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OM nucleic - nucleic search, using sw model

Run on: October 30, 2004, 05:38:57 : Search time 1793 Seconds
(without alignments)
7841.542 Million cell updates/sec

Title: US-09-787-677A-7

Perfect score: 2742

Sequence: 1 agaaagcagccgcgcagcagaga.....ggcgcataatcgtcgtacg 2742

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/prodata/1/pubpna/US09_PCT_NEW_PUB.seq:*
- 3: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
- 4: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:*
- 5: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
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- 12: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
- 13: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
- 14: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
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- 19: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
- 20: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2715	99.0	2863	15	US-10-301-822-23
2	1482.8	54.1	1918	9	US-09-988-598-2589
3	1472	53.7	1475	10	US-09-888-257A-1
4	1472	53.7	1475	10	US-09-946-374-133
5	1472	53.7	1475	13	US-10-006-867-79
6	1472	53.7	1475	13	US-10-063-547-79
7	1472	53.7	1475	13	US-10-063-551-79
8	1472	53.7	1475	14	US-10-028-072-491
9	1472	53.7	1475	14	US-10-063-616-79
10	1472	53.7	1475	14	US-10-140-808-491
11	1472	53.7	1475	14	US-10-063-569-79
12	1472	53.7	1475	14	US-10-063-513-79

13	1472	53.7	1475	14	US-10-063-515-79	Sequence 79, Appl
14	1472	53.7	1475	14	US-10-063-512-79	Sequence 79, Appl
15	1472	53.7	1475	14	US-10-121-049-491	Sequence 491, Appl
16	1472	53.7	1475	14	US-10-123-904-491	Sequence 491, Appl
17	1472	53.7	1475	14	US-10-140-470-491	Sequence 491, Appl
18	1472	53.7	1475	14	US-10-063-502-79	Sequence 79, Appl
19	1472	53.7	1475	14	US-10-175-746-491	Sequence 491, Appl
20	1472	53.7	1475	14	US-10-176-918-491	Sequence 491, Appl
21	1472	53.7	1475	14	US-10-176-921-491	Sequence 491, Appl
22	1472	53.7	1475	14	US-10-063-548-79	Sequence 79, Appl
23	1472	53.7	1475	14	US-10-137-865-491	Sequence 491, Appl
24	1472	53.7	1475	14	US-10-140-474-491	Sequence 491, Appl
25	1472	53.7	1475	14	US-10-142-431-491	Sequence 491, Appl
26	1472	53.7	1475	14	US-10-143-114-491	Sequence 491, Appl
27	1472	53.7	1475	14	US-10-140-002-491	Sequence 491, Appl
28	1472	53.7	1475	14	US-10-063-554-79	Sequence 79, Appl
29	1472	53.7	1475	14	US-10-006-856A-133	Sequence 133, Appl
30	1472	53.7	1475	14	US-10-142-419-491	Sequence 491, Appl
31	1472	53.7	1475	14	US-10-063-553-79	Sequence 79, Appl
32	1472	53.7	1475	14	US-10-063-518-79	Sequence 79, Appl
33	1472	53.7	1475	14	US-10-123-262-491	Sequence 491, Appl
34	1472	53.7	1475	14	US-10-142-423-491	Sequence 491, Appl
35	1472	53.7	1475	14	US-10-063-598-79	Sequence 79, Appl
36	1472	53.7	1475	14	US-10-227-693-79	Sequence 79, Appl
37	1472	53.7	1475	14	US-10-006-818A-133	Sequence 133, Appl
38	1472	53.7	1475	14	US-10-121-050-491	Sequence 491, Appl
39	1472	53.7	1475	14	US-10-141-755-491	Sequence 491, Appl
40	1472	53.7	1475	14	US-10-143-032-491	Sequence 79, Appl
41	1472	53.7	1475	14	US-10-063-563-79	Sequence 79, Appl
42	1472	53.7	1475	14	US-10-006-485A-133	Sequence 133, Appl
43	1472	53.7	1475	14	US-10-013-907A-133	Sequence 133, Appl
44	1472	53.7	1475	14	US-10-015-499A-133	Sequence 79, Appl
45	1472	53.7	1475	14	US-10-063-555-79	Sequence 79, Appl

ALIGNMENTS

RESULT 1

US-10-301-822-23

Sequence 23, Application US/10301822

Publication No. US20030148410A1

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: Berger, Allison

APPLICANT: Guillemette, Tracy L.

APPLICANT: Kamakazi, Shubhangt

APPLICANT: Schlegel, Robert

APPLICANT: Monahan, John E.

APPLICANT: Thibodeau, Stephen N.

APPLICANT: Burgart, Lawrence J.

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND

TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

FILE REFERENCE: MEMO1-0292RNM

CURRENT APPLICATION NUMBER: US/10/301,822

CURRENT FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US 60/339,971

PRIOR FILING DATE: 2001-12-10

PRIOR APPLICATION NUMBER: US 60/361,978

PRIOR FILING DATE: 2002-03-05

PRIOR APPLICATION NUMBER: US 60/381,988

PRIOR FILING DATE: 2002-05-20

NUMBER OF SEQ ID NOS: 228

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 23

LENGTH: 2863

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (231)...(923)

US-10-301-822-23

Query Match 99.0%; Score 2715; DB 15; Length 2863;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2729; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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QY 61 GCTTACACCTGAAACAAAGGAGAGCTCCGTAAGAGGCTTCTAAGAGGTGTCAT 120
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QY 121 GGCCTCTCTTGGCCTCCAACTTGTGGCTTACATCTAGAGGCTTCTTGGGCTAC 180
DB 233 GGCCTCTCTTGGCCTCCAACTTGTGGCTTACATCTAGAGGCTTCTTGGGCTAC 292
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DB 413 CACCCAGTGTGACATCTATAGCACCCTTCTGGGCTGCTGCTGACATCCAGGCTGCCA 472
QY 361 GGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 473 GGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 532
QY 421 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
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QY 541 TGGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 600
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QY 601 AGAGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 660
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QY 781 CAATTCCTACAGCTGACAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 893 CAATTCCTACAGCTGACAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 952
QY 841 TGGGCTCTGTAAGAAAGTGTGTAAGAAAGTGTGTAAGAAAGTGTGTAAGAAAGTGTGTA 900
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QY 1381 CTGAATTAACCACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1440
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Db 2813 GTAAACCTTCTGAGTGGTGGGAGGAGCAGTATCTTCTGATCCTTCTGATCCTTCTGATCCT 2847

RESULT 2
US-09-998-598-2589
Sequence 2589, Application US/0998598
Patent No. US20020150922A1
GENERAL INFORMATION:
APPLICANT: Stolk, John A.
APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.561
CURRENT APPLICATION NUMBER: US/09/998,598
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 2589
LENGTH: 1918
TYPE: DNA
ORGANISM: Homo sapiens
US-09-998-598-2589

Query Match 54.1%; Score 1482.8; DB 9; Length 1918;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1487; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db 402 AGAAGTCAAGCTGACAGAGAGACTCTGAATGAGGATTAAGAGTGTTCAGAGAGAGAG 461

Qy 61 GTTACAGCCTGAAGACAGAGGAGCAGTCCCTGAAGAGCTTCTTACTGAGAGTCTGCAAT 120
Db 462 GTTACAGCCTGAAGACAGAGGAGCAGTCCCTGAAGAGCTTCTTACTGAGAGTCTGCAAT 521
Qy 121 GGCCTCTCTTGGCTCCCACTTGGGCTGATCTTAAAGCTTCTGAGGCTTTTGGGAC 180
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Qy 181 ACTGTTGCAATGCTGTCTCCCGAGTGGAAAAACAATTTCTTAATGTGGTGGCCAGCAATTT 240
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Qy 241 GACAGAGTGGCTTCTCCCAAGGAGGCTCTGATGATGATGATGATGATGATGATGATGATGAT 300
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Qy 301 CACCAAGTGTGACATCTATGACACCTTCTGAGGCTGTGCGGCTGACATCCAGGCTGCCA 360
Db 702 CACCAAGTGTGACATCTATGACACCTTCTGAGGCTGTGCGGCTGACATCCAGGCTGCCA 761
Qy 361 GGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 762 GGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 821
Qy 421 CATGAGATGACAGTCTTCTGAGGAGATCCGAGCAGCAAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 822 CATGAGATGACAGTCTTCTGAGGAGATCCGAGCAGCAAGAGAGAGAGAGAGAGAGAGAGAG 881
Qy 481 TGAAGTCTTTTCTATCTTGAAGGCTCTGAGGATTCATCTGTTGCTGGAATCTTCA 540
Db 882 TGAAGTCTTTTCTATCTTGAAGGCTCTGAGGATTCATCTGTTGCTGGAATCTTCA 941
Qy 541 TGGGATCTTACGGGACTTCTTACTACCACTGTGTGCTGAGAGAGAGAGAGAGAGAGAGAG 600
Db 942 TGGGATCTTACGGGACTTCTTACTACCACTGTGTGCTGAGAGAGAGAGAGAGAGAGAGAG 1001
Qy 601 AGAGGCTCTTACTGAGGAGATTAATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 1002 AGAGGCTCTTACTGAGGAGATTAATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1061
Qy 661 CTGCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
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Qy 721 ACTCTTGGCAGAGAGAGCTCTCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
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Qy 781 CAATTCCTACAGCTGACAGGAGTATGTGAAGAACAGAGGAGCAGAGCTGAGGAGGAGTGGC 840
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Db 1242 TGGGCTGTGAAAAACAGTGAAGAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1301
Qy 901 GGAATCTGTGAGAGAGTGTGCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 960
Db 1302 GGAATCTGTGAGAGAGTGTGCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1361
Qy 961 GCAAGAAATGGGAGGCTGATGTAAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1020
Db 1362 GCAAGAAATGGGAGGCTGATGTAAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1421
Qy 1021 CAGCCTTTCTGTTTCTCTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
Db 1422 CAGCCTTTCTGTTTCTCTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1481
Qy 1081 GAAACCCATTTCTTAAAGCAGAGAGTCAAGAGATCTTGTGCTTGTGCTTGTGCTTGTGCTGCT 1140
Db 1482 GAAACCCATTTCTTAAAGCAGAGAGTCAAGAGATCTTGTGCTTGTGCTTGTGCTTGTGCTGCT 1541

QY 1141 ACTTCATCCCAACCACTAATCATCCCACTGACTGACCTCTGTGATCAAAAGACC 1200
 Db 1542 ACTTCATCCCAACCACTAATCATCCCACTGACTGACCTCTGTGATCAAAAGACC 1601
 QY 1201 TCTCTCTGAGTGGTGGCTCTTAAGCTCAATGCTGGGAGATGGGAAGAGAGAGTGGC 1260
 Db 1602 TCTCTCTGAGTGGTGGCTCTTAAGCTCAATGCTGGGAGATGGGAAGAGAGAGTGGC 1661
 QY 1261 TTTTGTGGGATGCTCTTAACCTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCC 1320
 Db 1662 TTTTGTGGGATGCTCTTAACCTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCC 1721
 QY 1321 TGAACCTCATCCCACTCTTTTATGATCTCCACAGTGTCCAGCTAATTTGTGATGAA 1380
 Db 1722 TGAACCTCATCCCACTCTTTTATGATCTCCACAGTGTCCAGCTAATTTGTGATGAA 1781
 QY 1381 CTGAAATTAACCACTCTTACGATTCAGGGAAGAGAGAGATGAGAGATGGGAGGA 1440
 Db 1782 CTGAAATTAACCACTCTTACGATTCAGGGAAGAGAGAGATGAGAGATGGGAGGA 1841
 QY 1441 CAGGAAGCAGCCTGAGCACTTTTAAAAATTAATAATGAAAAAACCGAGAA 1494
 Db 1842 CAGGAAGCAGCCTGAGCACTTTTAAAAATTAATAATGAAAAAACCGAGAA 1895

RESULT 3
 US-09-888-257A-1
 / Sequence 1, Application US/09888257A
 / Publication No. US20030060612A1
 / GENERAL INFORMATION:
 / APPLICANT: Goddard, Audrey
 / APPLICANT: Godowski, Paul J.
 / APPLICANT: Gurney, Austin L.
 / APPLICANT: Hillan, Kenneth J.
 / APPLICANT: Polakis, Paul
 / APPLICANT: Smith, Victoria
 / APPLICANT: Wood, William I.
 / APPLICANT: Wu, Thomas D.
 / APPLICANT: Zhang, Zhen
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
 / TITLE OF INVENTION: TREATMENT OF TUMOR
 / FILE REFERENCE: P5002R1
 / CURRENT APPLICATION NUMBER: US/09/888,257A
 / CURRENT FILING DATE: 2002-04-30
 / PRIOR APPLICATION NUMBER: US 60/063,540
 / PRIOR FILING DATE: 1997-10-28
 / PRIOR APPLICATION NUMBER: US 60/089,653
 / PRIOR FILING DATE: 1998-05-17
 / PRIOR APPLICATION NUMBER: US 60/099,792
 / PRIOR FILING DATE: 1998-09-10
 / PRIOR APPLICATION NUMBER: US 60/103,678
 / PRIOR FILING DATE: 1998-10-08
 / PRIOR APPLICATION NUMBER: US 60/235,451
 / PRIOR FILING DATE: 2000-09-26
 / PRIOR APPLICATION NUMBER: PCT/US99/12252
 / PRIOR FILING DATE: 1999-06-02
 / PRIOR APPLICATION NUMBER: PCT/US99/20111
 / PRIOR FILING DATE: 1999-09-01
 / PRIOR APPLICATION NUMBER: PCT/US00/04342
 / PRIOR FILING DATE: 2000-02-18
 / PRIOR APPLICATION NUMBER: PCT/US00/05841
 / PRIOR FILING DATE: 2000-03-02
 / PRIOR APPLICATION NUMBER: PCT/US00/08439
 / PRIOR FILING DATE: 2000-03-30
 / PRIOR APPLICATION NUMBER: PCT/US00/23328
 / PRIOR FILING DATE: 2000-08-24
 / PRIOR APPLICATION NUMBER: PCT/US00/32678
 / PRIOR FILING DATE: 2000-12-01
 / PRIOR APPLICATION NUMBER: PCT/US01/06520
 / PRIOR FILING DATE: 2001-02-28
 / PRIOR APPLICATION NUMBER: PCT/US01/06666
 / PRIOR FILING DATE: 2001-03-01
 / NUMBER OF SEQ ID NOS: 10

/ SEQ ID NO 1
 / LENGTH: 1475
 / TYPE: DNA
 / ORGANISM: Homo Sapien
 US-09-888-257A-1

Query Match 53.7%; Score 1472; DB 10; Length 1475;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 GCTTCAGCGCTGAAG 120
 Db 64 GCTTCAGCGCTGAAG 123
 QY 121 GGCCTCTCTTGGCTCCAACTTGTGGGCTACATCTAGAGCTTCTGGGCTTTTGGGAC 180
 Db 124 GGCCTCTCTTGGCTCCAACTTGTGGGCTACATCTAGAGCTTCTGGGCTTTTGGGAC 183
 QY 181 ACTGTGGCCATGCTGTCTCCAGCTGAGAAACAGATTCTTATGTGGTCCAGCATGT 240
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 Db 304 CACCCAGTGTGACATCTATGACACCTTGTGGGCTTGGCCGCTGACATCCAGGCTGCCA 363
 QY 361 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 Db 364 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 423
 QY 421 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
 Db 424 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 483
 QY 481 TGAAGTCTTTTATCTCTTGAAGGCTCTGAGATTCATCTTGTGCTGGAATCTTCA 540
 Db 484 TGAAGTCTTTTATCTCTTGAAGGCTCTGAGATTCATCTTGTGCTGGAATCTTCA 543
 QY 541 TGGGATCTTACAGGAGCTTCTACACACAGGCTGAGAGAGAGAGAGAGAGAGAGAG 600
 Db 544 TGGGATCTTACAGGAGCTTCTACACACAGGCTGAGAGAGAGAGAGAGAGAGAGAG 603
 QY 601 AGAGGCTCTTACTTGGGATTAATTTCTTCCCTGTCTCCCTGATGATGATATCTCT 660
 Db 604 AGAGGCTCTTACTTGGGATTAATTTCTTCCCTGTCTCCCTGATGATGATATCTCT 663
 QY 661 CTGCTTTTCTGCTCATCTCCAGAGAAATGCTTCAACTACTAGAGAGAGAGAGAGAG 720
 Db 664 CTGCTTTTCTGCTCATCTCCAGAGAAATGCTTCAACTACTAGAGAGAGAGAGAGAG 723
 QY 721 ACCTTGGCACAAGAGCTCTCAAGGCTGGTCAACCTCCCAAGTCAAGAGTGA 780
 Db 724 ACCTTGGCACAAGAGCTCTCAAGGCTGGTCAACCTCCCAAGTCAAGAGTGA 783
 QY 781 CAATTCCTACAGCTGACAGGATATGTAAGAACCAAGAGGAGAGAGAGAGAGAGAGAG 840
 Db 784 CAATTCCTACAGCTGACAGGATATGTAAGAACCAAGAGGAGAGAGAGAGAGAGAGAG 843
 QY 841 TGGGCTGTGAAAAACAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
 Db 844 TGGGCTGTGAAAAACAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 903
 QY 901 GATTCGTGCAAGAGTGTGCTGAGAGATGATGATGATGATGATGATGATGATGATGATG 960
 Db 904 GATTCGTGCAAGAGTGTGCTGAGAGATGATGATGATGATGATGATGATGATGATGATG 963

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Query Match 53.7%; Score 1472; DB 10; Length 1475;
 Best Local Similarity 100.0%; Pred No. 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAGCTTGCGAGAGAGACTGGAATGAGGATTAGAGTTCAGGAGCAAG 60
 DB 4 AGAAGTCAGCTTGCGAGAGAGACTGGAATGAGGATTAGAGTTCAGGAGCAAG 63
 QY 61 GCTTCAGCTGGAAGCAAGGAGAGATCCCTGGAAGCCTTCTAATGAGAGTTCCTCAT 120
 DB 64 GCTTCAGCTGGAAGCAAGGAGAGATCCCTGGAAGCCTTCTAATGAGAGTTCCTCAT 123
 QY 121 GGCCTCTTGAGCTGCAACTTGAGGCTTACATCCTAGGCTTCTGAGGCTTTGAGGAC 180
 DB 124 GGCCTCTTGAGCTGCAACTTGAGGCTTACATCCTAGGCTTCTGAGGCTTTGAGGAC 183
 QY 181 ACTGTTGCGATGCTCTCCAGCTGGAACAACTTATGCTGCTGCGAGCATTT 240
 DB 184 ACTGTTGCGATGCTCTCCAGCTGGAACAACTTATGCTGCTGCGAGCATTT 243
 QY 241 GACAGCATGTTGCTTCTCCAGGAGCTCTGAGATGGAATGTCACACAGCAAGGCAAT 300
 DB 244 GACAGCATGTTGCTTCTCCAGGAGCTCTGAGATGGAATGTCACACAGCAAGGCAAT 303
 QY 301 CACCCAGTGAATCATATAGACACCTTCTGAGGCTGCGAGCTGATCATCAGGCTGCCA 360
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 QY 361 GGCATGATGATGATCATCATGATCATCTCTCCCTGAGGCTGATCATCTCTGATGAG 420
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 QY 421 CATGATGATGATCATCTCTGAGGATGATGATGATGATGATGATGATGATGATGATG 480
 DB 424 CATGATGATGATCATCTCTGAGGATGATGATGATGATGATGATGATGATGATGATG 483
 QY 481 TGAAGCTTTTATCATCTGAGGAGCTGAGGATCATCTCTGAGGATCATCTCTGAG 540
 DB 484 TGAAGCTTTTATCATCTGAGGAGCTGAGGATCATCTCTGAGGATCATCTCTGAG 543
 QY 541 TGGGATCTTACGGGATCTTACTACACATGATGATGATGATGATGATGATGATGATG 600
 DB 544 TGGGATCTTACGGGATCTTACTACACATGATGATGATGATGATGATGATGATGATG 603
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 DB 604 AGAGGCTTTTACTTGGGATTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 663
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QY 721 ACCTTGGCAGAGAGCTCTCAAGGCGCTGCTCACTCCCAAGTCAAGAGT 780
DB 724 ACCTTGGCAGAGAGCTCTCAAGGCGCTGCTCACTCCCAAGTCAAGAGT 783
QY 781 CAATTCCTACAGCTGACAGGCTATGTGTAAAGAACAGAGGCGCAGAGTGGGCGGTGC 840
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QY 841 TGGGCTGTGAAAAACGTGACAGCAGCAGGCGGCGCAGAGTGAAGGACATCACT 900
DB 844 TGGGCTGTGAAAAACGTGACAGCAGCAGGCGGCGCAGAGTGAAGGACATCACT 903
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* RESULT 5

US-10-006-867-79
; Sequence 79, Application US/10006867
; Publication No. US20020119130A1
; GENERAL INFORMATION:
; APPLICANT: Eateon, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/006, 867
; CURRENT FILING DATE: 2001-12-06

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Query Match 53.7%; Score 1472; DB 13; Length 1475;
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QY 1 AGAAGTCAGCTGGCAGAGAGACTGGAATAGAGGATTAGAGTTCAGAGAGCAAA 60
 DB 4 AGAAGTCAGCTGGCAGAGAGACTGGAATAGAGGATTAGAGTTCAGAGAGCAAA 63
 QY 61 GCTTCAGCTGGAAG 120
 DB 64 GCTTCAGCTGGAAG 123
 QY 121 GGCCTCTCTTGGCTTCAACTTGTGGGCTTACCTAGGCTTTTGGGCAAC 180
 DB 124 GGCCTCTCTTGGCTTCAACTTGTGGGCTTACCTAGGCTTTTGGGCAAC 183
 QY 181 ACTGTTGCTATGCTCTCCAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAG 240
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 DB 244 GACAGAGATGGCTTCTCAAGGAGCTTGAATGAGATGCAACAGAGAGAGAT 303
 QY 301 CACCAGATGATCATATAGCAACCTTGTGGGCTTCCCGCTGATCATCAGGCTGCCA 360
 DB 304 CACCAGATGATCATATAGCAACCTTGTGGGCTTCCCGCTGATCATCAGGCTGCCA 363
 QY 361 GGCATGATGATGATCATCATGAGCAATCTCTCCGCTGATCATCTCTGTGGTGG 420
 DB 364 GGCATGATGATGATCATCATGAGCAATCTCTCCGCTGATCATCTCTGTGGTGG 423
 QY 421 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 DB 424 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 483

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 1444 CAGAGAGCAGCTGGGAGATTTTAAAAAATA 1475

RESULT 6
 us-10-063-547-79
 ; Sequence 79, Application US/10063547

Publication No. US20020182638A1
 GENERAL INFORMATION:
 APPLICANT: Eaton, Dan L.
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gerltsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3230R1C1
 CURRENT APPLICATION NUMBER: US/10/063,547
 CURRENT FILING DATE: 2002-05-02
 Prior Application removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 170
 SEQ ID NO 79
 LENGTH: 1475
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-063-547-79

Query Match 53.7%; Score 1472; DB 13; Length 1475;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 4 AGAAGTCAAGCTTGGCAGAGAGACTTGAATGAGGATTTAGAGTGTTCAGAGAGCAAGA 63
 61 GCTTCAAGCTTGAAG 120
 64 GCTTCAAGCTTGAAG 123
 121 GGCCTCTTGTGAGCTTCAACTTGTGGGCTTACATCTAGAGCTTGTGGGCTTTTGGGCAAC 180
 124 GGCCTCTTGTGAGCTTCAACTTGTGGGCTTACATCTAGAGCTTGTGGGCTTTTGGGCAAC 183
 181 ACTGTTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 184 ACTGTTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 243
 241 GAGAGAGTGGTGTCTTCCAAAGGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 244 GAGAGAGTGGTGTCTTCCAAAGGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 303
 301 CACCAAGTGAATCTATGACACCTTCTGAGGCTGAGGCTGAGATGATGATGATGATGATGATGAT 360
 304 CACCAAGTGAATCTATGACACCTTCTGAGGCTGAGGCTGAGATGATGATGATGATGATGATGAT 363
 361 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 364 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 423
 421 CATGAGATGACAGTCTTGTGCAAGAGATCCGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 424 CATGAGATGACAGTCTTGTGCAAGAGATCCGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 483
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 601 AGAGGCTTTTACTTGGGAGTATTTCTTCTGTTCTCTGTTGCTGAGATGATGATGATGATGAT 660
 604 AGAGGCTTTTACTTGGGAGTATTTCTTCTGTTCTCTGTTGCTGAGATGATGATGATGATGAT 663
 661 CTGCTTTTCTGCTGATCCAGAGAAATGCTCAACTAGATGATGATGATGATGATGATGATGATGAT 720

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Db 664 CTGCTTTCTGCTCATCCAGAAATCGCTCAACTACTACATGCCCAAGCCCA 723
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Db 724 ACCCTTGCCACAAGAGCTCTCAAGAGCCTGCTCAACTCCCAAGTCAAGAGT 783
Qy 781 CAATTCCTACAGCTGACAGGGATATGTGTGAAGAACAGAGGGCCAGAGCTGGGGGTGC 840
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Qy 841 TGGGTCTGTGAAGAAACAGTGAACGACCCCGAGGGCCAGAGTGAAGGACATCAACT 900
Db 844 TGGGTCTGTGAAGAAACAGTGAACGACCCCGAGGGCCAGAGTGAAGGACATCAACT 903
Qy 901 GGATCGGTGAGAAAGTGTGCTGAGGATAGACTGACTTTGGCCATTGGAATGAGCAAG 960
Db 904 GGATCGGTGAGAAAGTGTGCTGAGGATAGACTGACTTTGGCCATTGGAATGAGCAAG 963
Qy 961 GCAGAAATGGGGGCTAGTGTAAACAGATGACAGGTTGAATGCCAAGGATGCTGGCATTGC 1020
Db 964 GCAGAAATGGGGGCTAGTGTAAACAGATGACAGGTTGAATGCCAAGGATGCTGGCATTGC 1023
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Db 1024 GACCTTTCTGTTTCTCTCACTTGTGCTGCTCCCTGCTTAAGTCCCAACCTCAACTT 1083
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Db 1084 GAAACCCATTCCTCTTAAGCAGAGACTCAGAGATCCCTTGGCCCTGTGTTTACCTGGG 1143
Qy 1141 ACTTCATCCCAACCCCATATATCATATCCCACTGATGACCTCTGTGTAAAGAACCC 1200
Db 1144 ACTTCATCCCAACCCCATATATCATATCCCACTGATGACCTCTGTGTAAAGAACCC 1203
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Db 1204 TCTCTCTGCTGAGTGTGCTCTTAAGTCAATGCTGTGGGGATGGGAAGAAAGAGTGGC 1263
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Db 1324 TGGAACTTCATCCCACTCTTTTATGATCTCAAGTGTCAAGCTAATTTGTGATGAA 1383
Qy 1381 CTGAATTAAGAAACATCTAGGATATCCAGGGAAACAGAAACAGATGAGATGGAGGA 1440
Db 1384 CTGAATTAAGAAACATCTAGGATATCCAGGGAAACAGAAACAGATGAGATGGAGGA 1443
Qy 1441 CAGGAAGCAGCCTGGGACATTTAAAAAATA 1472
Db 1444 CAGGAAGCAGCCTGGGACATTTAAAAAATA 1475

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RESULT 7

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US-10-063-551-79
; Sequence 79, Application US/10063551
; Publication No. US20020183494A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1

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; CURRENT APPLICATION NUMBER: US/10/063,551
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 79
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-551-79

Query Match 53.7%; Score 1472; DB 13; Length 1475;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Gaps 0;
Matches 1472; Conservative 0; Indels 0; Gaps 0;

Qy 1 AGAAGTCAGCCTGAGAGAGACTGTGAATGAGAGATTAGAGTGTTCAGAGAGAGA 60
Db 4 AGAAGTCAGCCTGAGAGAGACTGTGAATGAGAGATTAGAGTGTTCAGAGAGAGA 63
Qy 61 GCTTCAGCCTGAAAGACAGAGGAGACAGTCCCTGAAGACGCTTCTACTGAGAGTCTGCAT 120
Db 64 GCTTCAGCCTGAAAGACAGAGGAGACAGTCCCTGAAGACGCTTCTACTGAGAGTCTGCAT 123
Qy 121 GGCCTCTTGGCTCCCACTGTGGGCTACATCTAGGCTTCTGGGGCTTTTGGGCAC 180
Db 124 GGCCTCTTGGCTCCCACTGTGGGCTACATCTAGGCTTCTGGGGCTTTTGGGCAC 183
Qy 181 ACTGTTGCCATGCTGCTCCAGCTGAAACAGATTCTTATGTGCTGCCAGATTGT 240
Db 184 ACTGTTGCCATGCTGCTCCAGCTGAAACAGATTCTTATGTGCTGCCAGATTGT 243
Qy 241 GACAGCAGTTGGCTTCTCCAGGGGCTCTGATGGAATGTGCCACACAGCACAGGCAT 300
Db 244 GACAGCAGTTGGCTTCTCCAGGGGCTCTGATGGAATGTGCCACACAGCACAGGCAT 303
Qy 301 CACCAAGTGAATCATATATGACACCTTGGGCTGCGCGCTGACATCAGGCTGCCA 360
Db 304 CACCAAGTGAATCATATATGACACCTTGGGCTGCGCGCTGACATCAGGCTGCCA 363
Qy 361 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 364 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 423
Qy 421 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Db 424 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 483
Qy 481 TGAAGTCTTTTATCTTGAAGGCTGCTGAGATCATTCCTGTTGCTGGAATCTTCA 540
Db 484 TGAAGTCTTTTATCTTGAAGGCTGCTGAGATCATTCCTGTTGCTGGAATCTTCA 543
Qy 541 TGGGATCTACAGGAGCTTCTACTCAACACTGTGTGCTGACAGCATGAAATTTGATGG 600
Db 544 TGGGATCTACAGGAGCTTCTACTCAACACTGTGTGCTGACAGCATGAAATTTGATGG 603
Qy 601 AGAGGCTCTTACTTGGGCAATTTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCT 660
Db 604 AGAGGCTCTTACTTGGGCAATTTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCT 663
Qy 661 CTGCTTTCTGCTCATCCAGAAATGAGTCCCACTACTAGAGTCCCTACCAAGCCCA 720
Db 664 CTGCTTTCTGCTCATCCAGAAATGAGTCCCACTACTAGAGTCCCTACCAAGCCCA 723
Qy 721 ACCCTTGCCACAAGAGCTCTCAAGAGCCTGCTCAACTCCCAAGTCAAGAGT 780
Db 724 ACCCTTGCCACAAGAGCTCTCAAGAGCCTGCTCAACTCCCAAGTCAAGAGT 783
Qy 781 CAATTCCTACAGCTGACAGGGATATGTGTGAAGAACAGAGGGCCAGAGCTGGGGGTGC 840
Db 784 CAATTCCTACAGCTGACAGGGATATGTGTGAAGAACAGAGGGCCAGAGCTGGGGGTGC 843
Qy 841 TGGGTCTGTGAAGAAACAGTGAACGACCCCGAGGGCCAGAGTGAAGGACATCAACT 900
Db 844 TGGGTCTGTGAAGAAACAGTGAACGACCCCGAGGGCCAGAGTGAAGGACATCAACT 903

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QY 901 GGATCGTGCAGAGGCTGTGAGGATGAGTGAAGCTTTGGCCATTGATGAGCAAG 960
DB 904 GGATCGTGCAGAGGCTGTGAGGATGAGTGAAGCTTTGGCCATTGATGAGCAAG 963
QY 961 GCAGAAATGGGGCTAGTGTATACAGATGAGGTTGATTTCCAGAGATGCTGCCATGC 1020
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QY 1021 CAGCCTTTCTGTTTCTTCTACCTTGTCTGCTCCCTGCTTGAATGCCCACTTCACTT 1080
DB 1024 CAGCCTTTCTGTTTCTTCTACCTTGTCTGCTCCCTGCTTGAATGCCCACTTCACTT 1083
QY 1081 GAAACCCATTCCTTAAAGCAGAGACTCAGAGATCCCTTGGCCCTGTTTACCTGGG 1140
DB 1084 GAAACCCATTCCTTAAAGCAGAGACTCAGAGATCCCTTGGCCCTGTTTACCTGGG 1143
QY 1141 ACTGCATCCCAACCCACTATCATATCCCACTGATGACCTCTGTGATCAAGACCC 1200
DB 1144 ACTGCATCCCAACCCACTATCATATCCCACTGATGACCTCTGTGATCAAGACCC 1203
QY 1201 TCTCTCTGCTGAGTGGCTCTTACCTCATTTGCTGGGATGGAGAGAGACAGTGGC 1260
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QY 1321 TGGAACTCCATCCCACTCTTGTATGACTCAAGTGTCCAGACTAATTTGTGATGAA 1380
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DB 1444 CAGGAAGGAGCTGGGAGCATTTAAAAATA 1475

RESULT 8
US-10-028-072-491
Sequence 491, Application US/10028072
Publication No. US2003004311A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028, 072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
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 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07

Query Match 53.7%; Score 1472; DB 14; Length 1475;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAGCTGGCAGAGAGACTGGAATGAGGATTTAGAGTGTTCAGAGGAGAA 60
 DB 4 AGAAGTCAGCTGGCAGAGAGACTGGAATGAGGATTTAGAGTGTTCAGAGGAGAA 63
 QY 61 GCTTCAGCTGGAAG 120
 DB 64 GCTTCAGCTGGAAG 123
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 QY 361 GGCATGATGTGACATCTGCAATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
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 DB 424 CATGAGATGACAGTCTTCTGCAAGAGATCCGAGCAAGAGAGAGAGAGAGAGAGAGAG 483
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 DB 544 TGGGATCTTACGAGGATTTACTCACCACTGCTGCTGCAAGAGAGAGAGAGAGAGAG 603
 QY 601 AGAGGCTCTTACTTGGGATATTTCTCCCTGTTTCCGATGATGAGGAGATCACTCT 660
 DB 604 AGAGGCTCTTACTTGGGATATTTCTCCCTGTTTCCGATGATGAGGAGATCACTCT 663

QY 661 CTGCTTTTCTGCTCATCCAGAGAAATGCTCCACTACTAGATGCTTACCAAGCCCA 720
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QY 721 ACCTTTTGCACAGAGAGCTTCCAGAGGCTTGTCAACTTCCCAAGTCAAGTGAAT 780
DB 724 ACCTTTTGCACAGAGAGCTTCCAGAGGCTTGTCAACTTCCCAAGTCAAGTGAAT 783
QY 781 CAATTTCTACAGCTGACAGGATATGTGTGAAGAACAGAGGCTGAGGCTGAGGCTGAG 840
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DB 844 TGGGCTGTGAAAAACAGTGAAGACAGACCCGAGAGGCTCAAGTGAAGGACACTACCACT 903
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DB 1024 CAGGCTTTCTGTTTCTCTCACTTGTGCTGCTCCCTGCTCAAGTCCCAAGCTTCACTT 1083
QY 1081 GAAACCCCATTTCCCTTAAGCAGAGACTCAAGAGATCCCTTTGCTGTTTACTGCTGAG 1140
DB 1084 GAAACCCCATTTCCCTTAAGCAGAGACTCAAGAGATCCCTTTGCTGTTTACTGCTGAG 1143
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DB 1144 ACTTCATCCCAAAACCACTATATCATCCCATGACTGACCTCTGTGATCAAGACCC 1203
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DB 1204 TCTCTGCTGAGTGGTGGCTTGAAGTCAATGCTGAGGAGATGGAGAGAGAGAGTGGC 1263
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DB 1324 TGGAACTCCATCCCATCTTGTATATGATCTCAGAGTCCAGACTAATTTGTGATGAA 1383
QY 1381 CTGAATTAATAACATCTCTAGGATTCAGAGGACAGAAAGAGATGACAGATGGAGGA 1440
DB 1384 CTGAATTAATAACATCTCTAGGATTCAGAGGACAGAAAGAGATGACAGATGGAGGA 1443
QY 1441 CAGGAAGCAGCTGAGCAATTTAAAAATA 1472
DB 1444 CAGGAAGCAGCTGAGCAATTTAAAAATA 1475

RESULT 9

US-10-063-616-79
; Sequence 79, Application US/10063616
; Publication No. US2003013855A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 79
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-616-79
Query Match 53.7%; Score 1472; DB 14; Length 1475;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGAAGTCAGCTTGGCAGAGAGACTTGAATATGAGGATTTAGAGTGTTCAGAGACAGA 60
DB 4 AGAAGTCAGCTTGGCAGAGAGACTTGAATATGAGGATTTAGAGTGTTCAGAGACAGA 63
QY 61 GCTTCAAGCTGAGAGACAGAGGAGACAGTCCCTGAAGACGCTTCTATGAGAGTCTGCACT 120
DB 64 GCTTCAAGCTGAGAGACAGAGGAGACAGTCCCTGAAGACGCTTCTATGAGAGTCTGCACT 123
QY 121 GGCCTCTCTTGGCTCCCACTTGTGGCTATCATCTAGGCTTCTGAGGCTTTTGGGAC 180
DB 124 GGCCTCTCTTGGCTCCCACTTGTGGCTATCATCTAGGCTTCTGAGGCTTTTGGGAC 183
QY 181 ACTGTTTGCATGCTGCTCCCAAGCTGAGAAACAGATTCTTATGTGCTGCTCAGCATTT 240
DB 184 ACTGTTTGCATGCTGCTCCCAAGCTGAGAAACAGATTCTTATGTGCTGCTCAGCATTT 243
QY 241 GACAGAGTGGCTTCTCCCAAGGCTCTGAGATGGAATGAGCAACAGACAGACAGGAT 300
DB 244 GACAGAGTGGCTTCTCCCAAGGCTCTGAGATGGAATGAGCAACAGACAGACAGGAT 303
QY 301 CACCAAGTGAATCTATAGCAACCTTCTGAGGCTGCTCCGCTGACATCCAGGCTGCCA 360
DB 304 CACCAAGTGAATCTATAGCAACCTTCTGAGGCTGCTCCGCTGACATCCAGGCTGCCA 363
QY 361 GGCATGATGTGATCATCTGATGCAATCTCTCTGCTGCTGATATCTCTGTGCTGGG 420
DB 364 GGCATGATGTGATCATCTGATGCAATCTCTCTGCTGCTGATATCTCTGTGCTGGG 423
QY 421 CATGAGATGCAAGTCTTCTGCAAGAAATCCGAGGCCAAGACAGATGAGGATGAGG 480
DB 424 CATGAGATGCAAGTCTTCTGCAAGAAATCCGAGGCCAAGACAGATGAGGATGAGG 483
QY 481 TGAAGTCTTTTCACTCTTGAAGGCTCTGAGATTCATCTGTGCTGGAATCTTCA 540
DB 484 TGAAGTCTTTTCACTCTTGAAGGCTCTGAGATTCATCTGTGCTGGAATCTTCA 543
QY 541 TGGGATCTTACCGGAGCTTCTACTACCACTGTGCTGACAGATGAAATTTGAGATTGG 600
DB 544 TGGGATCTTACCGGAGCTTCTACTACCACTGTGCTGACAGATGAAATTTGAGATTGG 603
QY 601 AGAGGCTCTTACTTGGGCAATTTTCTTCCCTGTTCTCCCTGATGCTGGAATCATCT 660
DB 604 AGAGGCTCTTACTTGGGCAATTTTCTTCCCTGTTCTCCCTGATGCTGGAATCATCT 663
QY 661 CTGCTTTTCTGCTCATCCAGAGAAATGCTCCACTACTAGATGCTTACCAAGCCCA 720
DB 664 CTGCTTTTCTGCTCATCCAGAGAAATGCTCCACTACTAGATGCTTACCAAGCCCA 723
QY 721 ACCTTTTGCACAGAGAGCTTCCAGAGGCTTGTCAACTTCCCAAGTCAAGTGAAT 780
DB 724 ACCTTTTGCACAGAGAGCTTCCAGAGGCTTGTCAACTTCCCAAGTCAAGTGAAT 783
QY 781 CAATTTCTACAGCTGACAGGATATGTGTGAAGAACAGAGGCTGAGGCTGAGGCTGAG 840
DB 784 CAATTTCTACAGCTGACAGGATATGTGTGAAGAACAGAGGCTGAGGCTGAGGCTGAG 843
QY 841 TGGGCTGTGAAAAACAGTGAAGACAGACCCGAGAGGCTCAAGTGAAGGACACTACCACT 900

```
DB 844 TGGGTCTGTAAAAAGTGAAGACAGACCCGAGGGGCAAGGAGGACATCAACACT 903
QY 901 GGATCGGTGAGAAAGTGTCTGTAGAGATAGACTTTGGCCATTGATGAGCAAG 960
DB 904 GGATCGGTGAGAAAGTGTCTGTAGAGATAGACTTTGGCCATTGATGAGCAAG 963
QY 961 GCAGAAATGGGGGCTAGTGTAAACAGATGACAGGTTGAATGCCAAGATGCGCCATGC 1020
DB 964 GCAGAAATGGGGGCTAGTGTAAACAGATGACAGGTTGAATGCCAAGATGCGCCATGC 1023
QY 1021 GACCTTTCTGTTTCTCTCACTTGTCTGCTCCCTGCGCTTAAGTCCCAACCTCACTT 1080
DB 1024 GACCTTTCTGTTTCTCTCACTTGTCTGCTCCCTGCGCTTAAGTCCCAACCTCACTT 1083
QY 1081 GAAACCCCATTCCTTTAAGCAGAGACTCAAGAGATCCCTTTGCTGTTTAACTGGG 1140
DB 1084 GAAACCCCATTCCTTTAAGCAGAGACTCAAGAGATCCCTTTGCTGTTTAACTGGG 1143
QY 1141 ACTGCATCCCAACCCCACTAATCAATCCCACTGATGACCTCTGTATCAAAAGACC 1200
DB 1144 ACTGCATCCCAACCCCACTAATCAATCCCACTGATGACCTCTGTATCAAAAGACC 1203
QY 1201 TCTCTCTGCTGAGTGTGCTCTTAAGTCAATGCTGGGGATGGAAAGAAAGATGCG 1260
DB 1204 TCTCTCTGCTGAGTGTGCTCTTAAGTCAATGCTGGGGATGGAAAGAAAGATGCG 1263
QY 1261 TTTTGTGGGCAATTGCTTAACCTACTCTCAAGCTTCCCTCAAAAGAACTGATGGCC 1320
DB 1264 TTTTGTGGGCAATTGCTTAACCTACTCTCAAGCTTCCCTCAAAAGAACTGATGGCC 1323
QY 1321 TGAACCTCATCCCACTCTTTTATGATCTCAAGTCTCAAGTCTAATTTGTGATGAA 1380
DB 1324 TGAACCTCATCCCACTCTTTTATGATCTCAAGTCTCAAGTCTAATTTGTGATGAA 1383
QY 1381 CTGAATTAACCATCTCTAGGATCCAGGAAACAGAAACAGGATGCAAGATGGAGGA 1440
DB 1384 CTGAATTAACCATCTCTAGGATCCAGGAAACAGAAACAGGATGCAAGATGGAGGA 1443
QY 1441 CAGGAAGCAGCTGGGACATTTAAAAATA 1472
DB 1444 CAGGAAGCAGCTGGGACATTTAAAAATA 1475

RESULT 10
US-10-140-808-491
; Sequence 491, Application US/10140808
; Publication No. US20030017563A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForay, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C182
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
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; SEQ ID NO 491
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-808-491

Query Match 53.7%; Score 1472; DB 14; Length 1475;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAGCTGTGGCAGAGACTCTGAATATGAGGATTAAGAGTGTTCAGAGGACAGA 60
DB 4 AGAAGTCAGCTGTGGCAGAGACTCTGAATATGAGGATTAAGAGTGTTCAGAGGACAGA 63
QY 61 GCTTCAGCTGAAAGACAGAGGACAGTCCCTGTAAGACGCTTCTAATGAGAGTCTGCCAT 120
DB 64 GCTTCAGCTGAAAGACAGAGGACAGTCCCTGTAAGACGCTTCTAATGAGAGTCTGCCAT 123
QY 121 GGCCTCTCTTGGCTCCAACTTGTGGCTACATCTAGAGCTTCTGAGGCTTTTGGGAC 180
DB 124 GGCCTCTCTTGGCTCCAACTTGTGGCTACATCTAGAGCTTCTGAGGCTTTTGGGAC 183
QY 181 ACTGTTGCCATGCTGCTCCAGCTGGAACCAAGTTCTATGTGCTGCCAGACTTGT 240
DB 184 ACTGTTGCCATGCTGCTCCAGCTGGAACCAAGTTCTATGTGCTGCCAGACTTGT 243
QY 241 GACAGCAGTTGGCTTCTCCAGAGGCTCTGATGAAATGTCACACACAGCAGGCAAT 300
DB 244 GACAGCAGTTGGCTTCTCCAGAGGCTCTGATGAAATGTCACACACAGCAGGCAAT 303
QY 301 CACCCAGTGTGAATCTATAGACCCCTTCTGGGCTGCGGCTGACATCCAGGCTGCCA 360
DB 304 CACCCAGTGTGAATCTATAGACCCCTTCTGGGCTGCGGCTGACATCCAGGCTGCCA 363
QY 361 GGCCTAGATGATGATCAATCCAGTCAATCTCTCTGAGCTGATTAATCTGTGGTGG 420
DB 364 GGCCTAGATGATGATCAATCCAGTCAATCTCTCTGAGCTGATTAATCTGTGGTGG 423
QY 421 CATGAGATGACAGTCTTCTCCAGGAATCCGAGCCAAAGACAGATGGCGGTAGCAGG 480
DB 424 CATGAGATGACAGTCTTCTCCAGGAATCCGAGCCAAAGACAGATGGCGGTAGCAGG 483
QY 481 TGAAGTCTTTTATCTTGTGAGGCTCTGAGATTCATTTCTGTTGCTGGAATCTTCA 540
DB 484 TGAAGTCTTTTATCTTGTGAGGCTCTGAGATTCATTTCTGTTGCTGGAATCTTCA 543
QY 541 TGGGATCTCAAGGACCTTCACTCAACAGTGGGCTGACAGAGATGAATTTGAGATTGG 600
DB 544 TGGGATCTCAAGGACCTTCACTCAACAGTGGGCTGACAGAGATGAATTTGAGATTGG 603
QY 601 AGAGGCTCTTTACTTGGGCAATTAATTTCTTCCCTGTTCTCCCTGATAGTGAATCACT 660
DB 604 AGAGGCTCTTTACTTGGGCAATTAATTTCTTCCCTGTTCTCCCTGATAGTGAATCACT 663
QY 661 CTGCTTTTCTGTCTATCCCAAGAAATGGCTTCAACTATACATGAGTCTTACCAACCCA 720
DB 664 CTGCTTTTCTGTCTATCCCAAGAAATGGCTTCAACTATACATGAGTCTTACCAACCCA 723
QY 721 ACCTTTGACCAAGAGGCTCTCAAGGCTGGTCAACTGCCAAGTCAAGAGTGAATT 780
DB 724 ACCTTTGACCAAGAGGCTCTCAAGGCTGGTCAACTGCCAAGTCAAGAGTGAATT 783
QY 781 CAATTCCTACAGCTGACAGGGATATGTGAAGAAACAGGGGACAGAGCTGGGGGTGCG 840
DB 784 CAATTCCTACAGCTGACAGGGATATGTGAAGAAACAGGGGACAGAGCTGGGGGTGCG 843
QY 841 TGGGTCTGAAAAAAGATGACAGACCCCGAGGGGCAAGGTGAGGACATACACT 900
DB 844 TGGGTCTGAAAAAAGATGACAGACCCCGAGGGGCAAGGTGAGGACATACACT 903
QY 901 GGATCGGTGAGAAAGTGTCTGTAGAGATAGACTTTGGCCATTGATGAGCAAG 960
DB 904 GGATCGGTGAGAAAGTGTCTGTAGAGATAGACTTTGGCCATTGATGAGCAAG 963
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QY 961 GCAGAAATGGGGGCTAGTGTAAAGCATGAGGTTGAATTGCCAGGATGCTGCCATGC 1020
DB 964 GCAGAAATGGGGGCTAGTGTAAAGCATGAGGTTGAATTGCCAGGATGCTGCCATGC 1023
QY 1021 CAGCCTTTCTGTTTCTCACTTGTCTGCCCTGCTTAACTTGTCCCAACCTCACTT 1080
DB 1024 CAGCCTTTCTGTTTCTCACTTGTCTGCCCTGCTTAACTTGTCCCAACCTCACTT 1083
QY 1081 GAAACCCCATTCCTTAAGCAGAGACTCAAGAGATCCCTTGGCTTGTGTTAACTGGG 1140
DB 1084 GAAACCCCATTCCTTAAGCAGAGACTCAAGAGATCCCTTGGCTTGTGTTAACTGGG 1143
QY 1141 ACTCCATCCCAACCACTAATCAATCCCACTGATGACCTCTGTATCAAGACCC 1200
DB 1144 ACTCCATCCCAACCACTAATCAATCCCACTGATGACCTCTGTATCAAGACCC 1203
QY 1201 TCTCTGTGCTGAGTGTGCTTGTAGCTCATTTGCTGGAGATGGAGAGAGAGAGTGGC 1260
DB 1204 TCTCTGTGCTGAGTGTGCTTGTAGCTCATTTGCTGGAGATGGAGAGAGAGAGTGGC 1263
QY 1261 TTTTGTGGGCTTGTCTTAACCTTCTCAAGCTTCCCTCAAGAACTGATTTGGCCC 1320
DB 1264 TTTTGTGGGCTTGTCTTAACCTTCTCAAGCTTCCCTCAAGAACTGATTTGGCCC 1323
QY 1321 TGGACCTCCATCCCACTCTTGTATGACTCCACAGTCCAGACTAATTTGTGATGAA 1380
DB 1324 TGGACCTCCATCCCACTCTTGTATGACTCCACAGTCCAGACTAATTTGTGATGAA 1383
QY 1381 CTGAATTAATAACCATCTTACGATATCCAGGAAACAGAAACAGAGATGAGAGGA 1440
DB 1384 CTGAATTAATAACCATCTTACGATATCCAGGAAACAGAAACAGAGATGAGAGGA 1443
QY 1441 CAGGAAAGCAGCTGGGACATTTAAAAATA 1472
DB 1444 CAGGAAAGCAGCTGGGACATTTAAAAATA 1475

RESULT 11
US-10-063-569-79
Sequence 79, Application US/10063569
Publication No. US2003018168A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Pillerhoff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT FILING DATE: 2002-05-02
CURRENT APPLICATION NUMBER: US/10/063,569
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 79
LENGTH: 1475
TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-569-79

Query Match 53.7%; Score 1472; DB 14; Length 1475;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAGCTGGCAGAGACTCTGAATGAGGATTTAGAGTGTTCAGAGCAGAGA 60
DB 4 AGAAGTCAGCTGGCAGAGACTCTGAATGAGGATTTAGAGTGTTCAGAGCAGAGA 63

QY 61 GCTTCAGCTGAAAGACAGAGGACAGTCCCTGAAAGACGCTTCTAATGAGAGTCTGCCAT 120
DB 64 GCTTCAGCTGAAAGACAGAGGACAGTCCCTGAAAGACGCTTCTAATGAGAGTCTGCCAT 123
QY 121 GGCCTCTTGTGGCTTCAACTTGTGGCTTCACTTGAAGCTTCTGGGGCTTTTGGGCAC 180
DB 124 GGCCTCTTGTGGCTTCAACTTGTGGCTTCACTTGAAGCTTCTGGGGCTTTTGGGCAC 183
QY 181 ACTGTTGACATGCTGCTGCCAGCTGAAACAAAGTCTTATGTGGTGGCCAGACTTGT 240
DB 184 ACTGTTGACATGCTGCTGCCAGCTGAAACAAAGTCTTATGTGGTGGCCAGACTTGT 243
QY 241 GACAGAGTGTGGCTTCTCAAGGAGCTCTGATGAAATGTGCCACACAGCAGAGCAT 300
DB 244 GACAGAGTGTGGCTTCTCAAGGAGCTCTGATGAAATGTGCCACACAGCAGAGCAT 303
QY 301 CACCCAGTGTGACATCTAATGACACCTTGTGGCTTGGCTGACATCCAGCTGCCA 360
DB 304 CACCCAGTGTGACATCTAATGACACCTTGTGGCTTGGCTGACATCCAGCTGCCA 363
QY 361 GGCATGATGATGACATCCAGTGCATCTCCCTGGGCTGATTAATCTGTGGTGGG 420
DB 364 GGCATGATGATGACATCCAGTGCATCTCCCTGGGCTGATTAATCTGTGGTGGG 423
QY 421 CATGATGACAGCTCTTCTGCAAGAAATCCAGGCCAAGACAGATGAGCGTGAAGCAGG 480
DB 424 CATGATGACAGCTCTTCTGCAAGAAATCCAGGCCAAGACAGATGAGCGTGAAGCAGG 483
QY 481 TGAAGTCTTTTTCATCTTGAAGGCTCTGGGATTCATCTGTGCTGGAATCTTCA 540
DB 484 TGAAGTCTTTTTCATCTTGAAGGCTCTGGGATTCATCTGTGCTGGAATCTTCA 543
QY 541 TGGGATTCATAGGAGCTTCTTCACTCAACATGAGGCTGACAGATGAAATTTGAGATTGG 600
DB 544 TGGGATTCATAGGAGCTTCTTCACTCAACATGAGGCTGACAGATGAAATTTGAGATTGG 603
QY 601 AGAGGCTCTTAACTTGTGGGCAATTTTCTTCCCTGTCTCCCTGATAGCTGGAATCATCT 660
DB 604 AGAGGCTCTTAACTTGTGGGCAATTTTCTTCCCTGTCTCCCTGATAGCTGGAATCATCT 663
QY 661 CTGCTTTTCTGCTCATCCAGAGAAATGCTTCAACTTCAATGATGCTTCAAGGCCA 720
DB 664 CTGCTTTTCTGCTCATCCAGAGAAATGCTTCAACTTCAATGATGCTTCAAGGCCA 723
QY 721 ACCTTTTGGCAGAGAGCTTCCAGGCTGCTTCAACTTCCCAAGTCAAGAGTGAAT 780
DB 724 ACCTTTTGGCAGAGAGCTTCCAGGCTGCTTCAACTTCCCAAGTCAAGAGTGAAT 783
QY 781 CAATTCCTAAGCTGACAGGATGATGTGAAGAAACAGAGGAGCCAGAGTGGGGGTGGC 840
DB 784 CAATTCCTAAGCTGACAGGATGATGTGAAGAAACAGAGGAGCCAGAGTGGGGGTGGC 843
QY 841 TGGGCTGTGAAAAACAGTGAAGACACCCGAGGAGCCACAGGTGAGGAGCACTTCACT 900
DB 844 TGGGCTGTGAAAAACAGTGAAGACACCCGAGGAGCCACAGGTGAGGAGCACTTCACT 903
QY 901 GGAATGCTGAGAGAGGCTGCTGAGATGATGATGATGATGATGATGATGATGATGATG 960
DB 904 GGAATGCTGAGAGAGGCTGCTGAGATGATGATGATGATGATGATGATGATGATGATG 963
QY 961 GCAGAAATGGGGGCTAGTGTAAAGCATGAGGTTGAATTGCCAGGATGCTGCCATGC 1020
DB 964 GCAGAAATGGGGGCTAGTGTAAAGCATGAGGTTGAATTGCCAGGATGCTGCCATGC 1023
QY 1021 CAGCCTTTCTGTTTCTCACTTGTCTGCCCTGCTTAACTTGTCCCAACCTCACTT 1080
DB 1024 CAGCCTTTCTGTTTCTCACTTGTCTGCCCTGCTTAACTTGTCCCAACCTCACTT 1083
QY 1081 GAAACCCCATTCCTTAAGCAGAGACTCAAGAGATCCCTTGGCTTGTGTTAACTGGG 1140
DB 1084 GAAACCCCATTCCTTAAGCAGAGACTCAAGAGATCCCTTGGCTTGTGTTAACTGGG 1143
QY 1141 ACTCCATCCCAACCACTAATCAATCCCACTGATGACCTCTGTATCAAGACCC 1200

DB 1144 ACTCCATCCCAAAACCAATCAATCAATCCACGACGACCTCTGTGTCAAAAGACC 1203
 QY 1201 TCTCTGCTGAGTGTGCTCTTAGCTCATTCGTGGGATGGAGAGACAGTGGC 1260
 DB 1204 TCTCTGCTGAGTGTGCTCTTAGCTCATTCGTGGGATGGAGAGACAGTGGC 1263
 QY 1261 TTTTGTGGGATGTCTTAACCTAATTCGAGCTTCCTCAAGAACTGATTGGCC 1320
 DB 1264 TTTTGTGGGATGTCTTAACCTAATTCGAGCTTCCTCAAGAACTGATTGGCC 1323
 QY 1321 TGGACCTCATCCACTCTGTATGATCCAGATGTCAGACTAATTTGACATGA 1380
 DB 1324 TGGACCTCATCCACTCTGTATGATCCAGATGTCAGACTAATTTGACATGA 1383
 QY 1381 CTGAAATTAATAACCATCTCAAGCTATCCAGAGAAACAGAAACAGATGAGAGA 1440
 DB 1384 CTGAAATTAATAACCATCTCAAGCTATCCAGAGAAACAGAAACAGATGAGAGA 1443
 QY 1441 CAGGAAGCAGCTGGGACATTTAAAAATA 1472
 DB 1444 CAGGAAGCAGCTGGGACATTTAAAAATA 1475

RESULT 12
 US-10-063-513-79
 / Sequence 79, Application US/10063513
 / Publication No. US20030018172A1
 / GENERAL INFORMATION:
 / APPLICANT: Eaton, Dan L.
 / APPLICANT: Rilveroff, Ellen
 / APPLICANT: Geriltsen, Mary E.
 / APPLICANT: Goddard, Audrey
 / APPLICANT: Godowski, Paul J.
 / APPLICANT: Grimaldi, Christopher J.
 / APPLICANT: Guiney, Austin L.
 / APPLICANT: Matanabe, Colin K.
 / APPLICANT: Wood, William I.
 / TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 / FILE OF INVENTION: ACIDS ENCODING THE SAME
 / FILE REFERENCE: P3230R1C1
 / CURRENT APPLICATION NUMBER: US/10/063,513
 / PRIOR FILING DATE: 2002-05-01
 / PRIOR APPLICATION removed - See File Wrapper or Palm
 / NUMBER OF SEQ ID NOS: 170
 / SEQ ID NO 79
 / LENGTH: 1475
 / TYPE: DNA
 / ORGANISM: Homo Sapien
 / US-10-063-513-79

Query Match 53.7%; Score 1472; DB 14; Length 1475;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAGCTGGCAGAGAGACTCTGAATGAGGATTAAGAGTGTTCAGAGCAAGA 60
 DB 4 AGAAGTCAGCTGGCAGAGAGACTCTGAATGAGGATTAAGAGTGTTCAGAGCAAGA 63
 QY 61 GCTTCAGCTGAGAGAGAGAGAGAGTCCCTGAAGCGCTTCACTGAGAGGTCTCCAT 120
 DB 64 GCTTCAGCTGAGAGAGAGAGAGAGTCCCTGAAGCGCTTCACTGAGAGGTCTCCAT 123
 QY 121 GGCCTCTCTTGGCTCAACTTGTGGGCTACATCTAGGCTTCTGGGGCTTTTGGGCA 180
 DB 124 GGCCTCTCTTGGCTCAACTTGTGGGCTACATCTAGGCTTCTGGGGCTTTTGGGCA 183
 QY 181 ACTGTTGCCATGCTCTCCAGCTGAAACAGATTTTATGTCGGTCCAGCATTTGT 240
 DB 184 ACTGTTGCCATGCTCTCCAGCTGAAACAGATTTTATGTCGGTCCAGCATTTGT 243
 QY 241 GACAGAGTTGGTTTCTCAAGGGCTCTGGATGGAATGTCACACACAGCAGAGCAT 300

DB 244 GACAGAGTTGGTTTCTCAAGGGCTCTGGATGGAATGTCACACACAGCAGAGCAT 303
 QY 301 CACCCAGTGTGACATCTATAGCAACCTTCTGGGCTGCGCGTGAATCCAGGCTGCCA 360
 DB 304 CACCCAGTGTGACATCTATAGCAACCTTCTGGGCTGCGCGTGAATCCAGGCTGCCA 363
 QY 361 GGCATGATGTGTGACATCCAGTGAATCTCTCCCTGGGCTGCAATATCTCTGGTGGG 420
 DB 364 GGCATGATGTGTGACATCCAGTGAATCTCTCCCTGGGCTGCAATATCTCTGGTGGG 423
 QY 421 CATGATGTCAGAGTCTTCTGCGCAGGAAATCCGAGCAAAAGACAGATGGCGGTAGAG 480
 DB 424 CATGATGTCAGAGTCTTCTGCGCAGGAAATCCGAGCAAAAGACAGATGGCGGTAGAG 483
 QY 481 TGGAGTCTTTTTCATCTTGAAGGCTCTGGGATTCATTTCTGTTGCTGGAATCTTCA 540
 DB 484 TGGAGTCTTTTTCATCTTGAAGGCTCTGGGATTCATTTCTGTTGCTGGAATCTTCA 543
 QY 541 TGGATCTTAAGGAGCTTCTACACCACTGCTGCTGACAGCATGAATTTGAGATTGG 600
 DB 544 TGGATCTTAAGGAGCTTCTACACCACTGCTGCTGACAGCATGAATTTGAGATTGG 603
 QY 601 AGAGGCTCTTACTTGGGATTAATTTCTTCCCTGTTCTCCCTGATGCTGAATCATCC 660
 DB 604 AGAGGCTCTTACTTGGGATTAATTTCTTCCCTGTTCTCCCTGATGCTGAATCATCC 663
 QY 661 CTGCTTTTCTGCTCATCCAGAGAAATGCTTCAACTACATGATGCTTCAACCAAGCCA 720
 DB 664 CTGCTTTTCTGCTCATCCAGAGAAATGCTTCAACTACATGATGCTTCAACCAAGCCA 723
 QY 721 ACCTTTTGGCACAAGAGCTTCTCAAGGCTGCTGCTCACTCCCAAGTCAAGATGAT 780
 DB 724 ACCTTTTGGCACAAGAGCTTCTCAAGGCTGCTGCTCACTCCCAAGTCAAGATGAT 783
 QY 781 CAATTCCTACAGGCTGACAGGATGATGTGAAGAACAGAGGCGCAGAGCTGGGGGTGGC 840
 DB 784 CAATTCCTACAGGCTGACAGGATGATGTGAAGAACAGAGGCGCAGAGCTGGGGGTGGC 843
 QY 841 TGGGCTGTGAATAACAGTGAACAGACCCCGAGGCGCACAGTGAAGGACATCACTACT 900
 DB 844 TGGGCTGTGAATAACAGTGAACAGACCCCGAGGCGCACAGTGAAGGACATCACTACT 903
 QY 901 GATCTGTGACAGAGTGTCTGAGAGATTAAGTACTTTGGCATTTGATTAAGCAAG 960
 DB 904 GATCTGTGACAGAGTGTCTGAGAGATTAAGTACTTTGGCATTTGATTAAGCAAG 963
 QY 961 GCAGAAATGAGGCTGATGAACAGATGAGATGAATTTGCCAAGATGCTGCGCATG 1020
 DB 964 GCAGAAATGAGGCTGATGAACAGATGAGATGAATTTGCCAAGATGCTGCGCATG 1023
 QY 1021 CAGCTTTTCTGTTTCTCACTTGTGCTGCTCCCTGAGTCCCAAGTCCCAAGCTCAACT 1080
 DB 1024 CAGCTTTTCTGTTTCTCACTTGTGCTGCTCCCTGAGTCCCAAGTCCCAAGCTCAACT 1083
 QY 1081 GAAACCCCATTCCTTAAGCAGAGATCAGAGATTCCTTTGCTCTGTGTTTAACTGGG 1140
 DB 1084 GAAACCCCATTCCTTAAGCAGAGATCAGAGATTCCTTTGCTCTGTGTTTAACTGGG 1143
 QY 1141 ACTCATCCCAAAACCACTAATCAATCACTCACTGATGATGATGATGATGATGATGAT 1200
 DB 1144 ACTCATCCCAAAACCACTAATCAATCACTCACTGATGATGATGATGATGATGATGAT 1203
 QY 1201 TCTCTGCTGAGTGTGCTCTTACTGATGCTTGGGATGGAGAGAGAGAGAGTGGC 1260
 DB 1204 TCTCTGCTGAGTGTGCTCTTACTGATGCTTGGGATGGAGAGAGAGAGAGTGGC 1263
 QY 1261 TTTTGTGGGATTTGCTTAACCTAATCTGCAAGCTTCCCTCAAGAACTGATTGGCC 1320
 DB 1264 TTTTGTGGGATTTGCTTAACCTAATCTGCAAGCTTCCCTCAAGAACTGATTGGCC 1323
 QY 1321 TGGAACTTCATCCCACTTGTATGATCCACAGTGTCCAGATTAATTTTGGATGAA 1380
 DB 1324 TGGAACTTCATCCCACTTGTATGATCCACAGTGTCCAGATTAATTTTGGATGAA 1383

QY 1381 CTGAATTAACCATCTCTAGGTATCCAGGGAACAGAAAGAGAGATGGGAGGA 1440
DB 1384 CTAAATTAACCATCTCTAGGTATCCAGGGAACAGAAAGAGAGATGGGAGGA 1443
QY 1441 CAGGAAGCAGCTGGGACATTTAAAAATA 1472
DB 1444 CAGGAAGCAGCTGGGACATTTAAAAATA 1475

RESULT 13
US-10-063-515-79
; Sequence 79, Application US/10063515
; Publication No. US20030018173A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P9320R1C1
; CURRENT APPLICATION NUMBER: US/10/063,515
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 79
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-515-79

Query Match 53.7%; Score 1472; DB 14; Length 1475;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAGCCTGGCAGAGAGACTCTGAATAGAGGATTAAGGATTTCAAGAGAGAGAGA 60
DB 4 AGAAGTCAGCCTGGCAGAGAGACTCTGAATAGAGGATTAAGGATTTCAAGAGAGAGAGA 63
QY 61 GCTTCAAGCTGGAAG 120
DB 64 GCTTCAAGCTGGAAG 123
QY 121 GGCCTCTCTGGGCTCCAACTTGGGCTACATCTAGAGGCTTCTGGGGCTTTTGGGAC 180
DB 124 GGCCTCTCTGGGCTCCAACTTGGGCTACATCTAGAGGCTTCTGGGGCTTTTGGGAC 183
QY 181 ACTGATGCAATGCTGCTCCAG 240
DB 184 ACTGATGCAATGCTGCTCCAG 243
QY 241 GACAGCAGTGGCTTCTCCAG 300
DB 244 GACAGCAGTGGCTTCTCCAG 303
QY 301 CACCAAGTGAATCTATAG 360
DB 304 CACCAAGTGAATCTATAG 363
QY 361 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
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QY 481 TGGAGTCTTTTTCATCTCTGAG 540
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QY 841 TGGGCTCTGTAAG 900
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DB 1024 CAGGCTTTCTGTTTCTCTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1083
QY 1081 GAAACCCCATTTCTTTAAGCAG 1140
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QY 1141 ACTTCATCCCAAG 1200
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QY 1321 TGGAACTTCAATCCCAAG 1380
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QY 1381 CTGAATTAACCATCTCTAGGTATCCAGGGAACAGAAAGAGAGATGGGAGGA 1440
DB 1384 CTGAATTAACCATCTCTAGGTATCCAGGGAACAGAAAGAGAGATGGGAGGA 1443
QY 1441 CAGGAAGCAGCTGGGACATTTAAAAATA 1472
DB 1444 CAGGAAGCAGCTGGGACATTTAAAAATA 1475

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US-10-063-512-79
; Sequence 79, Application US/10063512
; Publication No. US20030018183A1

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; GENERAL INFORMATION:
; APPLICANT: Balon, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P9230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; CURRENT FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 79
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-063-512-79

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Query Match      53.7%; Score 1472; DB 14; Length 1475;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 421 CATGATGATCAGATGCTTCTGCGAGGATCCGAGCCAAAGACAGAGTGGCGGTAGCAG 480
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DB 544 TGGGATCTCAGGAGACTTCTACTACCACTGTGTGCTGAGAGATGAAATTTGAGATTGG 603
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QY 781 CAATTCCTACAGCTGACAGGATATGTGTGAGAACACAGGGGCTCAAGTCTGGGGTGGC 840
DB 784 CAATTCCTACAGCTGACAGGATATGTGTGAGAACACAGGGGCTCAAGTCTGGGGTGGC 843
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DB 844 TGGGCTGTGAAACAGTGTGACAGACCCCGAGGGCCACAGGTGAGGACATCACT 903
QY 901 GGATCTGTGACAGAGTGTGTGAGATAGCTGATCTTGGCATTGTGATGAGCAAG 960
DB 904 GGATCTGTGACAGAGTGTGTGAGATAGCTGATCTTGGCATTGTGATGAGCAAG 963
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RESULT 15
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; Sequence 491, Application US/10121049
; Publication No. US2003002239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.

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/ APPLICANT: Tumas, Daniel
 / APPLICANT: Matanabe, Colin K
 / APPLICANT: Wood, William
 / APPLICANT: Zhang, Zemin
 / TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 / TITLE OF INVENTION: ACIDS ENCODING THE SAME
 / FILE REFERENCE: P330R1C17
 / CURRENT APPLICATION NUMBER: US/10/121,049
 / PRIORITY FILING DATE: 2002-04-12
 / Prior Application removed - See File Wrapper or Palm
 / NUMBER OF SEQ ID NOS: 550
 / SEQ ID NO 491
 / LENGTH: 1475
 / TYPE: DNA
 / ORGANISM: Homo Sapien
 / US-10-121-049-491

Query Match 53.7%; Score 1472; DB 14; Length 1475;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 GCTTACGCTGAAGACAGAGGAGAGGAGTCCCTGAAGAGGCTTCTAGAGAGTGGCAT 120
 DB 64 GCTTACGCTGAAGACAGAGGAGAGGAGTCCCTGAAGAGGCTTCTAGAGAGTGGCAT 123
 QY 121 GGCCTCTCTGCGCTCCCACTTGTGGGCTACATCTAGAGGCTTGTGGGCTTGTGGGCT 180
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 27, 2004, 07:21:12 ; Search time 131 Seconds

(without alignments)
569.234 Million cell updates/sec

Title: US-09-787-677a-3

Perfect score: 1174

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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15	1174	100.0	230	14	US-10-063-512-80	Sequence 80, App1
16	1174	100.0	230	14	US-10-121-092-492	Sequence 492, App
17	1174	100.0	230	14	US-10-123-904-492	Sequence 492, App
18	1174	100.0	230	14	US-10-140-470-492	Sequence 492, App
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41	1174	100.0	230	14	US-10-143-032-492	Sequence 492, App
42	1174	100.0	230	14	US-10-063-563-80	Sequence 80, App1
43	1174	100.0	230	14	US-10-006-485A-134	Sequence 134, App
44	1174	100.0	230	14	US-10-013-907A-134	Sequence 134, App
45	1174	100.0	230	14	US-10-015-499A-134	Sequence 134, App

ALIGNMENTS

RESULT 1

US-09-998-598-2590

Sequence 2590, Application US/09998598

Patent No. US20020150922A1

GENERAL INFORMATION:

APPLICANT: Stolk, John A.

APPLICANT: Xu, Jiangchun

APPLICANT: Chenault, Ruth A.

APPLICANT: Meagher, Madelein Joy

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.561

CURRENT FILING DATE: 2001-11-16

CURRENT FILING DATE: 2001-11-16

NUMBER OF SEQ ID NOS: 2606

SOFTWARE: Corixa Invention Disclosure Database

SEQ ID NO 2590

LENGTH: 230

TYPE: PRT

ORGANISM: Homo sapiens

US-09-998-598-2590

Query Match 100.0%; Score 1174; DB 9; Length 230;

Best Local Similarity 100.0%; Pred. No. 3.8e-110;

Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MASIGQLVGYIGLGLGLGLTLVAMLPKSTSSVYAGSIVTAVGFSKGLMECATSTG 60

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RESULT 2

US-09-888-257A-6
; Sequence 6, Application US/09888257A
; Publication No. US20030060612A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Polakie, Paul
; APPLICANT: Smith, Victoria
; APPLICANT: Wood, William I.
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5002R1
; CURRENT APPLICATION NUMBER: US/09/888, 257A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/063,540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: US 60/089,653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/099,792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: US 60/103,678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: US 60/235,451
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US00/04342
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
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; ORGANISM: Homo Sapien
US-09-888-257A-6

Query Match 100.0%; Score 1174; DB 10; Length 230;
Best Local Similarity 100.0%; Pred. No. 3.8e-110;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASIGLQVGYIIGLIGLIPVAMNHGILRDFYSPVPSMKFEIGELALYIGIISLFLSINGIT 180
Db 1 MASIGLQVGYIIGLIGLIPVAMNHGILRDFYSPVPSMKFEIGELALYIGIISLFLSINGIT 180
Qy 61 ITQCDIYIITLIGLIPADIOAAQAMNVTSSAISIACIISVGMRCVFCQESRADRVAVA 120
Db 61 ITQCDIYIITLIGLIPADIOAAQAMNVTSSAISIACIISVGMRCVFCQESRADRVAVA 120

Qy 121 GGVEFIIIGLIGLIPVAMNHGILRDFYSPVPSMKFEIGELALYIGIISLFLSINGIT 180
Db 121 GGVEFIIIGLIGLIPVAMNHGILRDFYSPVPSMKFEIGELALYIGIISLFLSINGIT 180
Qy 181 LCFSCSSQRNRSNYYDAYQAQPLATRSSPRGQPPKYSFBNYSYLTGYV 230
Db 181 LCFSCSSQRNRSNYYDAYQAQPLATRSSPRGQPPKYSFBNYSYLTGYV 230

RESULT 3

US-09-946-374-134
; Sequence 134, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deeneyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tuma, Daniel
; APPLICANT: Williams, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946, 374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808

PRO 1356

PRIOR FILING DATE: 1998-09-10
 PRIOR APPLICATION NUMBER: 60/099812
 PRIOR FILING DATE: 1998-09-10
 PRIOR APPLICATION NUMBER: 60/099815
 PRIOR FILING DATE: 1998-09-10
 PRIOR APPLICATION NUMBER: 60/099816
 PRIOR FILING DATE: 1998-09-10
 PRIOR APPLICATION NUMBER: 60/100385
 PRIOR FILING DATE: 1998-09-15
 PRIOR APPLICATION NUMBER: 60/100388
 PRIOR FILING DATE: 1998-09-15
 PRIOR APPLICATION NUMBER: 60/100390
 PRIOR FILING DATE: 1998-09-15
 PRIOR APPLICATION NUMBER: 60/100584
 PRIOR FILING DATE: 1998-09-16
 PRIOR APPLICATION NUMBER: 60/100627
 PRIOR FILING DATE: 1998-09-16
 PRIOR APPLICATION NUMBER: 60/100661
 PRIOR FILING DATE: 1998-09-16
 PRIOR APPLICATION NUMBER: 60/100662
 PRIOR FILING DATE: 1998-09-16
 PRIOR APPLICATION NUMBER: 60/100664
 PRIOR FILING DATE: 1998-09-16
 PRIOR APPLICATION NUMBER: 60/100683
 PRIOR FILING DATE: 1998-09-17
 PRIOR APPLICATION NUMBER: 60/100684
 PRIOR FILING DATE: 1998-09-17
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 PRIOR FILING DATE: 1998-09-17
 PRIOR APPLICATION NUMBER: 60/100711
 PRIOR FILING DATE: 1998-09-17
 PRIOR APPLICATION NUMBER: 60/100848
 PRIOR FILING DATE: 1998-09-18
 PRIOR APPLICATION NUMBER: 60/100849
 PRIOR FILING DATE: 1998-09-18
 PRIOR APPLICATION NUMBER: 60/100919
 PRIOR FILING DATE: 1998-09-17
 PRIOR APPLICATION NUMBER: 60/100930
 PRIOR FILING DATE: 1998-09-17
 PRIOR APPLICATION NUMBER: 60/101014
 PRIOR FILING DATE: 1998-09-18
 PRIOR APPLICATION NUMBER: 60/101068
 PRIOR FILING DATE: 1998-09-18
 PRIOR APPLICATION NUMBER: 60/101071
 PRIOR FILING DATE: 1998-09-18
 PRIOR APPLICATION NUMBER: 60/101279
 PRIOR FILING DATE: 1998-09-22
 PRIOR APPLICATION NUMBER: 60/101471
 PRIOR FILING DATE: 1998-09-23
 PRIOR APPLICATION NUMBER: 60/101472
 PRIOR FILING DATE: 1998-09-23
 PRIOR APPLICATION NUMBER: 60/101474
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 PRIOR APPLICATION NUMBER: 60/101477
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 PRIOR APPLICATION NUMBER: 60/101479
 PRIOR FILING DATE: 1998-09-23
 PRIOR APPLICATION NUMBER: 60/101738
 PRIOR FILING DATE: 1998-09-24
 PRIOR APPLICATION NUMBER: 60/101741
 PRIOR FILING DATE: 1998-09-24
 PRIOR APPLICATION NUMBER: 60/101743
 PRIOR FILING DATE: 1998-09-24
 PRIOR APPLICATION NUMBER: 60/101915
 PRIOR FILING DATE: 1998-09-24
 PRIOR APPLICATION NUMBER: 60/101916
 PRIOR FILING DATE: 1998-09-24
 PRIOR APPLICATION NUMBER: 60/102207
 PRIOR FILING DATE: 1998-09-29

PRIOR APPLICATION NUMBER: 60/102240
 PRIOR FILING DATE: 1998-09-29
 PRIOR APPLICATION NUMBER: 60/102307
 PRIOR FILING DATE: 1998-09-29
 PRIOR APPLICATION NUMBER: 60/102330
 PRIOR FILING DATE: 1998-09-29
 PRIOR APPLICATION NUMBER: 60/102331
 PRIOR FILING DATE: 1998-09-29
 PRIOR APPLICATION NUMBER: 60/102484
 PRIOR FILING DATE: 1998-09-30
 PRIOR APPLICATION NUMBER: 60/102487
 PRIOR FILING DATE: 1998-09-30
 PRIOR APPLICATION NUMBER: 60/102570
 PRIOR FILING DATE: 1998-09-30
 PRIOR APPLICATION NUMBER: 60/102571
 PRIOR FILING DATE: 1998-09-30
 PRIOR APPLICATION NUMBER: 60/102684
 PRIOR FILING DATE: 1998-10-01
 PRIOR APPLICATION NUMBER: 60/102687
 PRIOR FILING DATE: 1998-10-01
 PRIOR APPLICATION NUMBER: 60/102965
 PRIOR FILING DATE: 1998-10-02
 PRIOR APPLICATION NUMBER: 60/103258
 PRIOR FILING DATE: 1998-10-06
 PRIOR APPLICATION NUMBER: 60/103314
 PRIOR FILING DATE: 1998-10-07
 PRIOR APPLICATION NUMBER: 60/103315
 PRIOR FILING DATE: 1998-10-07
 PRIOR APPLICATION NUMBER: 60/103328
 PRIOR FILING DATE: 1998-10-07
 PRIOR APPLICATION NUMBER: 60/103395
 PRIOR FILING DATE: 1998-10-07
 PRIOR APPLICATION NUMBER: 60/103396
 PRIOR FILING DATE: 1998-10-07
 PRIOR APPLICATION NUMBER: 60/103401
 PRIOR FILING DATE: 1998-10-07
 PRIOR APPLICATION NUMBER: 60/103449
 PRIOR FILING DATE: 1998-10-06
 PRIOR APPLICATION NUMBER: 60/103633
 PRIOR FILING DATE: 1998-10-08
 PRIOR APPLICATION NUMBER: 60/103678
 PRIOR FILING DATE: 1998-10-08
 PRIOR APPLICATION NUMBER: 60/103679
 PRIOR FILING DATE: 1998-10-08
 PRIOR APPLICATION NUMBER: 60/103711
 PRIOR FILING DATE: 1998-10-08
 PRIOR APPLICATION NUMBER: 60/104257
 PRIOR FILING DATE: 1998-10-14
 PRIOR APPLICATION NUMBER: 60/104987
 PRIOR FILING DATE: 1998-10-20
 PRIOR APPLICATION NUMBER: 60/105000
 PRIOR FILING DATE: 1998-10-20
 PRIOR APPLICATION NUMBER: 60/105002
 PRIOR FILING DATE: 1998-10-20
 PRIOR APPLICATION NUMBER: 60/105104
 PRIOR FILING DATE: 1998-10-21
 PRIOR APPLICATION NUMBER: 60/105169
 PRIOR FILING DATE: 1998-10-22
 PRIOR APPLICATION NUMBER: 60/105266
 PRIOR FILING DATE: 1998-10-22
 PRIOR APPLICATION NUMBER: 60/105693
 PRIOR FILING DATE: 1998-10-26
 PRIOR APPLICATION NUMBER: 60/105694
 PRIOR FILING DATE: 1998-10-26
 PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 1174; DB 10; Length 230;
 Best Local Similarity 100.0%; Pred. No. 3 8e-110;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MASIGLGVGYIIGLLGLCTLVAMLLPSWKTSSYVGASIVTAVGSGKGLMECAHTSTG 60
 Db 1 MASIGLGVGYIIGLLGLCTLVAMLLPSWKTSSYVGASIVTAVGSGKGLMECAHTSTG 60

[illegible]

PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/119287
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/119525
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/120014
PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: 60/129122
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: 60/129674
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/138387
PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: 60/144791
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/175481
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 60/191007
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/199397
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/380139
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 09/311832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/380137
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380142

Query Match 100.0%; Score 1174; DB 13; Length 230;
Best Local Similarity 100.0%; Pred. No. 3.8e-110;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYIIGLGLGLTLVAMLLPSMKTSSYVGASIVTVAVGSKGLMECATHTSTG 60
DB 1 MASLGQLVGYIIGLGLGLTLVAMLLPSMKTSSYVGASIVTVAVGSKGLMECATHTSTG 60
QY 61 ITQCDIYSTLLGLPADIOAQAAMWTSASISLACIISVGMKCTVFCQESRAKDRVAVA 120
DB 61 ITQCDIYSTLLGLPADIOAQAAMWTSASISLACIISVGMKCTVFCQESRAKDRVAVA 120
QY 121 GGVFFILGLGLFIPVAMNLHGILRDFYSPVDPDSMKFEIGALYIGIISLFSLIAGII 180
DB 121 GGVFFILGLGLFIPVAMNLHGILRDFYSPVDPDSMKFEIGALYIGIISLFSLIAGII 180
QY 181 LCFSCSSQRRNSNYDAYOAOPLATRSSPRPGQPPVKSEFNSYSLTGYV 230
DB 181 LCFSCSSQRRNSNYDAYOAOPLATRSSPRPGQPPVKSEFNSYSLTGYV 230

RESULT 7

US-10-063-547-80
Sequence 80; Application US/10063547
Publication No. US20020182636A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,547
CURRENT FILING DATE: 2002-05-02
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 80
LENGTH: 230
TYPE: PRT
ORGANISM: Homo Saplen
US-10-063-547-80

Query Match 100.0%; Score 1174; DB 13; Length 230;
Best Local Similarity 100.0%; Pred. No. 3.8e-110;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYIIGLGLGLTLVAMLLPSMKTSSYVGASIVTVAVGSKGLMECATHTSTG 60
DB 1 MASLGQLVGYIIGLGLGLTLVAMLLPSMKTSSYVGASIVTVAVGSKGLMECATHTSTG 60
QY 61 ITQCDIYSTLLGLPADIOAQAAMWTSASISLACIISVGMKCTVFCQESRAKDRVAVA 120
DB 61 ITQCDIYSTLLGLPADIOAQAAMWTSASISLACIISVGMKCTVFCQESRAKDRVAVA 120
QY 121 GGVFFILGLGLFIPVAMNLHGILRDFYSPVDPDSMKFEIGALYIGIISLFSLIAGII 180
DB 121 GGVFFILGLGLFIPVAMNLHGILRDFYSPVDPDSMKFEIGALYIGIISLFSLIAGII 180
QY 181 LCFSCSSQRRNSNYDAYOAOPLATRSSPRPGQPPVKSEFNSYSLTGYV 230
DB 181 LCFSCSSQRRNSNYDAYOAOPLATRSSPRPGQPPVKSEFNSYSLTGYV 230

RESULT 8

US-10-063-551-80
Sequence 80; Application US/10063551
Publication No. US20020183494A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,551
CURRENT FILING DATE: 2002-05-02
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 80
LENGTH: 230
TYPE: PRT
ORGANISM: Homo Saplen
US-10-063-551-80

Query Match 100.0%; Score 1174; DB 13; Length 230;
Best Local Similarity 100.0%; Pred. No. 3.8e-110;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYIIGLGLGLTLVAMLLPSMKTSSYVGASIVTVAVGSKGLMECATHTSTG 60
DB 1 MASLGQLVGYIIGLGLGLTLVAMLLPSMKTSSYVGASIVTVAVGSKGLMECATHTSTG 60
QY 61 ITQCDIYSTLLGLPADIOAQAAMWTSASISLACIISVGMKCTVFCQESRAKDRVAVA 120
DB 61 ITQCDIYSTLLGLPADIOAQAAMWTSASISLACIISVGMKCTVFCQESRAKDRVAVA 120
QY 121 GGVFFILGLGLFIPVAMNLHGILRDFYSPVDPDSMKFEIGALYIGIISLFSLIAGII 180

Db 121 GGVFFILGLGFIPLVAMNHLGRDYSPLVPSDKMFIEGALYGLTISLFFLGLGII 180
Qy 181 LCPSCSSQRNRSNYYDAYOAOPLATRSSPRGCPKKSFFNSYSLTGYV 230
Db 181 LCPSCSSQRNRSNYYDAYOAOPLATRSSPRGCPKKSFFNSYSLTGYV 230

RESULT 9

US-10-028-072-492
; Sequence 492, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bertelini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tuma, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028, 072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059836
; PRIOR FILING DATE: 1997-09-24
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062285
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062814
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/062816
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063082
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/063127
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063327

; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063329
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063550
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063561
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063704
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063733
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063735
; PRIOR FILING DATE: 1997-10-29
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; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063755
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; PRIOR FILING DATE: 1997-11-03
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; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065846
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066453
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066511
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; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069212
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069278
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069334
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069694
; PRIOR FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: 60/072320
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: 60/073612
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: 60/074086
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074092
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081695
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081818
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082999
; PRIOR FILING DATE: 1998-04-24

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330R1C182
CURRENT APPLICATION NUMBER: US/10/140,808
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 492
LENGTH: 230
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-808-492

Query Match 100.0%; Score 1174; DB 14; Length 230;
Best Local Similarity 100.0%; Pred. No. 3.8e-110;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASIGQLVGYIIGLGLGTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60
DB 1 MASIGQLVGYIIGLGLGTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60
QY 61 ITQCDIYSTLLGHPADIQAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120
DB 61 ITQCDIYSTLLGHPADIQAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120
QY 121 GGVFFILGLGLGFIPIVAMNLHGILRDFYSPVDSMKFEIGALYIGIISLPSLIAGII 180
DB 121 GGVFFILGLGLGFIPIVAMNLHGILRDFYSPVDSMKFEIGALYIGIISLPSLIAGII 180
QY 181 LCFSSSQRRNSNYDAYOQAPLATRSSPRGQPPVKSEFNSYSLTGYV 230
DB 181 LCFSSSQRRNSNYDAYOQAPLATRSSPRGQPPVKSEFNSYSLTGYV 230

RESULT 12

US-10-063-569-80
Sequence 80, Application US/10063569
Publication No. US20030018168A1
GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,569
CURRENT FILING DATE: 2002-05-02
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 80
LENGTH: 230
TYPE: PRT
ORGANISM: Homo Sapien
US-10-063-569-80

Query Match 100.0%; Score 1174; DB 14; Length 230;
Best Local Similarity 100.0%; Pred. No. 3.8e-110;

Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASIGQLVGYIIGLGLGTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60
DB 1 MASIGQLVGYIIGLGLGTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60
QY 61 ITQCDIYSTLLGHPADIQAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120
DB 61 ITQCDIYSTLLGHPADIQAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120
QY 121 GGVFFILGLGLGFIPIVAMNLHGILRDFYSPVDSMKFEIGALYIGIISLPSLIAGII 180
DB 121 GGVFFILGLGLGFIPIVAMNLHGILRDFYSPVDSMKFEIGALYIGIISLPSLIAGII 180
QY 181 LCFSSSQRRNSNYDAYOQAPLATRSSPRGQPPVKSEFNSYSLTGYV 230
DB 181 LCFSSSQRRNSNYDAYOQAPLATRSSPRGQPPVKSEFNSYSLTGYV 230

RESULT 13

US-10-063-513-80
Sequence 80, Application US/10063513
Publication No. US20030018172A1
GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,513
CURRENT FILING DATE: 2002-05-01
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 80
LENGTH: 230
TYPE: PRT
ORGANISM: Homo Sapien
US-10-063-513-80

Query Match 100.0%; Score 1174; DB 14; Length 230;
Best Local Similarity 100.0%; Pred. No. 3.8e-110;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASIGQLVGYIIGLGLGTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60
DB 1 MASIGQLVGYIIGLGLGTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60
QY 61 ITQCDIYSTLLGHPADIQAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120
DB 61 ITQCDIYSTLLGHPADIQAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120
QY 121 GGVFFILGLGLGFIPIVAMNLHGILRDFYSPVDSMKFEIGALYIGIISLPSLIAGII 180
DB 121 GGVFFILGLGLGFIPIVAMNLHGILRDFYSPVDSMKFEIGALYIGIISLPSLIAGII 180
QY 181 LCFSSSQRRNSNYDAYOQAPLATRSSPRGQPPVKSEFNSYSLTGYV 230
DB 181 LCFSSSQRRNSNYDAYOQAPLATRSSPRGQPPVKSEFNSYSLTGYV 230

RESULT 14

US-10-063-515-80
Sequence 80, Application US/10063515
Publication No. US20030018173A1
GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.

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; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,515
; PRIOR APPLICATION: 2002-05-01
; PRIOR APPLICATION removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 80
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-515-80

Query Match          100.0%; Score 1174; DB 14; Length 230;
Best Local Similarity 100.0%; Pred. No. 3 8e-110;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MASIGLQLVGYIIGLIGLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60
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QY 61 ITQCDIYSTLLGLPADIOAQAAMWVTSSAISLACIISVGMCRCTVFCQESRAKDRVAVA 120
Db 61 ITQCDIYSTLLGLPADIOAQAAMWVTSSAISLACIISVGMCRCTVFCQESRAKDRVAVA 120
QY 121 GGVPFLLGGLGFIPIVAMNHLGILRDYSPPLVPSDKMKEIGEALYLGIIISLPSLIAGII 180
Db 121 GGVPFLLGGLGFIPIVAMNHLGILRDYSPPLVPSDKMKEIGEALYLGIIISLPSLIAGII 180
QY 181 LCFSSCSQRNRNSNYDAYOAOPLATRSSPRPGQPPKVKSEFNYSYLTGYV 230
Db 181 LCFSSCSQRNRNSNYDAYOAOPLATRSSPRPGQPPKVKSEFNYSYLTGYV 230
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RESULT 15
US-10-063-512-80
; Sequence 80, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Batton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 80
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-512-80
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Query Match          100.0%; Score 1174; DB 14; Length 230;
Best Local Similarity 100.0%; Pred. No. 3 8e-110;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MASIGLQLVGYIIGLIGLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60
Db 1 MASIGLQLVGYIIGLIGLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60
QY 61 ITQCDIYSTLLGLPADIOAQAAMWVTSSAISLACIISVGMCRCTVFCQESRAKDRVAVA 120
Db 61 ITQCDIYSTLLGLPADIOAQAAMWVTSSAISLACIISVGMCRCTVFCQESRAKDRVAVA 120
QY 121 GGVPFLLGGLGFIPIVAMNHLGILRDYSPPLVPSDKMKEIGEALYLGIIISLPSLIAGII 180
Db 121 GGVPFLLGGLGFIPIVAMNHLGILRDYSPPLVPSDKMKEIGEALYLGIIISLPSLIAGII 180
QY 181 LCFSSCSQRNRNSNYDAYOAOPLATRSSPRPGQPPKVKSEFNYSYLTGYV 230
Db 181 LCFSSCSQRNRNSNYDAYOAOPLATRSSPRPGQPPKVKSEFNYSYLTGYV 230
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Search completed: October 27, 2004, 07:33:03
Job time : 133 secs

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Db	2161	GGGATTTGACGTGAGGTGGAGGTGAGATGTTTCCACGAAAGACAGTTTCCACTTTAAG	2220
QY	2221	GTCCGAAAATGTTCCCTTTACCTTCGAGATGGAGAGGGGTCAATACCAAGATATTT	2280
Db	2221	GTCCGAAAATGTTCCCTTTACCTTCGAGATGGAGAGGGGTCAATACCAAGATATTT	2280
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Db	2461	TCAGAGCTTGAGAACTTCTCAGAGGTCACTCTTCAATGAGACCTTCTGTATCACTGCA	2520
QY	2521	TTCCCTCTCTCAACCCCTCCCTCCCCCAACCTCAATGATTAATGCTTCTTGATGCTTAG	2580
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QY	2581	CATTCAACAATTTTGAATGATCGTATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2640
Db	2581	CATTCAACAATTTTGAATGATCGTATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2640
QY	2641	GTTAAACCTTGGTGGGTGGGGGCGCATATCTGATGACTCTCTGTATATCCCGAGACTATCT	2700
Db	2641	GTTAAACCTTGGTGGGTGGGGGCGCATATCTGATGACTCTCTGTATATCCCGAGACTATCT	2700
QY	2701	GTTAAACGTGCGACGACCAAGAGGTGATCAATATTTGCTAGC 2742	
Db	2701	GTTAAACGTGCGACGACCAAGAGGTGATCAATATTTGCTAGC 2742	
RESULT 2			
AK075405		2959 bp	linear
LOCUS			
DEFINITION			
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ACCESSION			
VERSION			
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SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			

cdna library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center.
location/Qualifiers
1..2959
source

CDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center.

Location/Qualifiers

1. .2959

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="NT2RP2002060"

/cell_line="NT2"

/cell_type="teratocarcinoma"

/clone_id="NT2RP2"

/note="Cloning vector: pME18SFL3-mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"

Query Match	99.2%	Score	7021.4	DB	9	Length	2959		
Best Local Similarity	99.9%	Pred. No.	0						
Matches	2733	Conservative	0	Mismatches	1	Indels	1	Gaps	
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DB	209	AGAAGT	CAGCGCTGG	CAAGAGAG	ACTCTGA	AAATGAGGGAT	TGAGAGTGTTCAGAGAG	CAAGA	268
QY	61	GCTT	CACCTG	GAACAA	CAAGGGAG	AGTCCCTGA	AGAGCGTTC	CTAGAGAGTCTG	120
DB	269	GCTT	CACCTG	GAACAA	CAAGGGAG	AGTCCCTGA	AGAGCGTTC	CTAGAGAGTCTG	328
QY	121	GGCCT	CTCTTGG	CTCCAA	CTTGTG	GGGCTACAT	CTAGAGCGTTC	TG	180
DB	329	GGCCT	CTCTTGG	CTCCAA	CTTGTG	GGGCTACAT	CTAGAGCGTTC	TG	388
QY	181	ACTG	GTGCCAT	GTCTGCTCC	CCAGCTG	GAACAA	AGTTC	TATGTG	240
DB	389	ACTG	GTGCCAT	GTCTGCTCC	CCAGCTG	GAACAA	AGTTC	TATGTG	448
QY	241	GACAG	CAGTGGGCTT	CTCCAA	GGGCTCTG	GAATG	TGTC	CAACACAG	300
DB	449	GACAG	CAGTGGGCTT	CTCCAA	GGGCTCTG	GAATG	TGTC	CAACACAG	508
QY	301	CACCC	AGGTGACAT	CTAT	TAGCAC	CCCTTCTG	GGGCTTG	CCGCTG	360
DB	509	CACCC	AGGTGACAT	CTAT	TAGCAC	CCCTTCTG	GGGCTTG	CCGCTG	568
QY	361	GGCC	ATATG	TGTGACAT	CCAGTGA	ATCTCCTCC	TGGCC	CTG	420
DB	569	GGCC	ATATG	TGTGACAT	CCAGTGA	ATCTCCTCC	TGGCC	CTG	628
QY	421	CATG	AGATG	ACATCTT	CTGTC	CAAGAA	TCCCG	AGCCAA	480
DB	629	CATG	AGATG	ACATCTT	CTGTC	CAAGAA	TCCCG	AGCCAA	688
QY	481	TG	AGTCTT	TTCA	TCTTG	AGGCTCT	TGG	ATTC	540
DB	689	TG	AGTCTT	TTCA	TCTTG	AGGCTCT	TGG	ATTC	748
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DB	749	TGG	ATCTCT	GAAGG	ACTTCTA	CTAC	CACTG	GTGCTG	808
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DB	809	AG	AGGCTCT	TTACTT	TGGG	CA	TTATTTCT	CCCTGTCT	868
QY	661	CTG	CTTTTCT	CGCTCAT	TCCG	AGAA	ATGCTT	CCAC	720
DB	869	CTG	CTTTTCT	CGCTCAT	TCCG	AGAA	ATGCTT	CCAC	928
QY	721	AC	CTTCTG	CCACA	AGAG	CTCT	CCAG	GC	780
DB	929	AC	CTTCTG	CCACA	AGAG	CTCT	CCAG	GC	988
QY	781	CA	ATTCT	CA	AGCCT	GCAG	GGATAT	TGTGTGA	840

Db 989 CAATTCTTACAGCTGACAGGATATGTGTAAAGAACCGGGGCCAGAGCTGGGGGGTGGC 1048
 Qy 841 TGGGTCTGTGAAAAACAGTGAAGACACCCGAGGGGACAGGTGAGGAGCACTAACCT 900
 Db 1049 TGGGTCTGTGAAAAACAGTGAAGACACCCGAGGGGACAGGTGAGGAGCACTAACCT 1108
 Qy 901 GGAATGTGTGAGAAAGGTGTGTGAGGATAGACTGTGTTGGCATTGGATTGAGCAAG 960
 Db 1109 GGAATGTGTGAGAAAGGTGTGTGAGGATAGACTGTGTTGGCATTGGATTGAGCAAG 1168
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 Db 1229 CAGGCTTCTGTGTTTCCCTACAGCTGTGCTGCTCCCTGAGCTTGAAGCCCTCACTT 1288
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 Qy 1141 ACTTCATCCCAAAACCACTTAATCAATCCCACTGATGACCTCTGTGATCAAAAGCC 1200
 Db 1349 ACTTCATCCCAAAACCACTTAATCAATCCCACTGATGACCTCTGTGATCAAAAGCC 1408
 Qy 1201 TCTCTGTGCTGAGGTGGCTCTTAGCTCATTTGCTGGGATGGGAAAGAGAGAGTGGC 1260
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 Db 1469 TTTTGTGGGCAATGTCTTAACCTTCTCAAGCTTCCCTCAAAAGAACTGATTTGCC 1528
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 Db 1529 TGAACCTCATCCCACTCTTGTATAGATCCCAAGTCCAGCTAATTTGGCAAGAA 1588
 Qy 1381 CTGAATAAATAACATCTTACGGTATCCAGGGAGCAGAAAGCAGGATGAGGAGGA 1440
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 Qy 1441 CAGAAAGCAGCTGGGACATTTAAATAAATAAATAAATAAATAAATAAATAAATAA 1500
 Db 1649 CAGAAAGCAGCTGGGACATTTAAATAAATAAATAAATAAATAAATAAATAAATAA 1708
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 Db 1829 ACTTCACTGAGAACTGTCTCAAGAGTGGGATCAAACTTTGGCTGAGAGCCCTGCTC 1888
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 Qy 1801 GTGTGGAGCTGTGGGGTACTGAGAAAGACCACTTCTTGAAGGTGTCTTAAGAGCCAG 1860
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Db 2069 GTGTGGAGCTGTGGGGTACTGAGAAAGACCACTTCTTGAAGGTGTCTTAAGAGCCAG 2128
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 Db 2129 AGAAACTCTTCAAGCGCTAATGAAATAACAGCTCAATGAGATGAGGCCCCCAGGGTCC 2188
 Qy 1981 ACCCAAGAGCACTACAGAGCTCTGAAAGACATATGACACCAAGGAGCCCTTCAAGATT 2040
 Db 2189 ACCCAAGAGCACTACAGAGCTCTGAAAGACATATGACACCAAGGAGCCCTTCAAGATT 2248
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 Db 2309 TGGCATATCCATGCCCAAGGTGTGTCTGATGATGATGATGATGATGATGATGATGATGAT 2368
 Qy 2161 GGGATTGAGCTGAGAGTGGGAGTGGAGATGTTTCCAGAGACAGTTCCACTCTTAAG 2220
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 Qy 2221 GTCCGAAATGTTCCCTTTACCTGAGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGT 2280
 Db 2429 GTCCGAAATGTTCCCTTTACCTGAGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGT 2488
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 Db 2489 TCCCTCAGCAGTCTAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2548
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 Db 2549 CATTTGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2608
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 Qy 2461 TCAAGCTTGGAGAACTTCTCAGAGCTCACTCTCTTCAATGAGGCTTCTGATCACTCCA 2520
 Db 2669 TCAAGCTTGGAGAACTTCTCAGAGCTCACTCTCTTCAATGAGGCTTCTGATCACTCCA 2728
 Qy 2521 TCCCTGCTTCAAGCTTCT 2580
 Db 2729 TCCCTGCTTCAAGCTTCT 2788
 Qy 2581 CATTCACATTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640
 Db 2789 CATTCACATTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2848
 Qy 2641 GTAACCTCTTGGTGGGTCATATCTTGAAGCTCTCTGATTCCTCCAGACTATCT 2700
 Db 2849 GTAACCTCTTGGTGGGTCATATCTTGAAGCTCTCTGATTCCTCCAGACTATCT 2808
 Qy 2701 GTTACAGTGCAGGAC-CAGAAAGTATCAATTA 2734
 Db 2909 GTTACAGTGCAGGACACAGTATGATCAATTA 2943

RESULT 3
 AL158821
 LOCUS 109465 bp DNA linear PRI 08-FEB-2002
 DEFINITION Human DNA sequence from clone Rpl-75H8 on chromosome Xq22.3-23
 containing the CLDN2 gene for claudin 2, the gene for a novel protein
 similar to KIAA0136, a eukaryotic translation elongation factor 1
 alpha 1 (EBF1A1) pseudogene and a Cpg island, complete sequence.
 AL158821
 VERSION AL158821.16 GI:14329875
 KEYWORDS HTG; claudin; CLDN2; Cpg island; EBF1A1; KIAA0136.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (Pages 1 to 109465)
AUTHORS Heath, P.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humbrey@sanger.ac.uk
On Jun 8, 2001 this sequence version replaced gi:14160908.

COMMENT

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chrx>

RP1-75H8 is from the library RPCI-1 constructed by the group of Peter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pCYRAC2
IMPORTANT: This sequence is not the entire insert of clone RP1-75H8 It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true left end of clone RP1-75H8 is at 1 in this sequence. The true left end of clone RP13-383K5 is at 109366 in this sequence.

FEATURES

Source

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/mol_type="Genomic DNA"

/db_xref="taxon:9606"

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/clone="RP1-75H8"

/clone_1kb="RPCI-1"

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gene

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Query Match 99.2%; Score 2721.4; DB 9; Length 109465;
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Matches 2733; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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VERSION	AX136129.1	GI:14272537	
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SOURCE			
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REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
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JOURNAL	Secretory protein or membrane protein Patent: BP 1067182-A 51-10-JUN-2001,		
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KEYWORDS	AK075371.1	VERSION	GI:22761413	oligo capping; f1s (full insert sequence).	
SOURCE		ORGANISM	Homo sapiens (human)		
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REFERENCE	1		Oca,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayaishi,K., Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T., Nakamura,Y., Nagahari,K., Sugano,S. and Isogai,T.		
AUTHORS			HRI human cDNA sequencing project		
			Unpublished		
TITLE			2 (bases 1 to 2863)		
JOURNAL			Isogai,T. and Yamamoto,J.		
REFERENCE			Direct Submission		
AUTHORS			Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 229-0812, Japan (E-mail:genomic@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)		
TITLE			HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass sequencing, clone selection and full insert sequencing; Helix Research Institute (supported by Japan Key Technology Center etc.); cDNA library construction; Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center.		
COMMENT					

FEATURES
source

CDS

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Query Match 99.0%; Score 2715; DB 9; Length 2863;
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AUTHORS	Bukaryote, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria (1506)		
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	Straussberg, R.L., Feingold, E.A., Grouse, L.H., Dergs, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Ruidin, G.M., Hong, L., Scapleton, M., Soares, M.B., Bonaldi, M.F., Casavant, T.L., Schreier, T.E., Brownstein, M.J., Ubedin, T.B., Tothylaki, S., Carninci, P., Prange, C., Raha, S.S., Loguigliano, N.A., Peters, G.J., Aramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulik, S.W., Villalón, D.K., Muñoz, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,		

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Fahney, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shervenchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grilmond, J., Schmutz, J., Myers, R.M., Butlerfield, J.S., Krzywinski, M.I., Skalska, U., Smalins, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

2 (bases 1 to 1506)
 Straubeberg, R.
 Direct Submission
 Submitted (17-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
 Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Tekla Olson, Diana Palmquist, Anna Petrascu, Anna Liisa Prabhu, Parvaneh Saedi, UR Santos, Angelique Schnerch, Ursula Skalska, Duane Smalins, Jeff Stott, Miranda Tsai, George Yang, Jacque Schein, Asim Siddiqui, Rob Holt, Marco Marra.

FEATURES
SOURCE

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 DEFINITION AF177340
 ACCESSION AF177340.1 GI:10503979
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 REFERENCE
 1 (bases 1 to 1918)
 Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P.,
 Qin,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y.,
 Yu,J. and Han,L.H.
 Novel human cDNA clone with function of inhibiting cancer cell
 growth
 TITLE
 Unpublished
 2 (bases 1 to 1918)
 Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P.,
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 Direct Submission
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 Submitted (06-AUG-1999) National Laboratory for Oncogenes & Related
 Genes, Shanghai Cancer Institute, 25/Lin 2200 Xie Tu Road, Shanghai
 200032, P.R. China
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Matches 1487; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 121 GGCCTCTTGGCCTCCAGCTTGGGCTTACATCTAGGCTTGGGGCTTTTGGGAC 180
DB 522 GGCCTCTTGGCCTCCAGCTTGGGCTTACATCTAGGCTTGGGGCTTTTGGGAC 581
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LOCUS AX092348
DEFINITION Sequence 79 from Patent WO0116318.
ACCESSION AX092348
VERSION AX092348.1 GI:13444488
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1
Eaton, D.L., Filvaroff, E., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Watanabe, C.K. and
Wood, W.I.
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Patent: WO 0116318-A 79 08-MAR-2001;
JOURNAL Genentech, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAGCTGGCAGAGAGACTCTGAAATGAGGATTAAGGTGTTCAAGAGCAGA 60
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QY 61 GCTTCAGCTGAAAGCAAGGAGAGATCCTGAAAGAGCTTTCTAAGAGGTTCGCAT 120
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ACCESSION AX299996
VERSION AX299996.1 GI:17129473
KEYWORDS
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REFERENCE
1 Eaton, D.L., Fong, S., Goddard, A., Godowski, P.J., Grimaldi, C.J.,
Gurney, A.L., Tumas, D., Malanbe, C.K., Wood, W.I. and Zhang, C.
Compositions and methods for the treatment of immune related
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Patent: WO 0166740-A 1 13-SEP-2001;

JOURNAL Genentech, Inc. (US)
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DEFINITION Sequence 1 from Patent WO20216429.
ACCESSION AX395213
VERSION AX395213.1 GI:21066244
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1 Goddard, A., Goddard, P.J., Gurney, A.L., Hillen, K.J., Polakis, P.,
Smith, V., Wood, W.I., Wu, T.D. and Zhang, Z.
Composition and methods for the diagnosis and treatment of tumor
Patent: WO 0216429-A 1 28-FEB-2002;
Genentech, Inc. (US)
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VERSION AX464358.1 GI:21899195
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Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E.,
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VERSION AX491084.1 GI:22323879

KEYWORDS
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REFERENCE
AUTHORS
1 Baker, K.P., Ferrera, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurey, A.L., Hillan, K.J., Marek, S.A., Pan, J.,
Pao, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
Patent: WO 020690-A 191 03-JAN-2002;
Genentech, Inc. (US)
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ACCESSION AX697065 GI:29498042
VERSION AX697065.1 GI:29498042
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REFERENCE
1 Ferrara, N., Stewart, T. A., Williams, P. M., Baker, K. P., Desnoyers, L.,
Baton, D. L., Gao, W. Q., Pan, J., Botstein, D., Fong, S., Goddard, A.,
Geddes, P. J., Gunney, A. L., Smith, V., Tunas, D., Wood, W. I.,
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Patent: WO 0078961-A 133 28-DEC-2000;
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2521 TCCCTCTCCCAACCTTCTCCCAACCTTCTCCCAACCTTCTCCCAACCTTCTCCCAACCTTCTCC 2580
Qy 2581 CATTCACATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640
Db 2581 CATTCACATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640
Qy 2641 GTAAACCTTCTCGGTGGGTGGGGGCAATATCTTGAAGCTTCTTGTATCCCCAGATATCT 2700
Db 2641 GTAAACCTTCTCGGTGGGTGGGGGCAATATCTTGAAGCTTCTTGTATCCCCAGATATCT 2700
Qy 2701 GTAAACCTTCTCGGTGGGTGGGGGCAATATCTTGAAGCTTCTTGTATCCCCAGATATCT 2742
Db 2701 GTAAACCTTCTCGGTGGGTGGGGGCAATATCTTGAAGCTTCTTGTATCCCCAGATATCT 2742

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AAF93769
ID AAF93769 standard; cDNA; 2863 BP.
AC AAF93769;
XX
XX
XX 23-MAY-2001 (first entry)
DE Human cDNA encoding a membrane or secretory protein clone PSEC0059.
KM Human; secretory protein; membrane protein; vaccine; gene therapy;
KM rheumatoid arthritis; diabetes; ss.
OS Homo sapiens.
PN EP1067182-A2.
PD 10-JAN-2001.
PF 07-JUL-2000; 2000EP-00114090.
PR 08-JUL-1999; 99JP-00194179.
PR 11-JAN-2000; 2000JP-00118775.
PR 02-MAY-2000; 2000JP-00183766.
XX
XX (HELI-) HELIX RES INST.
PI Oca T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
XX WPI; 2001-093989/11.
DR P-PSDB; AAB88342.
XX
XX Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT gene therapy or as candidate target molecules in drug development.
PS Claim 1; SEQ ID NO 51; 603pp + Sequence listing; English.
XX
XX This invention relates to nucleic acid sequences AAF93744 - AAF93916
XX which encode human secretory or membrane proteins represented by AAB88317
XX - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
XX AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
XX invention. The invention also includes methods for the production of
XX antibodies directed against the proteins, and cDNA sequences, which can
XX be used in vaccines. The polynucleotide sequences can be used in gene
XX therapy. The polynucleotide sequences and the proteins they encode may be
XX used in the prevention, treatment and diagnosis of diseases associated
XX with inappropriate secretory protein/membrane protein expression. The
XX nucleic acids and complementary sequences may also be used as DNA probes
XX in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
XX and quantitate the presence of similar nucleic acid sequences in samples.
XX They may also be used to study the expression and function of secretory
XX proteins/membrane polypeptides and their role in metabolism. The
XX polypeptides may be used as antigens in the production of antibodies
XX against them and in assays to identify modulators (agonists and
XX antagonists) of expression and activity. The antibodies and antagonists
XX may also be used as therapeutic agents to down regulate expression and
XX activity. The antibodies may also be used as diagnostic agents for
XX detecting the presence of the polypeptides in samples (e.g. by enzyme
XX linked immunosorbent assay (ELISA)). Examples of diseases which may be
XX treated include rheumatoid arthritis and diabetes
XX
XX Sequence 2863 BP; 670 A; 794 C; 711 G; 688 T; 0 U; 0 Other;
XX
XX Query Match 99.0%; Score 2715; DB 5; Length 2863;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 2729; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
Qy 1 AGAAGTCAGCTGAGAGAGAGCTGTAATGAGGATGAGGTGTTCAAGAGCAAGA 60
Db 113 AGAAGTCAGCTGAGAGAGAGCTGTAATGAGGATGAGGTGTTCAAGAGCAAGA 172
Qy 61 GCTTCAGCTGGAAGACAGAGGAGCAAGTCCCTGAAGAGCTTCTTACTGAGAGGTCTGCAAT 120
Db 173 GCTTCAGCTGGAAGACAGAGGAGCAAGTCCCTGAAGAGCTTCTTACTGAGAGGTCTGCAAT 232

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QY	121	96CCCTCTTG6GCTCCAACTGT66GGCTACATCCGAA6GCTCTTG66GCTTTTG66AC	180
Db	223	GGCTCTCTTG6GCTCCAACTGT66GGCTACATCCGAA6GCTCTTG66GCTTTTG66AC	292
QY	181	ACTGTTGGCAGTCTGTCTCCAGCTGGAAAACAATTCTTAATGTCTG6TCCAGCATTTG	240
Db	293	ACTGTTGGCAGTCTGTCTCCAGCTGGAAAACAATTCTTAATGTCTG6TCCAGCATTTG	352
QY	241	GACAGCAGTTGGCTTCTCCAA6GGCTCTG6ATG6AATGTGCAACACAGCAGCGAT	300
Db	353	GACAGCAGTTGGCTTCTCCAA6GGCTCTG6ATG6AATGTGCAACACAGCAGCGAT	412
QY	301	CACCCAGTGTGACATCTAATAGCAACCCTTG66GCTCCGCGTGACATCAGCTG6CCA	360
Db	413	CACCCAGTGTGACATCTAATAGCAACCCTTG66GCTCCGCGTGACATCAGCTG6CCA	472
QY	361	GGCCATGATGTGTGACATCCAGTGCATCTCTCCCTG6CTTG6CATTTATCTGTGTGTGG	420
Db	473	GGCCATGATGTGTGACATCCAGTGCATCTCTCCCTG6CTTG6CATTTATCTGTGTGTGG	532
QY	421	CATGAGATGCAAGTCTTCTGCCAGGAATCCGAGCCAAAGACAAGTGTG6GCTG6CAG	480
Db	533	CATGAGATGCAAGTCTTCTGCCAGGAATCCGAGCCAAAGACAAGTGTG6GCTG6CAG	592
QY	481	TG6AGTCTTTTTCATCTGTGAGG6GCTCCTG6GATTCATCTCTGTGCTG6GATCTTCA	540
Db	593	TG6AGTCTTTTTCATCTGTGAGG6GCTCCTG6GATTCATCTCTGTGCTG6GATCTTCA	652
QY	541	TGGATCTTAAGGAACTTCTACTCAACACTGTGTGCTTGACAGCATGAATTTGAGATTGG	600
Db	653	TGGATCTTAAGGAACTTCTACTCAACACTGTGTGCTTGACAGCATGAATTTGAGATTGG	712
QY	601	AGAGGCTCTTTTACTTGGGCAATTAATTTCTCCCTGTCTCCCTG6ATG6CTGAAATGATCT	660
Db	713	AGAGGCTCTTTTACTTGGGCAATTAATTTCTCCCTGTCTCCCTG6ATG6CTGAAATGATCT	772
QY	661	CTGCTTTTCTG6CTCATCCAGAGAAATG6CTCCAACTAGTACATG6CTTACCAAGCCCA	720
Db	773	CTGCTTTTCTG6CTCATCCAGAGAAATG6CTCCAACTAGTACATG6CTTACCAAGCCCA	832
QY	721	ACTCTTGTCCACAGAGAGCTCTCCAA6GCTGTG6CTCAACTCTCCCAAGTCAAGATGAGTT	780
Db	833	ACTCTTGTCCACAGAGAGCTCTCCAA6GCTGTG6CTCAACTCTCCCAAGTCAAGATGAGTT	892
QY	781	CAATTCCTACAGGCTGACAGGTAATGTGTGAAGAACAGGGGCTCAGACTGTGGGGGTGGC	840
Db	893	CAATTCCTACAGGCTGACAGGTAATGTGTGAAGAACAGGGGCTCAGACTGTGGGGGTGGC	952
QY	841	TGGGTCTGTGAAAAACAGTGTGACAGCACTCCGAGGGGCAAGGTGTAGGGGACACTACACT	900
Db	953	TGGGTCTGTGAAAAACAGTGTGACAGCACTCCGAGGGGCAAGGTGTAGGGGACACTACACT	1012
QY	901	GGATCTGTCAAGAGGTGTGTGAGATAGCTGACATTTTG6CCATTG6ATTGAGCAAG	960
Db	1013	GGATCTGTCAAGAGGTGTGTGAGATAGCTGACATTTTG6CCATTG6ATTGAGCAAG	1072
QY	961	GCAGAAATGGGGGCTAAGTGAACACATGAGAGGTGAATTTG6CAAGATGCTCCGCAAGC	1020
Db	1073	GCAGAAATGGGGGCTAAGTGAACACATGAGAGGTGAATTTG6CAAGATGCTCCGCAAGC	1132
QY	1021	CAGCTTTCTGTTTTCTCACTTGTGTCTCTCCCTG6CTTAAGTGTCCCAACCTCAACTT	1080
Db	1133	CAGCTTTCTGTTTTCTCACTTGTGTCTCTCCCTG6CTTAAGTGTCCCAACCTCAACTT	1192
QY	1081	GAAACCCCAATTCCTTAAGCCAGAGCTGAGAGATCCCTTTG6CTTGTGTTTACTGTGG	1140
Db	1193	GAAACCCCAATTCCTTAAGCCAGAGCTGAGAGATCCCTTTG6CTTGTGTTTACTGTGG	1252
QY	1141	ACTCCATCCCAAAACCACTAATCAATCCCACTG6ACCTGTGATCAAGAGACC	1200
Db	1253	ACTCCATCCCAAAACCACTAATCAATCCCACTG6ACCTGTGATCAAGAGACC	1312

QY	1201	TCCTCTGAGCGTAGGTTGGCTCTTACCTCAATTTGCTGGGGATGGGAAGGAAAGCAGTGGC	1260
DB	1313	TCCTCTGAGCGTAGGTTGGCTCTTACCTCAATTTGCTGGGGATGGGAAGGAAAGCAGTGGC	1372
QY	1261	TTTTGTGGGACATTTGCTCTAAACCTTACTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCC	1330
DB	1373	TTTTGTGGGACATTTGCTCTAAACCTTACTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCC	1432
QY	1321	TGGAACCTCCATCCCACTCTTGTATTAGCTCCACAGTGTCCAGACTAAATTTGTGCATGA	1380
DB	1433	TGGAACCTCCATCCCACTCTTGTATTAGCTCCACAGTGTCCAGACTAAATTTGTGCATGA	1492
QY	1381	CTGAATAAATAACCATCTCAGGTATCCAGGGAACGAAGAAGCATGTGAGATGGGAAGA	1440
DB	1493	CTGAATAAATAACCATCTCAGGTATCCAGGGAACGAAGAAGCATGTGAGATGGGAAGA	1552
QY	1441	CAGGAAGCGACCTGGGACATTTAAAAAATAATGAAAAAATCCAGAACCCATT	1500
DB	1553	CAGGAAGCGACCTGGGACATTTAAAAAATAATGAAAAAATCCAGAACCCATT	1612
QY	1501	TCCTCAGGGCACTTTCAGAAATTCCTCATATTTGTGGGCTGGGATCAAGCTGCAGCTTG	1560
DB	1613	TCCTCAGGGCACTTTCAGAAATTCCTCATATTTGTGGGCTGGGATCAAGCTGCAGCTTG	1672
QY	1561	AGGAAGCAACAAGAAAGGAAGAAGATCTGGTGGAAAGCTCAGGTGGCACGGACCTTG	1620
DB	1673	AGGAAGCAACAAGAAAGGAAGAAGATCTGGTGGAAAGCTCAGGTGGCACGGACCTTG	1732
QY	1621	ACTCACACTGAGAACTGCGCTCAGAAAGCTGCAGATCACAACTTTCGCTGAAGCCCTGCCTC	1680
DB	1733	ACTCACACTGAGAACTGCGCTCAGAAAGCTGCAGATCACAACTTTCGCTGAAGCCCTGCCTC	1792
QY	1681	ACTCTAGGGCACTTGACCTTGCGCTTCTGCTTAACCAAGGCTTAAGGCTATTAGACAT	1740
DB	1793	ACTCTAGGGCACTTGACCTTGCGCTTCTGCTTAACCAAGGCTTAAGGCTATTAGACAT	1852
QY	1741	GGTTTCCTTGAAGAACGTAAACCAAGTTTTTCTAGGGAATGGCCCTTGGGGGATGACA	1800
DB	1853	GGTTTCCTTGAAGAACGTAAACCAAGTTTTTCTAGGGAATGGCCCTTGGGGGATGACA	1912
QY	1801	GTGTGGGAGCTGTGGGGTACTGTAGGAAGACACATTTCTCTTGAACGGTGTCTAAGAACCCAG	1860
DB	1913	GTGTGGGAGCTGTGGGGTACTGTAGGAAGACACATTTCTTGAACGGTGTCTAAGAACCCAG	1972
QY	1861	GTGATGTGTGTGTGGTCTCAAGTGGGTGTTTCTACTCTGCCAGTGAAGGACAGCCCTCT	1920
DB	1973	GTGATGTGTGTGTGGTCTCAAGTGGGTGTTTCTACTCTGCCAGTGAAGGACAGCCCTCT	2032
QY	1921	AGAAACTCTTCAGGCGTAATGAAAAATCAGCTCAAAATGAATCAGGCCCCCAGGGTCC	1980
DB	2033	AGAAACTCTTCAGGCGTAATGAAAAATCAGCTCAAAATGAATCAGGCCCCCAGGGTCC	2092
QY	1981	ACCAACAGAGCACTACAGAGCCCTGAAAGACATATAGCAACCAAGGAGACCCCTTCAGATT	2040
DB	2093	ACCAACAGAGCACTACAGAGCCCTGAAAGACATATAGCAACCAAGGAGACCCCTTCAGATT	2152
QY	2041	CCCCCACTGTCCATCCGAAGATGCTTCAAGATGGCTAGAGGGCATCTAAGGACTTCCAGCA	2100
DB	2153	CCCCCACTGTCCATCCGAAGATGCTTCAAGATGGCTAGAGGGCATCTAAGGACTTCCAGCA	2212
QY	2101	TGGCATATCCATCCCAAGCGGTGTGTGTTCATGATCTGAATGATAGCTGCACGTGCTCT	2160
DB	2213	TGGCATATCCATCCCAAGCGGTGTGTGTTCATGATCTGAATGATAGCTGCACGTGCTCT	2272
QY	2161	GGGATTTGCAGCTGAGGTGGAGTGGAGATGGTTCCAGGAAGACAGTTTCCACTCTAAG	2220
DB	2273	GGGATTTGCAGCTGAGGTGGAGTGGAGATGGTTCCAGGAAGACAGTTTCCACTCTAAG	2332
QY	2221	GTCCGAAAAATGTTCCCTTTAAACCTGGAGTGGGAGTGAAGGATCATACCAAAAGTATTT	2280
DB	2333	GTCCGAAAAATGTTCCCTTTAAACCTGGAGTGGGAGTGAAGGATCATACCAAAAGTATTT	2392
QY	2281	TCCTCAACAGTCTAGGCAATGACGTGGCTTCTGAAAAATTTCCAGCAACCTTCGAACT	2340

Db	1093	CTGGCTTTTTCGTGCTCATCCGAGGAAATCGGCTCAACTACATACGATGCTTACGAAGCCA	1092z
Qy	721	ACCTCTTGCCACAGGAGCTCTCCAAAGCCCTGGTCAACCTCCCAAGTCAAGATGAGTT	780
Db	1093	ACCTCTTGCCACAGGAGCTCTCCAAAGCCCTGGTCAACCTCCCAAGTCAAGATGAGTT	1152z
Qy	781	CAATTCTCAGACGCTGACAGGGTATGTGTGAAGAACAGAGGGCCAGAGCTGGGGGTGGC	840
Db	1153	CAATTCTCAGACGCTGACAGGGTATGTGTGAAGAACAGAGGGCCAGAGCTGGGGGTGGC	1212z
Qy	841	TGGGTCTGTGAAAAACAGTGGACAGCAACCCGAGGGCCACAGGTGAGGAACATCACT	900
Db	1213	TGGGTCTGTGAAAAACAGTGGACAGCAACCCGAGGGCCACAGGTGAGGAACATCACT	1272z
Qy	901	GGATCGTGTCAAGAGGTGCTGTGAGATAGACTGACCTTTGGCCATTGATGAGCAAG	960
Db	1273	GGATCGTGTCAAGAGGTGCTGTGAGATAGACTGACCTTTGGCCATTGATGAGCAAG	1332z
Qy	961	GCAGAAATGGGGGCTAGTGAACAGCATGACAGTTGAATTGCAAGATGCTGCGCATGC	1020
Db	1333	GCAGAAATGGGGGCTAGTGAACAGCATGACAGTTGAATTGCAAGATGCTGCGCATGC	1392z
Qy	1021	CAGCCTTCTGTTTTCTCACCCTTGCTGCTCCCTGGCCCTAAATGCCAACCTTCACTT	1080
Db	1393	CAGCCTTCTGTTTTCTCACCCTTGCTGCTCCCTGGCCCTAAATGCCAACCTTCACTT	1452z
Qy	1081	GAAACCCCATTTCCCTTAAGCCAGGACTCAGAGATCCCTTTGACCCTGTGTTTACTGGG	1140
Db	1453	GAAACCCCATTTCCCTTAAGCCAGGACTCAGAGATCCCTTTGACCCTGTGTTTACTGGG	1512z
Qy	1141	ACTGCATCCCAAAACCACTAATCAATCCAATGACTGACCTTGTGTATCAAAAGCC	1200
Db	1513	ACTGCATCCCAAAACCACTAATCAATCCAATGACTGACCTTGTGTATCAAAAGCC	1572z
Qy	1201	TCTCTGTCGCGAGGGTGGCTCTTAAGCTCATTTGCTGGGGATGGGAAAGGAAGAGTGGC	1260
Db	1573	TCTCTGTCGCGAGGGTGGCTCTTAAGCTCATTTGCTGGGGATGGGAAAGGAAGAGTGGC	1632z
Qy	1261	TTTTGTGGGCAATTGCTCTAACCTTCTCAAGCTTCCCTCAAGAAACTGATTTGGCC	1320
Db	1633	TTTTGTGGGCAATTGCTCTAACCTTCTCAAGCTTCCCTCAAGAAACTGATTTGGCC	1692z
Qy	1321	TGGAACCTCCCATCCCATCTTGTATATGACTCAAGGTCCAGACTTAATTGTGATGA	1380
Db	1693	TGGAACCTCCCATCCCATCTTGTATATGACTCAAGGTCCAGACTTAATTGTGATGA	1752z
Qy	1381	CTGAATTAACCAATCTCAACGCTATCCAGGAAACAGAAAGCAGATGCGATGGAGGA	1440
Db	1753	CTGAATTAACCAATCTCAACGCTATCCAGGAAACAGAAAGCAGATGCGATGGAGGA	1812z
Qy	1441	CAGGAAGCAGCCTGGGACATTTAATAAAATGAATAAAATAAAACCCAGAACCAATT	1500
Db	1813	CAGGAAGCAGCCTGGGACATTTAATAAAATGAATAAAATAAAACCCAGAACCAATT	1872z
Qy	1501	TCTCAGGGCACTTCCAGAAATTCTCTCATTTTGTGGGCTGGGATCAAGCCTGACGCTG	1560
Db	1873	TCTCAGGGCACTTCCAGAAATTCTCTCATTTTGTGGGCTGGGATCAAGCCTGACGCTG	1932z
Qy	1561	AGGAAGACAGAGAAAGGAAGAAGATCTGTGGAAAGCTCAGGTGGCAACGGACCTG	1620
Db	1933	AGGAAGACAGAGAAAGGAAGAAGATCTGTGGAAAGCTCAGGTGGCAACGGACCTG	1992z
Qy	1621	ACTCCTCAGAGGAATCGCTCATGAAGCTGGGATCACAACTTTGGCTGAAGCCCTGCTC	1680
Db	1993	ACTCCTCAGAGGAATCGCTCATGAAGCTGGGATCACAACTTTGGCTGAAGCCCTGCTC	2052z
Qy	1681	ACTCTAGGGCACCTGACCTGGCTCTTGCCCTAACAACAAGGCTTAAGGGCTATGACAAAT	1740
Db	2053	ACTCTAGGGCACCTGACCTGGCTCTTGCCCTAACAACAAGGCTTAAGGGCTATGACAAAT	2112z
Qy	1741	GGTTTCTTAAGAAACAGTAAACAATTTTCTAAGGATGGCCTTTGGCTGGGGATGACA	1800

Db	2113	GGTTTCCTTGAAGAACAGTAAACAGATTTTTCTAGAGATAGCCCTTGCTGCGGAGATGACA	2172
Qy	1801	GTGTGGAGAGCTGTGGGGTATCTGAGAAAGACACATTCCTTGAAGGTGTCTAAGAAAGCCAG	1866
Db	2173	GTGTGGAGAGCTGTGGGGTATCTGAGAAAGACACATTCCTTGAAGGTGTCTAAGAAAGCCAG	2232
Qy	1861	GTGATGTGTGTGTGTGCTCCAGTGGGTGTTTCTACTGTGCAGTGAAGGAGCCCTT	1930
Db	2293	AGAAACTTTCAGGCGTAAATGAGAAATCAGCTCAATATGATATCAGGCCCTCCAGGGTCC	2352
Qy	1981	ACCACAGAGACCTACAGAGGCTCTGAAAGAACAATAGACACAAAGCGAGCCCTTCAGATT	2040
Db	2353	ACCACAGAGACCTACAGAGGCTCTGAAAGAACAATAGACACAAAGCGAGCCCTTCAGATT	2412
Qy	2041	CCCCCACTGTTCATCGAAGATGCTCCAGATGGCTAGAAGGCAATCTAAGGGCTCCAGCA	2100
Db	2413	CCCCCACTGTTCATCGAAGATGCTCCAGATGGCTAGAAGGCAATCTAAGGGCTCCAGCA	2472
Qy	2101	TGGATATTCATATGCCACAGGTGCTGTCCATATGATCTGAGATATAGCTGCACATGTGCT	2166
Db	2473	TGGATATTCATATGCCACAGGTGCTGTCCATATGATCTGAGATATAGCTGCACATGTGCT	2532
Qy	2161	GGGATTCAGCTGAGTGGAGTGGAGATGGTATCCAGAGAAAGACAGTTCACACTCTAAG	2220
Db	2533	GGGATTCAGCTGAGTGGAGTGGAGATGGTATCCAGAGAAAGACAGTTCACACTCTAAG	2592
Qy	2221	GTCCGAAATATGTTCCCTTTACCCCTGAGATGGAGATGAGGGGTCAATACAAAGATATT	2280
Db	2593	GTCCGAAATATGTTCCCTTTACCCCTGAGATGGAGATGAGGGGTCAATACAAAGATATT	2652
Qy	2281	TCCCTCACAGCTACAGGACATGACATGGGCTTCGAAAAATTCACAGACACCTCTCGAACT	2340
Db	2653	TCCCTCACAGCTACAGGACATGACATGGGCTTCGAAAAATTCACAGACACCTCTCGAACT	2712
Qy	2341	CATTGTACAGCAGAGAGGCCCATCTGTTGTCTGTACATGCTTTCAATGTCCACTTC	2400
Db	2713	CATTGTACAGCAGAGAGGCCCATCTGTTGTCTGTACATGCTTTCAATGTCCACTTC	2772
Qy	2401	TTTGCCATGTTCCAGGCTCTCTCCCAACCTGGAAGGCCGTCTCCCTTAGCCAAAGTCCCTC	2460
Db	2773	TTTGCCATGTTCCAGGCTCTCTCCCAACCTGGAAGGCCGTCTCCCTTAGCCAAAGTCCCTC	2832
Qy	2461	TCAGGCTTGGAGAACTTCTCAAGGTCACCTCTTCAATGAGCCTTCTGTATCACTCA	2520
Db	2833	TCAGGCTTGGAGAACTTCTCAAGGTCACCTCTTCAATGAGCCTTCTTTCCTCCACTCA	2892
Qy	2521	TTCCTCTTCCTAACCCCTCCCTCCCCCAACCTCAATGTATTAATTTGCTTTTGAATGCTTAG	2580
Db	2893	TTCCTCTTCCTAACCCCTCCCTCCCCCAACCTCAATGTATTAATTTGCTTTTGAATGCTTAG	2952
Qy	2581	CATTCACAATTTTGAATGATGTTATTTTGTGTGTGTGTGTGCAGATCTCAAAATATTT	2640
Db	2953	CATTCACAATTTTGAATGATGTTATTTTGTGTGTGTGTGTGCAGATCTCAAAATATTT	3012
Qy	2641	GTAACCCCTTCGATGGGTGGGGGCATATATCTTAGACCTCTCTGTATCCCCAGACTATCT	2700
Db	3013	GTAACCCCTTCGATGGGTGGGGGCATATATCTTAGACCTCTCTGTATCCCCAGACTATCT	3072
Qy	2701	GTAACAGTGCAGGCAAC-CAGAAAGTATCAATAA	2734
Db	3073	GTAACAGTGCAGGCAACAGTATGATATCAATAA	3107
RESULT 4			
AB271540			
ID AB271540 standard; DNA; 3126 BP.			
XX AC AB271540;			

RESULT 4
ABZ71540
ID ABZ71540 standard; DNA; 3126 BP

DT 03-APR-2003 (first entry)
XX Secreted protein gene 168 genomic fragment HTP1H83, SEQ ID NO:650.
XX
XX
XX Human; secreted protein; digestive disorder; gastrointestinal disorder;
XX mout; oesophagus; stomach; small intestine; large intestine; liver;
XX biliary tract; pancreas; cancer; tumor; hyperproliferative disorder;
XX immune disorder; inflammation; infection; wound healing; drug screening;
XX chromosome identification; chromosome mapping; cytostatic; gene therapy;
XX anti-inflammatory; immunosuppressive; vulnerary; chromosome Xq22.3-23;
XX gene; ds.
XX Homo sapiens.
XX
XX W0200276488-A1.
XX
XX 03-OCT-2002.
XX
XX 19-MAR-2002; 2002MO-US008276.
XX PF
XX 21-MAR-2001; 2001US-0277340P.
XX PR 19-JUL-2001; 2001US-0306171P.
XX PR 13-NOV-2001; 2001US-0331287P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI; 2003-029900/02.
XX
XX New human secreted proteins and nucleic acids, useful for detecting,
XX preventing, diagnosing, prognosticating, treating and/or ameliorating,
XX e.g. gastrointestinal diseases and disorders, or cancers.
XX
XX Disclosure, Page 1211-1212; 1216pp; English.
XX
XX AB271190-AB271478 represent cDNAs corresponding to 178 human secreted
XX protein genes, and ABP00011-ABP00299 represent the proteins they encode.
XX CC AB271479-AB271540 represent human secreted protein genomic fragments. The
XX CC invention also encompasses antibodies specific for the secreted proteins,
XX CC the use of the secreted proteins in drug screening, and recombinant
XX CC vectors and host cells comprising a nucleic acid of the invention. The
XX CC secreted proteins, nucleic acids encoding them, antibodies or antibody
XX CC fragments specific for the secreted proteins, and modulators of protein
XX CC activity are useful for diagnosing, treating, ameliorating or preventing
XX CC digestive disorders. Such conditions include disorders of the mouth,
XX CC oesophagus, stomach, small intestine, large intestine, liver, biliary
XX CC tract and pancreas, and include cancers of these organs and tissues. The
XX CC secreted proteins and their nucleic acids may also be used in the
XX CC treatment of immune disorders, inflammation, infection,
XX CC hyperproliferative disorders, and to promote wound healing. Nucleic acids
XX CC of the invention may be used for chromosome identification, chromosome
XX CC mapping, in gene therapy, for identifying individuals from minute
XX CC biological samples, as hybridisation probes, and as molecular weight
XX CC markers. The present sequence represents a human secreted protein genomic
XX CC fragment referred to in the disclosure of the invention
XX
XX
SQ Sequence 3126 BP; 739 A; 848 C; 761 G; 778 T; 0 U; 0 Other;
Query Match 99.0%; Score 2715; DB 8; Length 3126;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 272; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Db 493 GGCCTCTCTGGCCCTCCAACTGTGTGGGCTAATCTTAAGCCCTTGTGGGCTTTGGGCAC 552
Qy 181 ACTGTTGCATGCTGCTGCTCCAGCTGGAAGAAAGATTCTTATGTGGTCCAGCATTTGT 240
Db 553 ACTGTTGCATGCTGCTGCTCCAGCTGGAAGAAAGATTCTTATGTGGTCCAGCATTTGT 612
Qy 241 GACAGCAGTTGGCTTCTCCAAAGGCGCTGTGATGTAATGTGCCACACAGCACAGGCAT 300
Db 613 GACAGCAGTTGGCTTCTCCAAAGGCGCTGTGATGTAATGTGCCACACAGCACAGGCAT 672
Qy 301 CACCCAGTGTGAATCTTATGACACCTTTCGGGCGCCCGGCTGACATCCAGGCTGCCA 360
Db 673 CACCCAGTGTGAATCTTATGACACCTTTCGGGCGCCCGGCTGACATCCAGGCTGCCA 732
Qy 361 GGCATGATGTGATCAATCCAGTCAATCTCTCCCTGGCCCTGATTAATCTGTGTGG 420
Db 733 GGCATGATGTGATCAATCCAGTCAATCTCTCCCTGGCCCTGATTAATCTGTGTGG 792
Qy 421 CATGATGATGATGATCTTTCGAGGAATCCGAGCCAAAGACAGATGCGGTAGCAG 480
Db 793 CATGATGATGATGATCTTTCGAGGAATCCGAGCCAAAGACAGATGCGGTAGCAG 852
Qy 481 TGGAGTCTTTTCAATCTTGGAGGCGCTCCGTGATTCATCTCTGTGGCTGTGAATCTTCA 540
Db 853 TGGAGTCTTTTCAATCTTGGAGGCGCTCCGTGATTCATCTCTGTGGCTGTGAATCTTCA 912
Qy 541 TGGAGTCTTACGAGGATCTTCTACTACCACTGATGCTGACAGCATGAATTTGAGATTGG 600
Db 913 TGGAGTCTTACGAGGATCTTCTACTACCACTGATGCTGACAGCATGAATTTGAGATTGG 972
Qy 601 AGAGGCTCTTTACTTGGGCAATTAATTTCTTCTCTGTTCTCCCTGATGCTGAATCATCT 660
Db 973 AGAGGCTCTTTACTTGGGCAATTAATTTCTTCTCTGTTCTCCCTGATGCTGAATCATCT 1032
Qy 661 CTGCTTTTCTGCTCATCTCCAGGAATATGCTCTCACTATGAGTCCATCCAGGCCA 720
Db 1033 CTGCTTTTCTGCTCATCTCCAGGAATATGCTCTCACTATGAGTCCATCCAGGCCA 1092
Qy 721 ACCCTTGGCACAAGAGCTCTCCAAAGGCTGTGCAACCTCCAAAGTCAAGATGAGTT 780
Db 1093 ACCCTTGGCACAAGAGCTCTCCAAAGGCTGTGCAACCTCCAAAGTCAAGATGAGTT 1152
Qy 781 CAATTCCTACAGCTGACAGGATATGTGTGAAGAACCAAGGAGGCAAGCTGGGGGTGGC 840
Db 1153 CAATTCCTACAGCTGACAGGATATGTGTGAAGAACCAAGGAGGCAAGCTGGGGGTGGC 1212
Qy 841 TGGGCTGTGAAAAACAGTGAACAGCACCCCGAGGGCCACAGGTGAGGGACATCACT 900
Db 1213 TGGGCTGTGAAAAACAGTGAACAGCACCCCGAGGGCCACAGGTGAGGGACATCACT 1272
Qy 901 GGATCGTGTGAAAGGCTGCTGAGGATGAGCTTGGGCAATTTGGGCAATTTGAGCAAG 960
Db 1273 GGATCGTGTGAAAGGCTGCTGAGGATGAGCTTGGGCAATTTGGGCAATTTGAGCAAG 1332
Qy 961 GCAAAATGAGGCTGATGTGAACAGCATGCAAGTTGAATTCGAAGATCTGCCATGC 1020
Db 1333 GCAAAATGAGGCTGATGTGAACAGCATGCAAGTTGAATTCGAAGATCTGCCATGC 1392
Qy 1021 CAGCTTCTGTTTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 1393 CAGCTTCTGTTTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1452
Qy 1081 GAAACCCATTCCTTAAGCAGAGATCCAGAGATCCCTTGGCCCTGTGTTTAACTGGG 1140
Db 1453 GAAACCCATTCCTTAAGCAGAGATCCAGAGATCCCTTGGCCCTGTGTTTAACTGGG 1512
Qy 1141 ACTTCATCCCAACCAACCACTAATCAATCCCACTGACTGACCTCTGTGATCAAGACC 1200
Db 1513 ACTTCATCCCAACCAACCACTAATCAATCCCACTGACTGACCTCTGTGATCAAGACC 1572
Qy 1201 TCTCTGTGATGAGTTGGCTTTAGCTCAATGCTGTGGGATGAGAAAGAGACAGTGGC 1260
Db 1573 TCTCTGTGATGAGTTGGCTTTAGCTCAATGCTGTGGGATGAGAAAGAGACAGTGGC 1632

OY	1261	TTTTGTGGGCAATGCTCTAAACCTTCTCAAGCTTCCTCCAAAGAACAATGATTGGGCC	13308
Dp	1693	TTTGTGTGGGCATTGCTCTAACCTTACTTCTCAAGCTTCCTCCAAAGAACAATGATTGGGCC	16992
OY	1321	TGGAACCTCATCCCACTCTTGTTATGACTCCAAGTGTCCAAGCTAATTTTGTGCATGAA	13808
Dp	1693	TGGAACCTCATCCCACTCTTGTTATGACTCCAAGTGTCCAAGCTAATTTTGTGCATGAA	17522
OY	1381	CTGAATAATAAAACAATCCTTAGGGTATCGAGGGAAACGAAGAAGATGTGAGGATGGGAGGA	14408
Dp	1753	CTGAATAATAAAACAATCCTTAGGGTATCGAGGGAAACGAAGAAGATGTGAGGATGGGAGGA	18122
OY	1441	CAGGAAGGCAGCCTGGGACATTTAAAAAATGAAAAAAAAAATGAAAAAAAAAACCAGAACCCATT	15008
Dp	1813	CAGGAAGGCAGCCTGGGACATTTAAAAAATGAAAAAAAAAATGAAAAAAAAAACCAGAACCCATT	18722
OY	1501	TCTCAGGGCACTTTTCCANAATTTCTCTCATTTTGTGGGCTGGGATTCMAAGCTGCAAGCTTG	15608
Dp	1873	TCTCAGGGCACTTTTCCANAATTTCTCTCATTTTGTGGGCTGGGATTCMAAGCTGCAAGCTTG	19322
OY	1561	AGGAAGACACAAGGAAAGAAAGAAAGATCTGTGTGAAGGCTCAAGTGGCACGGAATCTG	16208
Dp	1993	AGGAAGACACAAGGAAAGAAAGAAAGATCTGTGTGAAGGCTCAAGTGGCACGGAATCTG	19992
OY	1621	ACTCACAAGGAACCTGCTCTAGAAAGCTGCGATCACAACTTTGGCTGAAGCCTTGCTCTC	16808
Dp	1993	ACTCACAAGGAACCTGCTCTAGAAAGCTGCGATCACAACTTTGGCTGAAGCCTTGCTCTC	20522
OY	1681	ACTCTAAGGGACCTGAACCTGGCCCTTTCCTTAACCAAGGCTAAGGGCTAATGACAT	17408
Dp	2053	ACTCTAAGGGACCTGAACCTGGCCCTTTCCTTAACCAAGGCTAAGGGCTAATGACAT	21122
OY	1741	GATTTCCTTAGGAACAGTAAACAAGTTTTCCTAAGGATGACCCTTGCTGGGGGATGACA	18008
Dp	2113	GATTTCCTTAGGAACAGTAAACAAGTTTTCCTAAGGATGACCCTTGCTGGGGGATGACA	21722
OY	1801	GTTGTGGGAGCTGTGGGGTATCTGAAGGAACACCAATTCCTTAACGATGCTTAAGAACCCAG	18608
Dp	2173	GTTGTGGGAGCTGTGGGGTATCTGAAGGAACACCAATTCCTTAACGATGCTTAAGAACCCAG	22322
OY	1861	GTTGATGTGTGTGGCTCAGTGGGCTTCTACTCTGCAATGAGGCAAGCCCTCT	19208
Dp	2233	GTTGATGTGTGTGGCTCAGTGGGCTTCTACTCTGCAATGAGGCAAGCCCTCT	22922
OY	1921	AGAAACTCTTAGCGGCTAATGAAAAATCAGTCAATATGATCAGGCCCTCCACGGGCTC	19808
Dp	2293	AGAAACTCTTAGCGGCTAATGAAAAATCAGTCAATATGATCAGGCCCTCCACGGGCTC	23522
OY	1981	ACCACAGAGCACTACAGAGCCTGTGAAGAACAATGAGCAACCAAGCGGCCCTCAGATT	20408
Dp	2353	ACCACAGAGCACTACAGAGCCTGTGAAGAACAATGAGCAACCAAGCGGCCCTCAGATT	24122
OY	2041	CCCCCACTGTCAATCGAAGATGCTCCAGATGGGCTGAAGGGCATTTAAGGGCTCCAGCA	21008
Dp	2413	CCCCCACTGTCAATCGAAGATGCTCCAGATGGGCTGAAGGGCATTTAAGGGCTCCAGCA	24722
OY	2101	TGGGATATCCATGCCCACGGGCTGTGTCCATATGAGTGAATAGCTGTGCACTGTCTCCT	21608
Dp	2473	TGGGATATCCATGCCCACGGGCTGTGTCCATATGAGTGAATAGCTGTGCACTGTCTCCT	25322
OY	2161	GGGATTTGACGTGAGTGGGAGTGGAGNAATGTTCCAGAGAAAGACAGTTCACCTCTAAG	22208
Dp	2533	GGGATTTGACGTGAGTGGGAGTGGAGNAATGTTCCAGAGAAAGACAGTTCACCTCTAAG	25922
OY	2221	GTCGGAANAATGTTCCCTTTACCTCTGAGTGGGAGTGAAGGGCTCATPACCAACAAAGTATT	22808
Dp	2593	GTCGGAANAATGTTCCCTTTACCTCTGAGTGGGAGTGAAGGGCTCATPACCAACAAAGTATT	26522
OY	2281	TTCCTCAACAATAGAGATGACATGAGCTTCTGAAAAATTCAGAGCAACCTCCTTGAAACT	23408
Dp	2653	TTCCTCAACAATAGAGATGACATGAGCTTCTGAAAAATTCAGAGCAACCTCCTTGAAACT	27122

QY	2341	CATTGTGAGCAGAGAGGAGCCCATCTGTTGTCTGTAAACATGCTTTCACATGTCACCTTC	2400
Db	2713	CATTGTGAGCAGAGAGGAGCCCATCTGTTGTCTGTAAACATGCTTTCACATGTCACCTTC	2772
QY	2401	TTGCGCATGTTTCACAGCTGCTCTCCCAACCTGGAGAGCGCGTCTCCCTTAGCCAACTCTCC	2460
Db	2773	TTGCGCATGTTTCACAGCTGCTCTCCCAACCTGGAGAGCGCGTCTCCCTTAGCCAACTCTCC	2833
QY	2461	TCAGGCTTGGAGAACTTCTCTCAGGCTCAGCTCTCTTCAATGAGCCTTCTCTGATCACTTCA	2522
Db	2833	TCAGGCTTGGAGAACTTCTCTCAGGCTCAGCTCTCTTCAATGAGCCTTCTCTTCCCACTTCA	2892
QY	2521	TTCCCTCTCTACCCCTGCTCCCTCCCAACCCCTCAATGATAAATGCTCTTGATGCTTAG	2580
Db	2893	TTCCCTCTCTACCCCTGCTCCCTCCCAACCCCTCAATGATAAATGCTCTTGATGCTTAG	2955
QY	2581	CATTCACAATTTTGTATGTAATCGTTATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2640
Db	2953	CATTCACAATTTTGTATGTAATCGTTATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	3012
QY	2701	GTAACAGTGCAGGACAC-CAGAAGTGATCAATAA	2734
Db	3073	GTAACAGTGCAGGACACAGTAGTGATCAATAA	3107

RESULT 5
ADB91911

ID	ADB91911	standard; DNA, 3126 BP.
XX	AC	ADB91911;
XX	DT	04-DEC-2003 (first entry)
DE	XX	Human secreted protein related DNA #SEQ ID 857.
XX	XX	Secreted protein; gene therapy; antidiabetic; diabetes; human; ds.
KW	XX	Homo sapiens.
OS	XX	WO2003004622-A2.
PN	PD	16-JAN-2003.
XX	PF	19-MAR-2002; 2002WO-US008124.
XX	PR	21-MAR-2001; 2001US-0277340P.
PR	PR	19-JUL-2001; 2001US-0306171P.
XX	PR	13-NOV-2001; 2001US-0331287P.
XX	PA	(HUMA-) HUMAN GENOME SCI INC.
XX	PI	Rosen CA, Ruben SM;
PT	DR	WPI; 2003-229407/22.

Nucleic acid encoding a human secreted protein is useful in diagnosing or treating diabetes or conditions related to diabetes.

Disclosure; SEQ ID NO 857, 1537bp; English.

The invention relates to isolated nucleic acid molecules ADB91065-ADB91448 and ADB91835-ADB91911 encoding human secreted proteins ADB91449-ADB91834. Also disclosed is a recombinant vector comprising a polynucleotide of the invention, and a recombinant host cell comprising the recombinant vector. The polypeptide of the invention is useful in identifying a binding partner by contacting the polypeptide with a binding partner, and determining whether the binding partner increases or decreases activity of the polypeptide. The polypeptide, polynucleotide, antibody or its fragment, agonist or antagonist are useful for preparing

CC a pharmaceutical composition for diagnosing or treating diabetes or
CC conditions related to diabetes. The present sequence is that of the human
CC immunoglobulin Fc portion used to generate fusion proteins, increasing
CC the stability of the fused protein as compared to the secreted protein
CC only. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPD at ftp.wipo.int/pub/published_pat_sequences.

XX
Sequence 3126 BP; 739 A; 848 C; 761 G; 778 T; 0 U; 0 Other;

Query Match 99.0%; Score 2715; DB 9; Length 3126;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2729; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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QY 1 AGAAGTCAGCTGCGAGAGAGACTGTAAATAGAGGATAGAGTGTTCAGAGAGAGA 60
DB 373 AGAAGTCAGCTGCGAGAGAGACTGTAAATAGAGGATAGAGTGTTCAGAGAGAGA 432
QY 61 GCTTCAGCTGAGAGACAGAGAGAGAGTCCCTGAAAGAGCTTCTAAGAGAGTCTG 120
DB 433 GCTTCAGCTGAGAGACAGAGAGAGAGTCCCTGAAAGAGCTTCTAAGAGAGTCTG 492
QY 121 GGCCTCTCTTGGCCTCCAACTTGTGGGCTAATCTAAGGCTTCTGGGCTTTTGG 180
DB 493 GGCCTCTCTTGGCCTCCAACTTGTGGGCTAATCTAAGGCTTCTGGGCTTTTGG 552
QY 181 ACTGTTGGCATGTGTCTCCCACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 553 ACTGTTGGCATGTGTCTCCCACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 612
QY 241 GACAGCAGTGGCTTCTCAAGAGGCTCTGAGATGAGATGAGCAGACAGACAGAG 300
DB 613 GACAGCAGTGGCTTCTCAAGAGGCTCTGAGATGAGATGAGCAGACAGACAGAG 672
QY 301 CACCCAGTGTGACATCTAAGACACCTTCTGGGCTTGGGCTGACATCCAGGCTG 360
DB 673 CACCCAGTGTGACATCTAAGACACCTTCTGGGCTTGGGCTGACATCCAGGCTG 732
QY 361 GGCCTCTCTTGGCCTCCAACTTGTGGGCTAATCTAAGGCTTCTGGGCTTTTGG 420
DB 733 GGCCTCTCTTGGCCTCCAACTTGTGGGCTAATCTAAGGCTTCTGGGCTTTTGG 792
QY 421 CATGAGATGACAGTCTTCTGCGAGAGATCCCGAGCCAGAGACAGAGAGAGAGAG 480
DB 793 CATGAGATGACAGTCTTCTGCGAGAGATCCCGAGCCAGAGACAGAGAGAGAGAG 852
QY 481 TGAAGTCTTCTTCACTCTGAGAGGCTCTGAGATTCATCTCTGTTGCTTGA 540
DB 853 TGAAGTCTTCTTCACTCTGAGAGGCTCTGAGATTCATCTCTGTTGCTTGA 912
QY 541 TGGGATCTTACGGGACTTCTAAGTCACTGATGCTGAGACAGATGAAATTTGAG 600
DB 913 TGGGATCTTACGGGACTTCTAAGTCACTGATGCTGAGACAGATGAAATTTGAG 972
QY 601 AGAGGCTCTTCACTTGGGCAATTAATTTCTGCTGCTGCTGCTGCTGCTGCTG 660
DB 973 AGAGGCTCTTCACTTGGGCAATTAATTTCTGCTGCTGCTGCTGCTGCTGCTG 1032
QY 661 CTGCTTCTCTGCTCATCTCCAGAGAAATGCTCCAACTACTACGATGCTCAAGCCA 720
DB 1033 CTGCTTCTCTGCTCATCTCCAGAGAAATGCTCCAACTACTACGATGCTCAAGCCA 1092
QY 721 ACCTCTTGGCAAGAGGCTCTCAAGGCTGCTGCACTTCCAAAGTCAAGAGTGA 780
DB 1093 ACCTCTTGGCAAGAGGCTCTCAAGGCTGCTGCACTTCCAAAGTCAAGAGTGA 1152
QY 781 CAATTCCTAAGAGCTGACAGGCTATGTGTAAGAACAGAGGAGGAGAGAGAGAG 840
DB 1153 CAATTCCTAAGAGCTGACAGGCTATGTGTAAGAACAGAGGAGGAGAGAGAGAG 1212
QY 841 TGGGCTCTGTGAAAAACAGTGAAGAGACCCCGAGAGGAGAGAGTGAAGAGAGAG 900
DB 1213 TGGGCTCTGTGAAAAACAGTGAAGAGACCCCGAGAGGAGAGAGTGAAGAGAGAG 1272
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QY 901 GATCTGTGACAGAGGTGCTGAGATAGACTGACTTTTGGCATTGATGAGCAAG 960
DB 1273 GATCTGTGACAGAGGTGCTGAGATAGACTGACTTTTGGCATTGATGAGCAAG 1332
QY 961 GCAGAAATGGGGCTAGTGTAAACAGATCAGAGTGAATTTGCCAGAGATGCTGCCATGC 1020
DB 1333 GCAGAAATGGGGCTAGTGTAAACAGATCAGAGTGAATTTGCCAGAGATGCTGCCATGC 1392
QY 1021 CAGCCTTCTGTTTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1393 CAGCCTTCTGTTTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1452
QY 1081 GAAACCCCATTCCTTAAAGCAGAGACTCAGAGAGATCCCTTGGCTCTGTTTACCTGG 1140
DB 1453 GAAACCCCATTCCTTAAAGCAGAGACTCAGAGAGATCCCTTGGCTCTGTTTACCTGG 1512
QY 1141 ACTCATTCGCCAAGCCCACTAATCAATCCATGACCTGCTGTGATCAAGAGCC 1200
DB 1513 ACTCATTCGCCAAGCCCACTAATCAATCCATGACCTGCTGTGATCAAGAGCC 1572
QY 1201 TCTCTGTGAGTGTGGCTCTTAAGTCTAAGTGTGGGATGGGAGAGAGAGAGAGAG 1260
DB 1573 TCTCTGTGAGTGTGGCTCTTAAGTCTAAGTGTGGGATGGGAGAGAGAGAGAGAG 1632
QY 1261 TTTTGTGGGATGTGCTTAACTTCTCAAGCTTCCCTCAAGAAAGTGAATGGGCC 1320
DB 1633 TTTTGTGGGATGTGCTTAACTTCTCAAGCTTCCCTCAAGAAAGTGAATGGGCC 1692
QY 1321 TGAACCTTCATCCACTCTTGTATGACTCCAGATGTCAGACTAATTTGTGATGAA 1380
DB 1693 TGAACCTTCATCCACTCTTGTATGACTCCAGATGTCAGACTAATTTGTGATGAA 1752
QY 1381 CTGAATTAAGCAATCTTAAGGTATCCAGAGAGACAGAAAGCAGAGATGGAGAGA 1440
DB 1753 CTGAATTAAGCAATCTTAAGGTATCCAGAGAGACAGAAAGCAGAGATGGAGAGA 1812
QY 1441 CAGAAAGGACGCTGGGACATTTAAATAAATAAATAAATAAATAAATAAATAAATAA 1500
DB 1813 CAGAAAGGACGCTGGGACATTTAAATAAATAAATAAATAAATAAATAAATAAATAA 1872
QY 1501 TCTCAAGGACCTTTCAGAAATTCCTCATATTTGTGGGCTGGGATCAAGCTGCACTTG 1560
DB 1873 TCTCAAGGACCTTTCAGAAATTCCTCATATTTGTGGGCTGGGATCAAGCTGCACTTG 1932
QY 1561 AGGAAAGCAGAGAAAGAGAAAGAAATCTGTGTGAAGTCAAGTGGCAGCCGACTTG 1620
DB 1933 AGGAAAGCAGAGAAAGAGAAAGAAATCTGTGTGAAGTCAAGTGGCAGCCGACTTG 1992
QY 1621 ACTCACTGAGAACTGCTCAGAGCTGAGATCAAACTTTGGCTGAAGCCCTGCTG 1680
DB 1993 ACTCACTGAGAACTGCTCAGAGCTGAGATCAAACTTTGGCTGAAGCCCTGCTG 2052
QY 1681 ACTCTAGGAGCCTGACCTGCTCTTGTGCTTAAGCAAGAGCTTAAGAGCTATAGA 1740
DB 2053 ACTCTAGGAGCCTGACCTGCTCTTGTGCTTAAGCAAGAGCTTAAGAGCTATAGA 2112
QY 1741 GGTTCCTTAAGAACTGTAACAGATTTTCTAGGATGAGGCTTGGCTGGGAGATGACA 1800
DB 2113 GGTTCCTTAAGAACTGTAACAGATTTTCTAGGATGAGGCTTGGCTGGGAGATGACA 2172
QY 1801 GTGTGGAGAGCTGTGGGATGCTGAGAGAGACAGATTCCTTGAAGAGGTCTTAAGAGCAG 1860
DB 2173 GTGTGGAGAGCTGTGGGATGCTGAGAGAGACAGATTCCTTGAAGAGGTCTTAAGAGCAG 2232
QY 1861 GTGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1920
DB 2233 GTGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2292
QY 1921 AGAAACTCTTCAAGGCTTAATGAAATTCAGCTCAATAGATCAAGGCTCCCTCAAGGCTC 1980
DB 2293 AGAAACTCTTCAAGGCTTAATGAAATTCAGCTCAATAGATCAAGGCTCCCTCAAGGCTC 2352
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QY	1981	ACCACGACAGCACTACAGAGCCCTCGAAAGACATAGAGACCAAGGAGACCCCTTCAGTT	2048
Db	2353	ACCACGACAGCACTACAGAGCCCTCGAAAGACATAGAGACCAAGGAGACCCCTTCAGTT	2412
QY	2041	CCCCCACTGTCATCGAAGATGCTCCAGATGGCTAGAGGGCATCTAAGG3CTTCAGCA	2100
Db	2413	CCCCCACTGTCATCGAAGATGCTCCAGATGGCTAGAGGGCATCTAAGG3CTTCAGCA	2472
QY	2101	TGGCATATCCATGGCCACGAGGTGCTGTGTCATATCTAGATGATAGCTGACCTGCTGCT	2166
Db	2473	TGGCATATCCATGGCCACGAGGTGCTGTGTCATATCTAGATGATAGCTGACCTGCTGCT	2532
QY	2161	GGGATTTGCACTGAGGTGGAGATGGTTTCCAGAGACAGCATTTCCACTCTAAG	2220
Db	2513	GGGATTTGCACTGAGGTGGAGATGGTTTCCAGAGACAGCATTTCCACTCTAAG	2592
QY	2221	GTCCGAAAATGTTCCCTTTTACCCTGAGATGGAGATGAGGGGTATATCCAAAGATATT	2280
Db	2593	GTCCGAAAATGTTCCCTTTTACCCTGAGATGGAGATGAGGGGTATATCCAAAGATATT	2652
QY	2281	TCCCTCACACGATCTAAGGATGACTGGCTTCTGAAAATAATTCAGACACACTCTCGAACC	2340
Db	2653	TCCCTCACACGATCTAAGGATGACTGGCTTCTGAAAATAATTCAGACACACTCTCGAACC	2712
QY	2341	CATTGTCAAGACAGAGGGCCCATCTGTTGTCTGTAACATGTCCTTTCAATGTCCACTTC	2400
Db	2713	CATTGTCAAGACAGAGGGCCCATCTGTTGTCTGTAACATGTCCTTTCAATGTCCACTTC	2722
QY	2401	TTGGCATATTCAGATGCTCTCCCAACCTGGAAAGGCGCTCCCTTAGGCAAGTCCGCC	2460
Db	2773	TTGGCATATTCAGATGCTCTCCCAACCTGGAAAGGCGCTCTCCCTTAGGCAAGTCCGCC	2832
QY	2461	TCAGGCTTTGGAGAACTTCTCAGAGCTCACCTCTTCATTGAGACCTTCTGTATCACTCA	2520
Db	2833	TCAGGCTTTGGAGAACTTCTCAGAGCTCACCTCTTCATTGAGACCTTCTGTATCACTCA	2892
QY	2521	TCCCTCTCTACCCCTCCCTCCCAACCCCTCAATGTTAATTTGCTTCTTGATGCTTAG	2580
Db	2893	TCCCTCTCTACCCCTCCCTCCCAACCCCTCAATGTTAATTTGCTTCTTGATGCTTAG	2952
QY	2581	CATTACAAATTTTGTATGATTCGTATTTGTGTGTGTGTGCCATCTCACAATATATT	2640
Db	2953	CATTACAAATTTTGTATGATTCGTATTTGTGTGTGTGTGCCATCTCACAATATATT	3012
QY	2641	GTAACACCTCTTGTTGGTGGTGGGGGCCATATCTTACATCTCTCTGTATCCCAAGCTATCT	2700
Db	3013	GTAACACCTCTTGTTGGTGGTGGGGGCCATATCTTACATCTCTCTGTATCCCAAGCTATCT	3072
QY	2701	GTAACAGTGCACAGGAC-CAGAAAGGTATCAATAA	2734
Db	3073	GTAACAGTGCACAGGAC-CAGAAAGGTATCAATAA	3107
RESULT 6			
ID	ADCT4722	standard; DNA; 3126 BP.	
XX	ADCT4722;		
XX	01-JAN-2004	(first entry)	
DE	Human secreted protein-related DNA - SEQ ID 1355.		
KM	antianaemic; antirheumatic; antiarthritic; antiinflammatory; antihypoid;		
KM	antidiabetic; immunosuppressive; dermatological; nephrotropic;		
KM	antiParkinsonian; neuroprotective; noctropic; antibacterial; virocid;		
KM	fungicide; antiparasitic; antiaerotoxic; vulnary; cytostatic;		
KM	haemopoietic; haematologic; anaemia; autoimmune disorder;		
KM	rheumatoid arthritis; inflammation; Grave's disease; diabetes;		
KM	systemic lupus erythematosus; glomerulonephritis; neurodegenerative;		
KM	Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;		
KM	cancer; Dacterial; viral; fungal; parasitic infection; gene therapy;		
KM	human; ds.		

OS	XX	Hom sapiens.
XX	XX	WO2003038063-A2.
XX	XX	08-MAY-2003.
XX	XX	19-MAR-2002; 2002MO-US008277.
XX	XX	21-MAR-2001; 2001US-0277340P.
XX	XX	19-JUL-2001; 2001US-0306171P.
XX	XX	13-NOV-2001; 2001US-0331287P.
XX	XX	(HUMA-) HUMAN GENOME SCI INC.
XX	XX	Rosen CA, Ruden SM;
XX	XX	WPI; 2003-430516/40.
XX	XX	New human secreted polypeptide for diagnosing, preventing or treating
XX	XX	hematopoietic or hematologic disorders (e.g. anemia), autoimmune
XX	XX	disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
XX	XX	atherosclerosis).
XX	XX	Diaclosure; SEQ ID NO 1355; 2272bp; English.
XX	XX	The invention relates to a novel human secreted polypeptide comprising a
XX	XX	defined sequence given in the specification. The polypeptide, nucleic
XX	XX	acid molecule, antibody, agonist or antagonist of the invention may be
XX	XX	useful for preparing a composition for diagnosing or treating a
XX	XX	hematopoietic or hematologic disorder such as anaemia, autoimmune
XX	XX	disorders such as rheumatoid arthritis, inflammation, Grave's disease,
XX	XX	diabetes, systemic lupus erythematosus or glomerulonephritis,
XX	XX	neurodegenerative disorders including Parkinson's disease and Alzheimer's
XX	XX	diseases, wounds and hyperproliferative disorders including
XX	XX	atherosclerosis or cancer, as well as bacterial, viral, fungal or
XX	XX	parasitic infections. The polypeptide may also be used during gene
XX	XX	therapy procedures and for identifying a binding partner by contacting
XX	XX	the polypeptide with a binding partner and determining whether the
XX	XX	binding partner increases or decreases the activity of the polypeptide.
XX	XX	The current sequence is that of the human secreted protein-related DNA of
XX	XX	the invention.
XX	XX	Sequence 3126 BP; 739 A; 848 C; 761 G; 778 T; 0 U; 0 Other;
XX	XX	Query Match 99.0%; Score 2715; DB 10; Length 3126;
XX	XX	Best Local Similarity 99.8%; Pred. No. 0;
XX	XX	Matches 2729; Conservative 0; Mismatches 5; Indels 1; Gaps 1.
XX	XX	1 AGAAGTCAGCGCTGGCAGACAGAACCTCTGAAATGAGAGGATTAAAGGTCTTCAGAGACACA 60
XX	XX	373 AGAAGTCAGCGCTGGCAGACAGAACCTCTGAAATGAGAGGATTAAAGGTCTTCAGAGACACA 432
XX	XX	61 GCTTCAGCGCTGAAACAAAGGAGAGCTCCCTGAAAGACGCTCTACTGAGAGGTCTGCCAT 120
XX	XX	433 GCTTCAGCGCTGAAACAAAGGAGAGCTCCCTGAAAGACGCTCTACTGAGAGGTCTGCCAT 492
XX	XX	121 GGCCTCTCTTGGGCTTCCAACTTGTGGGCTACATCCTAGGCGCTTCTGGGGCTTTTGGGCAC 180
XX	XX	493 GGCCTCTCTTGGGCTTCCAACTTGTGGGCTACATCCTAGGCGCTTCTGGGGCTTTTGGGCAC 552
XX	XX	181 ACTGGTTGGCAATGTCGTCCTCCCACTGGGAAACAAAGTTCTTAATGTCGGTGCAGACATTGT 240
XX	XX	553 ACTGGTTGGCAATGTCGTCCTCCCACTGGGAAACAAAGTTCTTAATGTCGGTGCAGACATTGT 612
XX	XX	241 GACAGCAGTTGGCTTCTTCCAAAGGCGCTCTGGATGGAATGTGCCACACACAGACAGGCGAT 300
XX	XX	613 GACAGCAGTTGGCTTCTTCCAAAGGCGCTCTGGATGGAATGTGCCACACACAGACAGGCGAT 672
XX	XX	301 CACCCAGTGTGACATCTATAGCACCCCTTCTGGGCGCTGCGCGCTGACATCCAGGCTGCCCA 360
XX	XX	673 CACCCAGTGTGACATCTATAGCACCCCTTCTGGGCGCTGCGCGCTGACATCCAGGCTGCCCA 732

Db 1399 GGGCATATGATGACATCCAGTCATCTCCCTGGCCCTGCATTTATCTTGTTGGG 1340
 Qy 421 CATGAGATGACAGCTCTTCTGCGCAGAAATCCGAGCCAAAGACAGATGGCGGTAGCAGG 480
 Db 1339 CATGAGATGACAGCTCTTCTGCGCAGAAATCCGAGCCAAAGACAGATGGCGGTAGCAGG 1280
 Qy 481 TGGAGTCTTTTTCATCTTGGAGGCTCTCTGGGATTCATTCCTGTGTGGTATCTTCA 540
 Db 1279 TGGAGTCTTTTTCATCTTGGAGGCTCTCTGGGATTCATTCCTGTGTGGTATCTTCA 1220
 Qy 541 TGGAGTCTTACGGGACTTCTTACCACTGTGCTGACAGAGTGAATTTGATTTGG 600
 Db 1219 TGGAGTCTTACGGGACTTCTTACCACTGTGCTGACAGAGTGAATTTGATTTGG 1160
 Qy 601 AGAGGCTCTTAACTTGGGCAATTAATTTCTCCCTGTTCCTCTGATGAGTGAATCATCT 660
 Db 1159 AGAGGCTCTTAACTTGGGCAATTAATTTCTCCCTGTTCCTCTGATGAGTGAATCATCT 1100
 Qy 661 CTGCTTTTCTGCTCATCCAGAGAAATCGTCCAACTAATGATGCTTACCAAGCCCA 720
 Db 1099 CTGCTTTTCTGCTCATCCAGAGAAATCGTCCAACTAATGATGCTTACCAAGCCCA 1040
 Qy 721 ACCCTTGGCCAGAGAGCTCTCCAGAGGCTGTCAACCTCCCAAGTCAAGATGAGTT 780
 Db 1039 ACCCTTGGCCAGAGAGCTCTCCAGAGGCTGTCAACCTCCCAAGTCAAGATGAGTT 980
 Qy 781 CAATTCCTACAGCTGACAGGGTATGTGTGAAGAACAGGGGCGCAGAGCTGGGGGGTGGC 840
 Db 979 CAATTCCTACAGCTGACAGGGTATGTGTGAAGAACAGGGGCGCAGAGCTGGGGGGTGGC 920
 Qy 841 TGGGTCTGTGAAAAACAGTGAACGACCCGAGAGGCGCAGAGTGAAGGACATCAACT 900
 Db 919 TGGGTCTGTGAAAAACAGTGAACGACCCGAGAGGCGCAGAGTGAAGGACATCAACT 860
 Qy 901 GGAATCGTGAAGAGTGTGCTGAGAGTGAAGTGAATTTGCCAATTTGATTTGAGCAAG 960
 Db 859 GGAATCGTGAAGAGTGTGCTGAGAGTGAAGTGAATTTGCCAATTTGATTTGAGCAAG 800
 Qy 961 GCAGAAATGGGGGCTAGTGAACAGATGACAGTGAATTTGCCAAGATCTGCGCATGC 1020
 Db 799 GCAGAAATGGGGGCTAGTGAACAGATGACAGTGAATTTGCCAAGATCTGCGCATGC 740
 Qy 1021 GACCTTTCTGTTTCTCTCACTTGTGCTCTCCCTGCTTAAGTCCCAACCTCAACTT 1080
 Db 739 GACCTTTCTGTTTCTCTCACTTGTGCTCTCCCTGCTTAAGTCCCAACCTCAACTT 680
 Qy 1081 GAAACCCCATCTCCCTTAAGCAGAGTCAAGAGATCCCTTGGCCCTGTGTTTA--CTTG 1138
 Db 679 GAAACCCCATCTCCCTTAAGCAGAGTCAAGAGATCCCTTGGCCCTGTGTTTA--CTTG 620
 Qy 1139 GAACTGC--ATCCCCAAACCAATATCAATCCCACTGACCTGCTGTGATCAAA 1195
 Db 619 GAACTGC--ATCCCCAAACCAATATCAATCCCACTGACCTGCTGTGATCAAA 560
 Qy 1196 GACCTTCTCTGCTGAGTGTGGCTTTAGCTCATTTGCTGGGATTTGGAGAGAGCA 1255
 Db 559 GACCTTCTCTGCTGAGTGTGGCTTTAGCTCATTTGCTGGGATTTGGAGAGAGCA 500
 Qy 1256 GTGGCTTTTGTGGGCAATTTGCTTAACCTTCAAGCTTCCCTCCAAAGAAATGATTT 1315
 Db 499 GTGGCTTTTGTGGGCAATTTGCTTAACCTTCAAGCTTCCCTCCAAAGAAATGATTT 440
 Qy 1316 GGGCTTGGAACTTCATCCACTCTTGTATGACTCCAGAGTGCAGACTAATTTGTGC 1375
 Db 439 GGGCTTGGAACTTCATCCACTCTTGTATGACTCCAGAGTGCAGACTAATTTGTGC 380
 Qy 1376 ATGAACCTGAATAAATCAATCCATACGTATCCAGGAAACGAAAGCATGAGATGG 1435
 Db 379 ATGAACCTGAATAAATCAATCCATACGTATCCAGGAAACGAAAGCATGAGATGG 320
 Qy 1436 GAGAGCAGAGAGCAGCTGGGACATTTAAAAATTAATTAATTAATTAATTAATTAATTA 1495
 Db 319 GAGAGCAGAGAGCAGCTGGGACATTTAAAAATTAATTAATTAATTAATTAATTAATTA 260

Qy 1496 CCAATTTCTAGGGCACTTTTCAGAAATCTCTCATATTTGTGGCTGGGATCAAGCCTGCA 1555
 Db 259 CCAATTTCTAGGGCACTTTTCAGAAATCTCTCATATTTGTGGCTGGGATCAAGCCTGCA 200
 Qy 1556 GCTTGAAGAAAGCAACAAGAAAGAAAGAAAGATCTGTGGAAGCTCAGGTGCAGCGGA 1615
 Db 199 GCTTGAAGAAAGCAACAAGAAAGAAAGAAAGATCTGTGGAAGCTCAGGTGCAGCGGA 140
 Qy 1616 CTCTGACTCCTAGAGAACTGCTCCTCAGAGTGCATGATCAACTTTTGGCTGAAGCCCT 1675
 Db 139 CTCTGACTCCTAGAGAACTGCTCCTCAGAGTGCATGATCAACTTTTGGCTGAAGCCCT 80
 Qy 1676 GCTTCACTTAGGGCACTTGAAGCTGCTGCTTGTCTTAACACAGGCTTAAGGCTTAG 1735
 Db 79 GCTTCACTTAGGGCACTTGAAGCTGCTGCTTGTCTTAACACAGGCTTAAGGCTTAG 20
 Qy 1736 ACAATGCTTCTCTTAGGA 1753
 Db 19 ACAATGCTTCTCTTAGGA 2

RESULT 9
 ABV89278
 ID ABV89278 standard, cDNA, 1918 BP.
 XX
 AC ABV89278;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Human colon cancer related cDNA SEQ ID NO 2589.
 XX
 XX Human; colon; cancer; cytostatic; tumour; gene therapy; vaccine; gene;
 KM sg.
 OS Homo sapiens.
 XX
 XX NC020258534-A2.
 PN
 PD 01-AUG-2002.
 XX
 PF 16-NOV-2001; 2001MO-US043704.
 XX
 XX 20-NOV-2000; 2000US-0252222P.
 PR 06-FEB-2001; 2001US-0267011P.
 PR 28-MAR-2001; 2001US-0279670P.
 PR 10-JUL-2001; 2001US-0304037P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Stolk JA, Xu J, Chenault RA, Meagher MJ, Secret H, King GE;
 XX WPI; 2002-608400/65.
 DR P-PDB; ABP67991.
 XX
 XX New isolated tumor colon polynucleotide and polypeptide, useful for the
 PT diagnosis, prevention and/or treatment of cancer, in particular colon
 PT cancer.
 PS Claim 1; SEQ ID NO 2589; 266bp + Sequence Listing; English.
 XX
 CC The invention relates to a human colon tumour expressed polynucleotide
 CC (I) encoding a polypeptide (II), ABP67991-ABP67996 comprising: (i) any of
 CC 2600 fully defined nucleotide sequences (ABV8669-ABV89289); (ii)
 CC complements of (i); (iii) at least 20 contiguous residues of (i); (iv)
 CC sequences that hybridize to (i), under moderately stringent conditions;
 CC (v) sequences having at least 75% or 90% identity to (i); or (vi)
 CC degenerate variants of (i). The compositions and methods of the present
 CC invention are useful for the diagnosis, prevention and/or treatment of
 CC cancer, particularly colon cancer. (i) can be used in gene therapy and
 CC (I) and (II) are useful in pharmaceutical compositions such as vaccines.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO

CC at fep.wipo.int/pub/published_pct_sequences
 XX Sequence 1918 BP; 486 A; 525 C; 473 G; 434 T; 0 U; 0 Other;

Query Match 54.1%; Score 1482.8; DB 6; Length 1918;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 1487; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AGAAGTCAGCTTGGCAGAGAGACTCTGAATAGAGGATTAGAGTCTTCAAGAGCAGA 60
 DB 402 AGAAGTCAGCTTGGCAGAGAGACTCTGAATAGAGGATTAGAGTCTTCAAGAGCAGA 461
 QY 61 GCTTCAGCTTGAAGACAAAGGAGAGAGCTCCCTGAAGAGCTTCTACTAGAGAGCTGGCAT 120
 DB 462 GCTTCAGCTTGAAGACAAAGGAGAGAGCTCCCTGAAGAGCTTCTACTAGAGAGCTGGCAT 521
 QY 121 GGCCTCTCTTGGCCTCCCACTTGGGCTAATCTAGAGCTTCTGGGGCTTTTGGGAC 180
 DB 522 GGCCTCTCTTGGCCTCCCACTTGGGCTAATCTAGAGCTTCTGGGGCTTTTGGGAC 581
 QY 181 ACTGTTGGCATGTGCTCCCACTGGGCTGAAGAACTTCTATGTGGTGGCCAGCATTT 240
 DB 582 ACTGTTGGCATGTGCTCCCACTGGGCTGAAGAACTTCTATGTGGTGGCCAGCATTT 641
 QY 241 GACAGCAGTTGGGCTTCCCAAGGAGCTCTGAGATGAGATGCGCACACAGCAGCAGCAT 300
 DB 642 GACAGCAGTTGGGCTTCCCAAGGAGCTCTGAGATGAGATGCGCACACAGCAGCAGCAT 701
 QY 301 CACCAAGTGAACATCTATAGACACCTTCTGGGCTTGGGCTGACATCCAGGCTGCCA 360
 DB 702 CACCAAGTGAACATCTATAGACACCTTCTGGGCTTGGGCTGACATCCAGGCTGCCA 761
 QY 361 GGCATGATGTGATCATTCAGTGCATCTCTCCCTGGGCTGATTTCTCTGTGGTGG 420
 DB 762 GGCATGATGTGATCATTCAGTGCATCTCTCCCTGGGCTGATTTCTCTGTGGTGG 821
 QY 421 CATGAGATGACAGTCTTCTGGCAGAACTCCGAGCCAAAGACAGATGGGCGGTAGCAG 480
 DB 822 CATGAGATGACAGTCTTCTGGCAGAACTCCGAGCCAAAGACAGATGGGCGGTAGCAG 881
 QY 481 TGGAGTCTTTTTCATCTCTGGAGGCTCTGGGATTTCTCTGGTCTCTGATCTTCA 540
 DB 882 TGGAGTCTTTTTCATCTCTGGAGGCTCTGGGATTTCTCTGGTCTCTGATCTTCA 941
 QY 541 TGGGATCTTAAGGAGCTTCTACTCAACATGCTGAGCAGATGAATTTGAGATTGG 600
 DB 942 TGGGATCTTAAGGAGCTTCTACTCAACATGCTGAGCAGATGAATTTGAGATTGG 1001
 QY 601 AGAGGCTCTTAACTTGGGCAATTTCTCCCTGTTCTCCCTGATPAGCTGGAAATCATCT 660
 DB 1002 AGAGGCTCTTAACTTGGGCAATTTCTCCCTGTTCTCCCTGATPAGCTGGAAATCATCT 1061
 QY 661 CTGCTTTCTGCTCATCTCCAGAGAAATCGTCCCACTACTAGATGCTTCAAGGCCCA 720
 DB 1062 CTGCTTTCTGCTCATCTCCAGAGAAATCGTCCCACTACTAGATGCTTCAAGGCCCA 1121
 QY 721 ACCTCTTGGCAAGAGCTTCTCAAGGCTGATCACTTCCCAAGTCAAGATGAGTT 780
 DB 1122 ACCTCTTGGCAAGAGCTTCTCAAGGCTGATCACTTCCCAAGTCAAGATGAGTT 1181
 QY 781 CAATTCTTAAGCTGACAGGATATGTGTGAAGAACAGAGGCGCCAGAGCTGGGGGGTGGC 840
 DB 1182 CAATTCTTAAGCTGACAGGATATGTGTGAAGAACAGAGGCGCCAGAGCTGGGGGGTGGC 1241
 QY 841 TGGGCTGTGAAAAAGTGAAGACACCCGAGGGCCACAGTGAAGGACATTAACACT 900
 DB 1242 TGGGCTGTGAAAAAGTGAAGACACCCGAGGGCCACAGTGAAGGACATTAACACT 1301
 QY 901 GGATCGTGTGAAGAGTGTGCTGAGATTAAGTGAATTTGGCATTTGAGCAAG 960
 DB 1302 GGATCGTGTGAAGAGTGTGCTGAGATTAAGTGAATTTGGCATTTGAGCAAG 1361
 QY 961 GCAGAAATGGGGCTAGTGAACAGCATGACAGTGAATTTGCCAAGATGCTCCCATGC 1020

DB 1362 GCAGAAATGGGGCTAGTGAACAGCATGACAGTGAATTTGCCAAGATGCTCCCATGC 1421
 QY 1021 CAGCCTTTCTGTTTCTTCTACACTGCTGCCCTCCCTGAAGTCCCAACCTCAACTT 1080
 DB 1422 CAGCCTTTCTGTTTCTTCTACACTGCTGCCCTCCCTGAAGTCCCAACCTCAACTT 1481
 QY 1081 GAAACCCCATTCCTTAAAGCAGAGCTCAGAGATCCCTTGGCTCTGTTTACCTGGG 1140
 DB 1482 GAAACCCCATTCCTTAAAGCAGAGCTCAGAGATCCCTTGGCTCTGTTTACCTGGG 1541
 QY 1141 ACTGCATCCCAAAACCCCAATACATCCCACTGACTGACCTCTGTGATCAAGACCC 1200
 DB 1542 ACTGCATCCCAAAACCCCAATACATCCCACTGACTGACCTCTGTGATCAAGACCC 1601
 QY 1201 TCTCTCTGCTGAGTGTGGCTCTTACCTGATTCCTGGGAGATGGGAGAGAGCAGTGGC 1260
 DB 1602 TCTCTCTGCTGAGTGTGGCTCTTACCTGATTCCTGGGAGATGGGAGAGAGCAGTGGC 1661
 QY 1261 TTTTGGGCAATGCTCTAAGCTTCTCAAGCTTCCCTCCAAAGAACTGATTTGGCCC 1320
 DB 1662 TTTTGGGCAATGCTCTAAGCTTCTCAAGCTTCCCTCCAAAGAACTGATTTGGCCC 1721
 QY 1321 TGGAACTTCATCCACTCTTGTATGACTCCAGAGTTCAGACTTAATTTGTGATGA 1380
 DB 1722 TGGAACTTCATCCACTCTTGTATGACTCCAGAGTTCAGACTTAATTTGTGATGA 1781
 QY 1381 CTGAATTAAGAACTCTAGAGTATCCAGAGAAACAGAAAGCAGAGTGGAGGA 1440
 DB 1782 CTGAATTAAGAACTCTAGAGTATCCAGAGAAACAGAAAGCAGAGTGGAGGA 1841
 QY 1441 CAGAAAGCAGCTGGGACATTTAAATAAATAAATAAATAAATAAATAAATAAATAA 1494
 DB 1842 CAGAAAGCAGCTGGGACATTTAAATAAATAAATAAATAAATAAATAAATAAATAA 1895

RESULT 10
 ABA04424
 ID ABA04424 standard; cDNA; 1918 BP.
 XX AC ABA04424;
 XX AC
 DT 11-MAR-2002 (first entry)
 XX
 DE Human SP82 protein encoding cDNA SEQ ID NO:1/3.
 XX
 KW Human; SP82; cancer suppression; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH CDS 520..1212
 FT /*tag= a
 FT /product= "SP82"
 XX
 XX
 XX CNIJ33315-A.
 XX
 XX 19-SEP-2001.
 PD
 XX
 PF 13-MAR-2000; 2000CN-00111989.
 XX
 PR 13-MAR-2000; 2000CN-00111989.
 XX
 XX (SHAN-) SHANGHAI INST ONCOLOGY.
 PA
 XX
 PI Gu J, Yang S;
 XX
 XX WPI: 2002-042193/06.
 DR
 XX P-PSDB; ABB04707.
 DR
 XX
 PT New human protein able to suppress growth of cancer cells and its
 PT encoding polynucleotide sequence.
 XX

PS Claim 5; Page 11-12 (Disclosure); 42bp; Chinese.
 XX The present sequence encodes human SP82 protein, which has cancer-
 CC suppressing activity. The present invention also describes a method for
 CC the preparation of the protein by recombination, and the application of
 CC the protein in treating diseases such as cancer
 XX

SQ Sequence 1918 BP; 486 A; 525 C; 473 G; 434 T; 0 U; 0 Other;

Query Match 54.1%; Score 1482.8; DB 6; Length 1918;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 1487; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AGAAGTCAGCTGGCAGAGAGACTCTGAATGAGGATTTAGAGGTGTTCAAGAGCAAGA 60
 DB AGAAGTCAGCTGGCAGAGAGACTCTGAATGAGGATTTAGAGGTGTTCAAGAGCAAGA 461
 QY 61 GCTTCAGCTGAGAGCAAGGAGAGAGCTCCGTAAGAGAGCTTTCTAGAGAGTCTGCAAT 120
 DB GCTTCAGCTGAGAGCAAGGAGAGAGCTCCGTAAGAGAGCTTTCTAGAGAGTCTGCAAT 521
 QY 462 GCTTCAGCTGAGAGCAAGGAGAGAGCTCCGTAAGAGAGCTTTCTAGAGAGTCTGCAAT 521
 DB GCTTCAGCTGAGAGCAAGGAGAGAGCTCCGTAAGAGAGCTTTCTAGAGAGTCTGCAAT 581
 QY 121 GGCCTCTCTGGCTCCCACTTGTGGGCTACATCTAGAGCTTCTGGGCTTTTGGGAC 180
 DB GGCCTCTCTGGCTCCCACTTGTGGGCTACATCTAGAGCTTCTGGGCTTTTGGGAC 581
 QY 522 GGCCTCTCTGGCTCCCACTTGTGGGCTACATCTAGAGCTTCTGGGCTTTTGGGAC 581
 DB GGCCTCTCTGGCTCCCACTTGTGGGCTACATCTAGAGCTTCTGGGCTTTTGGGAC 641
 QY 181 ACTGTTGTCATGCTGCTGCTCCCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 DB ACTGTTGTCATGCTGCTGCTCCCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 641
 QY 582 ACTGTTGTCATGCTGCTGCTCCCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 641
 DB ACTGTTGTCATGCTGCTGCTCCCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 241
 QY 241 GAGAAGAGTGGGCTTCTCCCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 DB GAGAAGAGTGGGCTTCTCCCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 701
 QY 642 GAGAAGAGTGGGCTTCTCCCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 701
 DB GAGAAGAGTGGGCTTCTCCCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 301
 QY 301 CACCAAGTGAATCTATAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 DB CACCAAGTGAATCTATAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 701
 QY 702 CACCAAGTGAATCTATAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 761
 DB CACCAAGTGAATCTATAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 361
 QY 361 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 821
 QY 762 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 821
 DB GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 421
 QY 421 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 DB CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 881
 QY 882 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 881
 DB CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 481
 QY 481 TGAAGTCTTTTATCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 DB TGAAGTCTTTTATCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 941
 QY 882 TGAAGTCTTTTATCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 941
 DB TGAAGTCTTTTATCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 541
 QY 541 TGAAGTCTTTTATCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
 DB TGAAGTCTTTTATCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1001
 QY 942 TGAAGTCTTTTATCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1001
 DB TGAAGTCTTTTATCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 601
 QY 601 AGAGGCTCTTTATCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 DB AGAGGCTCTTTATCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1061
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 DB AGAGGCTCTTTATCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 661
 QY 661 CTGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 DB CTGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1121
 QY 1062 CTGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1121
 DB CTGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 721
 QY 721 ACCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 DB ACCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1122
 QY 1122 ACCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1181
 DB ACCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 781
 QY 781 CAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 DB CAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1182
 QY 1182 CAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1241
 DB CAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 841
 QY 841 TGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 DB TGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1242
 QY 1242 TGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1301
 DB TGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT

QY 901 GATTCGTGCTGAG 960
 DB GATTCGTGCTGAG 1302
 QY 1302 GATTCGTGCTGAG 1361
 DB GATTCGTGCTGAG 961
 QY 961 GATTCGTGCTGAG 1020
 DB GATTCGTGCTGAG 1362
 QY 1362 GATTCGTGCTGAG 1421
 DB GATTCGTGCTGAG 1021
 QY 1021 GATTCGTGCTGAG 1080
 DB GATTCGTGCTGAG 1422
 QY 1422 GATTCGTGCTGAG 1481
 DB GATTCGTGCTGAG 1081
 QY 1081 GATTCGTGCTGAG 1140
 DB GATTCGTGCTGAG 1482
 QY 1482 GATTCGTGCTGAG 1541
 DB GATTCGTGCTGAG 1141
 QY 1141 GATTCGTGCTGAG 1200
 DB GATTCGTGCTGAG 1542
 QY 1542 GATTCGTGCTGAG 1601
 DB GATTCGTGCTGAG 1201
 QY 1201 GATTCGTGCTGAG 1260
 DB GATTCGTGCTGAG 1602
 QY 1602 GATTCGTGCTGAG 1661
 DB GATTCGTGCTGAG 1261
 QY 1261 GATTCGTGCTGAG 1320
 DB GATTCGTGCTGAG 1662
 QY 1662 GATTCGTGCTGAG 1721
 DB GATTCGTGCTGAG 1321
 QY 1321 GATTCGTGCTGAG 1380
 DB GATTCGTGCTGAG 1722
 QY 1722 GATTCGTGCTGAG 1781
 DB GATTCGTGCTGAG 1381
 QY 1381 GATTCGTGCTGAG 1440
 DB GATTCGTGCTGAG 1782
 QY 1782 GATTCGTGCTGAG 1841
 DB GATTCGTGCTGAG 1441
 QY 1441 GATTCGTGCTGAG 1494
 DB GATTCGTGCTGAG 1842
 QY 1842 GATTCGTGCTGAG 1895
 DB GATTCGTGCTGAG

RESULT 11

AAA37060 standard; cDNA; 1475 BP.

AAA37060;

08-AUG-2000 (first entry)

Human PRO1356 (UNQ705) cDNA sequence SBQ ID NO:133.

Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;

transmembrane; secretion; immunoadhesion; pharmaceutical; screening; ss.

Homo sapiens.

MO200012708-A2.

09-MAR-2000.

01-SEP-1999; 99MO-US020111.

01-SEP-1998; 98US-0098716P.

01-SEP-1998; 98US-0098749P.

01-SEP-1998; 98US-0098750P.

02-SEP-1998; 98US-0098803P.

02-SEP-1998; 98US-0098821P.

02-SEP-1998; 98US-0098843P.

09-SEP-1998; 98US-0099536P.

09-SEP-1998; 98US-0099596P.

09-SEP-1998; 98US-0099602P.

09-SEP-1998; 98US-0099642P.

PR 10-SEP-1998; 98US-0097741P.
PR 10-SEP-1998; 98US-009754P.
PR 10-SEP-1998; 98US-009763P.
PR 10-SEP-1998; 98US-009792P.
PR 10-SEP-1998; 98US-009808P.
PR 10-SEP-1998; 98US-009812P.
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PR 16-SEP-1998; 98US-0100661P.
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PR 14-OCT-1998; 98US-0104257P.
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PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105693P.
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PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106023P.
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PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
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PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
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PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
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PR 17-NOV-1998; 98US-0108867P.
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PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.

(GETH) GENENTECH INC.

Baker K, Goddard A, Gurney AU, Smith V, Watanabe CK, Wood WT;

WPI; 2000-237871/20.

P-PSDB; AAY99378.

New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions.

Claim 2; Fig 77; 773pp; English.

AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding them have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention

Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

Query Match 53.7%; Score 1472; DB 3; Length 1475;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAAGTCAGCTGGCAGAGGACTCTGAATGAGGATTTAGAGCTTCAAGAGCAGA 60
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Db 4 AGAAGTCAGCTGGCAGAGGACTCTGAATGAGGATTTAGAGCTTCAAGAGCAGA 63
61 GCTTCAGCTGAGAGCAGAGGAGCAGTCCCTGAAGAGCTTCTACTGAGAGTCTCCAT 120

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Db 64 GCTTCAGCCGGAAGACAGAGGAGCAGTCCCTGAAGAGCTTCTACTAGAGGCTCTGCAT 123
Qy 121 GGGCTCTTGGGCTCCAACTGTGGGCTACCTCTAGAGGCTCTGGGGCTTTTGGGAC 180
Db 124 GGGCTCTTGGGCTCCAACTGTGGGCTACCTCTAGAGGCTCTGGGGCTTTTGGGAC 183
Qy 181 ACTGTTGCAATGCTGTCTCCAGCTGGAAAACAAAGTTCTTATGTGCGTCCAGCATTTG 240
Db 184 ACTGTTGCAATGCTGTCTCCAGCTGGAAAACAAAGTTCTTATGTGCGTCCAGCATTTG 243
Qy 241 GACAGCAGTTGGCTTCTCCAGGGGCTCTGGATGGAAATGTGCCACACACAGCAGGAT 300
Db 244 GACAGCAGTTGGCTTCTCCAGGGGCTCTGGATGGAAATGTGCCACACAGCAGGAT 303
Qy 301 CACCAAGTGAACATCTATAGCAACCTTCTGGGCTGCGGCTGACATCCAGGCTGCCA 360
Db 304 CACCAAGTGAACATCTATAGCAACCTTCTGGGCTGCGGCTGACATCCAGGCTGCCA 363
Qy 361 GGGCATTGATGATGATCATCATGTCATCTCTCTGGGCTGTCATTTATCTGTGTGGG 420
Db 364 GGGCATTGATGATGATCATCATGTCATCTCTCTGGGCTGTCATTTATCTGTGTGGG 423
Qy 421 CATGATATGACAGTCTTCTGCCAGGAATCCGAGCCAAAGACAGAGTGGCGGTAGCAG 480
Db 424 CATGATATGACAGTCTTCTGCCAGGAATCCGAGCCAAAGACAGAGTGGCGGTAGCAG 483
Qy 481 TGAAGTCTTTTTCATCTTGAAGGCTCTGGAGTTGATTCCTGTGGCTCTGATCTTCA 540
Db 484 TGAAGTCTTTTTCATCTTGAAGGCTCTGGAGTTGATTCCTGTGGCTCTGATCTTCA 543
Qy 541 TGGGATCTCTAAGGGAATCTTACTACCACTGTGCTGACAGCATGAAATTTGAGATTGG 600
Db 544 TGGGATCTCTAAGGGAATCTTACTACCACTGTGCTGACAGCATGAAATTTGAGATTGG 603
Qy 601 AGAGGCTCTTACTTGGGCAATTAATTTCTCCCTGTTCTCCCTGATAGCTGGAATCATCT 660
Db 604 AGAGGCTCTTACTTGGGCAATTAATTTCTCCCTGTTCTCCCTGATAGCTGGAATCATCT 663
Qy 661 CTGCTTTTCTGCTCATCCAGAAATGCTCCAACTACATGATGCTACCAAGGCCA 720
Db 664 CTGCTTTTCTGCTCATCCAGAAATGCTCCAACTACATGATGCTACCAAGGCCA 723
Qy 721 ACCTCTTGCACAAAGAGCTCTCCAAAGCTGTGCACTCTCCAAAGTCAAGATGAGTT 780
Db 724 ACCTCTTGCACAAAGAGCTCTCCAAAGCTGTGCACTCTCCAAAGTCAAGATGAGTT 783
Qy 781 CAATTTCTAAGGCTGACAGGCTATGTGTGAAGAACAGGGGCTCAGAGCTGGGGGCTGGC 840
Db 784 CAATTTCTAAGGCTGACAGGCTATGTGTGAAGAACAGGGGCTCAGAGCTGGGGGCTGGC 843
Qy 841 TGGGCTCTGTAAGAAACAGTGAAGCAGCCCGAGGGGCAAGGTGAGGAGCATACCACT 900
Db 844 TGGGCTCTGTAAGAAACAGTGAAGCAGCCCGAGGGGCAAGGTGAGGAGCATACCACT 903
Qy 901 GGATCTGTGAGAGGCTGTGAGAGTACATGACTTTTGGCCATTGATGAGCAAG 960
Db 904 GGATCTGTGAGAGGCTGTGAGAGTACATGACTTTTGGCCATTGATGAGCAAG 963
Qy 961 GCAGAAATGGGGGCTAGTGTAAACAGTGAAGTTGAATGGCAAGATCTGGCCATGC 1020
Db 964 GCAGAAATGGGGGCTAGTGTAAACAGTGAAGTTGAATGGCAAGATCTGGCCATGC 1023
Qy 1021 CAGCCTTTCTGTTTCTCTACCTTGTGCTGCCCTGAGGCTAAGTCCCAACCTCACTT 1080
Db 1024 CAGCCTTTCTGTTTCTCTACCTTGTGCTGCCCTGAGGCTAAGTCCCAACCTCACTT 1083
Qy 1081 GAAACCCCATCTCCCTTAAGCAGAGACTCAGAGATCCCTTTGCTGTGTTTAACTGGG 1140
Db 1084 GAAACCCCATCTCCCTTAAGCAGAGACTCAGAGATCCCTTTGCTGTGTTTAACTGGG 1143
Qy 1141 ACTCCATCCCAAAACCATTAATCACTCCCATGATGACCTCTGTGATCAAGAGCC 1200
Db 1144 ACTCCATCCCAAAACCATTAATCACTCCCATGATGACCTCTGTGATCAAGAGCC 1203
```

```
Db 1144 ACTCCATCCCAAAACCATTAATCACTCCCATGATGACCTCTGTGATCAAGAGCC 1203
Qy 1201 TCTCTGTGCTGAGTTGGCTCTTACCTATGCTGGGATGGGAAGAGACAGTGGC 1260
Db 1204 TCTCTGTGCTGAGTTGGCTCTTACCTATGCTGGGATGGGAAGAGACAGTGGC 1263
Qy 1261 TTTTGTGGGCAATGCTCTAACTTCTCAAGCTTCTCCAAAGAACTGATTGGCCC 1320
Db 1264 TTTTGTGGGCAATGCTCTAACTTCTCAAGCTTCTCCAAAGAACTGATTGGCCC 1323
Qy 1321 TGGAACTCATCCCACTCTGTATGACTCCCAAGTCCAGATCTAATTTGCAATGA 1380
Db 1324 TGGAACTCATCCCACTCTGTATGACTCCCAAGTCCAGATCTAATTTGCAATGA 1383
Qy 1381 CTGAATAATTAACCATCTACGATATCAGGGAACAGAAAGCAGATGAGATGGAGGA 1440
Db 1384 CTGAATAATTAACCATCTACGATATCAGGGAACAGAAAGCAGATGAGATGGAGGA 1443
Qy 1441 CAGGAAGCAGCCTGGGACATTTAAAAATA 1472
Db 1444 CAGGAAGCAGCCTGGGACATTTAAAAATA 1475

RESULT 12
AAFS4296
ID AAF54296 standard; DNA; 1475 BP.
XX
AC AAF54296;
XX
DT 02-APR-2001 (first entry)
XX
DE DNA encoding protein of the invention #39.
XX
KM Secreted; transmembrane; gene therapy; ss.
XX
OS Unidentified.
XX
PN WO200078961-A1.
XX
PD 28-DEC-2000.
XX
PF 18-FEB-2000; 2000MO-US004342.
XX
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99MO-US020111.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99MO-US028313.
PR 02-DEC-1999; 99MO-US028551.
PR 16-DEC-1999; 99MO-US030095.
PR 05-JAN-2000; 2000MO-US000219.
PR 06-JAN-2000; 2000MO-US000376.
XX
PA (GENT ) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Geo W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MB, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WT;
XX
DR WPI; 2001-071395/08.
XX
PT Secreted and transmembrane proteins and nucleic acids designated PRO,
PT useful as hybridization probes, in chromosome and gene mapping and gene
PT therapy.
XX
PS Claim 2; Fig 77; 787pp; English.
XX
CC The present invention relates to secreted and transmembrane proteins.
CC These proteins and the DNA encoding them may be used as hybridization
CC probes, in chromosome and gene mapping and in the generation of anti-
CC sense RNA and DNA. They may also be used to generate either
```

transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy

Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

Query Match 53.7%; Score 1472; DB 4; Length 1475;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AGAAGTGAAGCTTGGCAGAGAGACTTGAATGAGGATTAGAGTTTCAAGAGCAAGA 60
DB 4 AGAAGTGAAGCTTGGCAGAGAGACTTGAATGAGGATTAGAGTTTCAAGAGCAAGA 63
QY 61 GCTTACAGCTGAAGCAAGGAGAGAGCTTGAAGAGCTTCTAAGAGGTTGACAT 120
DB 64 GCTTACAGCTGAAGCAAGGAGAGAGCTTGAAGAGCTTCTAAGAGGTTGACAT 123
QY 121 GGCCTCTTGGCTCCCACTTGGGCTAATCTTGAAGGCTTCTGGGGCTTTTGGGAC 180
DB 124 GGCCTCTTGGCTCCCACTTGGGCTAATCTTGAAGGCTTCTGGGGCTTTTGGGAC 183
QY 181 ACTGTTGCAATGCTGCTCCCACTGAGGAAACAAAGTTCTTATGCTGCTGACATTTGT 240
DB 184 ACTGTTGCAATGCTGCTCCCACTGAGGAAACAAAGTTCTTATGCTGCTGACATTTGT 243
QY 241 GACAGCAGTTGGCTTCCCAAGGGCTCTGAGTGAATGAGGCAACAGACAGCAGGCAAT 300
DB 244 GACAGCAGTTGGCTTCCCAAGGGCTCTGAGTGAATGAGGCAACAGACAGCAGGCAAT 303
QY 301 CACCAAGTGAACATCTATAGCAACCTTCTGGGCTGCTCCGCTGACATCCAGCTGGCCA 360
DB 304 CACCAAGTGAACATCTATAGCAACCTTCTGGGCTGCTCCGCTGACATCCAGCTGGCCA 363
QY 361 GGCATGATGATGATCATCATGATGATCTCTCTGAGGCTGATATCTTGTGTGG 420
DB 364 GGCATGATGATGATCATCATGATGATCTCTCTGAGGCTGATATCTTGTGTGG 423
QY 421 CATGAGATGACAGTCTTCTGCGCAGGAATCCGAGCCAAAGACAGATGGCGGTAGCAG 480
DB 424 CATGAGATGACAGTCTTCTGCGCAGGAATCCGAGCCAAAGACAGATGGCGGTAGCAG 483
QY 481 TGAAGTCTTTTTCATCTCTGAGAGGCTCTGAGATTCATCTGTTGCTGGAATCTTCA 540
DB 484 TGAAGTCTTTTTCATCTCTGAGAGGCTCTGAGATTCATCTGTTGCTGGAATCTTCA 543
QY 541 TGGGATCTTACGAGACTTCTACCACTGAGTGTGCTGACAGCATGAATTTGAGATTGG 600
DB 544 TGGGATCTTACGAGACTTCTACCACTGAGTGTGCTGACAGCATGAATTTGAGATTGG 603
QY 601 AGAGGCTCTTATCTGAGGATTAATTTCTTCCCTGTTCTCCCTGATGACTGGAATCATCT 660
DB 604 AGAGGCTCTTATCTGAGGATTAATTTCTTCCCTGTTCTCCCTGATGACTGGAATCATCT 663
QY 661 CTGCTTTCTGCTCATCTCCAGAGAAATGCTCCAACTACAGATGCTTACCAAGCCA 720
DB 664 CTGCTTTCTGCTCATCTCCAGAGAAATGCTCCAACTACAGATGCTTACCAAGCCA 723
QY 721 ACCTCTTTCACCAAGAGCTTCTCAAGGCTGTGATCACTTCCAAAGTCAAGAGTGAATT 780
DB 724 ACCTCTTTCACCAAGAGCTTCTCAAGGCTGTGATCACTTCCAAAGTCAAGAGTGAATT 783
QY 781 CAATTTCTTACAGCTGACAGGATTAATGTAAGAAACAGAGGCTGAGGCTGGGGTGGC 840
DB 784 CAATTTCTTACAGCTGACAGGATTAATGTAAGAAACAGAGGCTGAGGCTGGGGTGGC 843
QY 841 TGGGCTCTGTAAGAAACAGTGAAGCAAGCCGAGAGGCTCAAGTGAAGGACATCAACCACT 900
DB 844 TGGGCTCTGTAAGAAACAGTGAAGCAAGCCGAGAGGCTCAAGTGAAGGACATCAACCACT 903
QY 901 GGAATCTGTGTAAGAGGCTGCTGAGAGTGAATGACTTTTGGCATTTGAGCAAG 960
DB 904 GGAATCTGTGTAAGAGGCTGCTGAGAGTGAATGACTTTTGGCATTTGAGCAAG 963

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QY 961 GCAGAAATGGGGCTAGTGAACAGATGAGGTTGAATTCAGAGATGCTGGCATGC 1020
DB 964 GCAGAAATGGGGCTAGTGAACAGATGAGGTTGAATTCAGAGATGCTGGCATGC 1023
QY 1021 CAGCCTTCTGTTTCTTCTCACTTGTCTGCTCTCCCTGCTTAAGTCCCAACCTCAACTT 1080
DB 1024 CAGCCTTCTGTTTCTTCTCACTTGTCTGCTCTCCCTGCTTAAGTCCCAACCTCAACTT 1083
QY 1081 GAAACCCATTCCTTAAAGCAGAGTCAAGAGATCCCTTGGCTCTGTTTAACTGGG 1140
DB 1084 GAAACCCATTCCTTAAAGCAGAGTCAAGAGATCCCTTGGCTCTGTTTAACTGGG 1143
QY 1141 ACTTCATCCCAACCAACCACTAATCACTCCCACTGACTGAACCTCTGTATCAAGACCC 1200
DB 1144 ACTTCATCCCAACCAACCACTAATCACTCCCACTGACTGAACCTCTGTATCAAGACCC 1203
QY 1201 TCTCTGCTGAGTGGCTGCTTAACTCACTGAGGAGTGGAGAGAGACAGATGGC 1260
DB 1204 TCTCTGCTGAGTGGCTGCTTAACTCACTGAGGAGTGGAGAGAGACAGATGGC 1263
QY 1261 TTTTGGGAGATTGCTTAACTTCACTTCAAGCTTCCCTCAAGAAACTGATTTGGCCC 1320
DB 1264 TTTTGGGAGATTGCTTAACTTCACTTCAAGCTTCCCTCAAGAAACTGATTTGGCCC 1323
QY 1321 TGGAACTTCATCCCACTCTTGTATGACTGCAAGTGTCAAGTCAATTTGTGATGAA 1380
DB 1324 TGGAACTTCATCCCACTCTTGTATGACTGCAAGTGTCAAGTCAATTTGTGATGAA 1383
QY 1381 CTGAATTAATAACCATCTTACGATATCCAGGAAACAGAAACAGATGAGATGGAGGA 1440
DB 1384 CTGAATTAATAACCATCTTACGATATCCAGGAAACAGAAACAGATGAGATGGAGGA 1443
QY 1441 CAGGAAGCAGCTTGGGACATTTAAAAATA 1472
DB 1444 CAGGAAGCAGCTTGGGACATTTAAAAATA 1475

```

RESULT 13
AAS21489 standard; cDNA; 1475 BP.
ID AAS21489;
XX AAS21489;
AC AAS21489;
XX 24-OCT-2001 (first entry)
DT
XX Human cDNA sequence encoding for PRO1356 polypeptide.
XX Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIa; gene therapy; ss.
XX Homo sapiens.
OS
XX
PN W0200140466-A2.
PD
XX 07-JUN-2001.
PD
XX 01-DEC-2000; 2000MO-US032678.
PF
XX
XX 01-DEC-1999; 99MO-US028301.
PR 01-DEC-1999; 99MO-US028634.
PR 02-DEC-1999; 99MO-US028551.
PR 02-DEC-1999; 99MO-US028564.
PR 02-DEC-1999; 99MO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99MO-US030095.
PR 20-DEC-1999; 99MO-US030911.
PR 20-DEC-1999; 99MO-US030999.
PR 30-DEC-1999; 99MO-US031243.
PR 30-DEC-1999; 99MO-US031274.
PR 05-JAN-2000; 2000MO-US000219.
PR

PR 06-JAN-2000; 2000OWO-US000277.
PR 06-JAN-2000; 2000OWO-US000376.
PR 11-FEB-2000; 2000OWO-US003555.
PR 18-FEB-2000; 2000OWO-US004341.
PR 18-FEB-2000; 2000OWO-US004342.
PR 22-FEB-2000; 2000OWO-US004414.
PR 24-FEB-2000; 2000OWO-US004914.
PR 24-FEB-2000; 2000OWO-US005004.
PR 01-MAR-2000; 2000OWO-US005601.
PR 02-MAR-2000; 2000OWO-US005841.
PR 03-MAR-2000; 2000OWO-US005841.
PR 10-MAR-2000; 2000OWO-US006319.
PR 15-MAR-2000; 2000OWO-US006884.
PR 20-MAR-2000; 2000OWO-US007377.
PR 21-MAR-2000; 2000OWO-US007532.
PR 30-MAR-2000; 2000OWO-US008439.
PR 17-MAY-2000; 2000OWO-US013705.
PR 22-MAY-2000; 2000OWO-US014042.
PR 30-MAY-2000; 2000OWO-US014941.
PR 02-JUN-2000; 2000OWO-US015264.
PR 05-JUN-2000; 2000OWO-US015264.
PR 28-JUL-2000; 2000OWO-US020710.
PR 11-AUG-2000; 2000OWO-US022031.
PR 23-AUG-2000; 2000OWO-US023522.
PR 24-AUG-2000; 2000OWO-US023326.
PR 08-NOV-2000; 2000OWO-US030952.
PR 10-NOV-2000; 2000OWO-US030873.

PA (CETH) GENENTECH INC.
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,
PI Gerritsen ME, Goddard A, Godowski PJ, Guney AL, Sherwood S,
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z,
XX WPI; 2001-408281/43.
DR P-PSDB; AAU12417.

PT Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung, breast, prostate, cervical.

PS Claim 3; Fig 491; 813pp; English.

AA52124/AA521518 encode for novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor- α (TNF- α) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes, or inhibit binding of A-peptide to factor VIIa. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy

Query Match	53.7%	Score 1472;	DB 4;	Length 1475;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1472; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

1 AGAAGTCAGCCTGGCAGAGACTCTGAATGAGGGATTGAGGCTTCAAGAGCAGA 600

[illegible]

QY 1141 ACTGCATCCCAACCACTATATCATGCCAATGACCCCTGTGATCAAGACCC 1200
DB 1144 ACTGCATCCCAACCACTATATCATGCCAATGACCCCTGTGATCAAGACCC 1203
QY 1201 TCTCTGCTGAGTGTGCTCTTACCTATGCTGAGGATGGAGAGAGAGAGAG 1260
DB 1204 TCTCTGCTGAGTGTGCTCTTACCTATGCTGAGGATGGAGAGAGAGAGAG 1263
QY 1261 TTTTGTGGGATGCTCTTAACTTCTCAAGTTCTCTTCAAGAACTGATGGCCC 1320
DB 1264 TTTTGTGGGATGCTCTTAACTTCTCAAGTTCTCTTCAAGAACTGATGGCCC 1323
QY 1321 TGGAACTCCATCCCACTCTTGTATGATCCACAGTCCAGCTAATTTGGCATGAA 1380
DB 1324 TGGAACTCCATCCCACTCTTGTATGATCCACAGTCCAGCTAATTTGGCATGAA 1383
QY 1381 CTGAATATTAACATCTCTACGCTATCCAGGAAAGAGAGAGAGAGAGAGAGAG 1440
DB 1384 CTGAATATTAACATCTCTACGCTATCCAGGAAAGAGAGAGAGAGAGAGAGAG 1443
QY 1441 CAGGAGGAGCTGCGGACATTTAAAAATA 1472
DB 1444 CAGGAGGAGCTGCGGACATTTAAAAATA 1475
RESULT 14
AAS15360
ID AAS15360 standard; cDNA; 1475 BP.
XX AAS15360;
AC AAS15360;
XX
DT 16-JAN-2002 (first entry)
XX
DE cDNA encoding human PRO1356 polypeptide.
XX
KW Human; PRO1356; clone DNA64886-1601; immune-related disorder;
KW inflammatory disorder; infectious disorder; immunodeficiency disorder;
KW autoimmune disorder; renal disease; demyelinating disease; skin disease;
KW neoplasia; transplantation associated disease; gene therapy;
KW immunosuppressive; anti-inflammatory; antidiabetic; ss.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 122..814
FT /tag= a
FT /product= "PRO1356 polypeptide"
FT sig_peptide 122..193
FT /tag= b
FT mat_peptide 194..811
FT /tag= c
XX
XX
PN WO20016740-A2.
XX
PD 13-SEP-2001.
XX
PE 01-MAR-2001; 2001WO-US006666.
XX
PR 03-MAR-2000; 2000US-0187202P.
PR 21-MAR-2000; 2000US-0191015P.
PR 30-MAY-2000; 2000WO-US014841.
PR 05-JUN-2000; 2000US-0209832P.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
XX
XX
PA (GENE) GENENTECH INC.
XX
PI Eaton DL, Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL,
PI Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2001-625876/72.
XX P-PSDB; AAU09178.
DR

XX Nucleic acid encoding PRO polypeptides, useful for detecting and
PT treating immune related diseases and disorders in mammals including
PT autoimmune diseases, inflammatory diseases and asthma.
XX
XX Claim 2; Fig 1; 122pp; English.
XX
XX The present invention relates to the isolation of 9 novel human PRO
XX polypeptides (AAU09178-AAU09186) and the cDNA sequences encoding them.
XX The novel PRO polypeptides include PRO1356, PRO1268, PRO1884, PRO3444,
XX PRO3151, PRO4322, PRO3964, PRO10008 and PRO19598. The cDNA sequences
XX encoding these PRO polypeptides have been designated as clones DNA6486-
XX 1601, DNA64903-1553, DNA64318-2520, DNA87997, DNA89273, DNA92223-2567,
XX DNA96973, DNA101921 and DNA145887 respectively. Compositions (e.g.
XX vaccines) containing PRO polypeptides and methods of using these
XX compositions are useful in the treatment and diagnosis of immune-related
XX disorders. Such disorders include immune-mediated inflammatory disorders
XX (e.g. osteoarthritis), non-immune-mediated inflammatory disorders (e.g.
XX diabetes mellitus), infectious disorders (e.g. granulomatous hepatitis),
XX immunodeficiency disorders (e.g. AIDS), autoimmune disorders (e.g.
XX rheumatoid arthritis), immune-related renal diseases (e.g. cirrhosis),
XX demyelinating diseases of the peripheral or central nervous system (e.g.
XX Guillain-Barre syndrome), immune-mediated skin diseases (e.g. contact
XX dermatitis), neoplasias and transplantation associated diseases. The
XX cDNA polynucleotide sequences of the invention may be used in gene therapy.
XX AAS15360-AAS15368 represent cDNA sequences encoding for the novel human
XX PRO polypeptides of the invention
XX
SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
XX
XX Query Match 53.7%; Score 1472; DB 4; Length 1475;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 AGAAGTACGCTGCGAGAGAGACTGTGAATGAGGATTTAGAGGTGTTCAAGAGCAAGA 60
DB 4 AGAAGTACGCTGCGAGAGAGACTGTGAATGAGGATTTAGAGGTGTTCAAGAGCAAGA 63
QY 61 GCTTACGCTGGAAG 120
DB 64 GCTTACGCTGGAAG 123
QY 121 GGCCTCTTGGGCTCCAACTTGTGGGCTACATCTAGAGCTTCTGGAGCTTTTGGGAC 180
DB 124 GGCCTCTTGGGCTCCAACTTGTGGGCTACATCTAGAGCTTCTGGAGCTTTTGGGAC 183
QY 181 ACTGTTGCCATGCTGCTCCAGCTGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 184 ACTGTTGCCATGCTGCTCCAGCTGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 243
QY 241 GACAGAGTTGGCTTCTCCAGAGGCTCTGAGATGAGATGAGATGAGATGAGATGAG 300
DB 244 GACAGAGTTGGCTTCTCCAGAGGCTCTGAGATGAGATGAGATGAGATGAGATGAG 303
QY 301 CACCCAGTGTGATCTATGACACCTTCTGGGCTGCGCCGCTGATCATCCAGGCTGCCA 360
DB 304 CACCCAGTGTGATCTATGACACCTTCTGGGCTGCGCCGCTGATCATCCAGGCTGCCA 363
QY 361 GGCATGATGTGATCATCCAGTCAATCTCTCTGCGCTGATATCTCTGTGTGGG 420
DB 364 GGCATGATGTGATCATCCAGTCAATCTCTCTGCGCTGATATCTCTGTGTGGG 423
QY 421 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
DB 424 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 483
QY 481 TGGAGTCTTTTATCTTGAAGGCTCTGAGATTCATCTGTTGCTGAGATCTTCA 540
DB 484 TGGAGTCTTTTATCTTGAAGGCTCTGAGATTCATCTGTTGCTGAGATCTTCA 543
QY 541 TGGAGTCTTACGGAGATCTTACTACCACTGAGTGTGCTGACAGATGAATTTAGATTGG 600
DB 544 TGGAGTCTTACGGAGATCTTACTACCACTGAGTGTGCTGACAGATGAATTTAGATTGG 603

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QY 601 AGAGGCTTTTACTGAGGCAATATTTCTCCCTGTTCTCCCTGATAGCTGGAATCATCT 660
DB 604 AGAGGCTTTTACTGAGGCAATATTTCTCCCTGTTCTCCCTGATAGCTGGAATCATCT 663
QY 661 CTGCTTTTCTGCTCAATCCAGAGAAATGCTCCCACTACTAGATGCTCCAGGCCA 720
DB 664 CTGCTTTTCTGCTCAATCCAGAGAAATGCTCCCACTACTAGATGCTCCAGGCCA 723
QY 721 ACCTCTTGCCAGAGAGCTCTCCAGAGGCTGCTCACTCCCAAGTCAAGAGT 780
DB 724 ACCTCTTGCCAGAGAGCTCTCCAGAGGCTGCTCACTCCCAAGTCAAGAGT 783
QY 781 CAATTCCTAAGGCTGACAGGATATGTTGTAAGAACAGAGGAGCCAGAGCTGAGGAGTGGC 840
DB 784 CAATTCCTAAGGCTGACAGGATATGTTGTAAGAACAGAGGAGCCAGAGCTGAGGAGTGGC 843
QY 841 TGGGTCTGTATAAACAAGTGAACAGCAGCAGCCAGAGGAGCAAGTGAAGGAGCACTACCACT 900
DB 844 TGGGTCTGTATAAACAAGTGAACAGCAGCAGCCAGAGGAGCAAGTGAAGGAGCACTACCACT 903
QY 901 GAATCGGTGAGAAAGTGTGCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 960
DB 904 GAATCGGTGAGAAAGTGTGCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 963
QY 961 GCAGAAATGGGGCTAGTGTAAACAGATGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1020
DB 964 GCAGAAATGGGGCTAGTGTAAACAGATGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1023
QY 1021 GACCTTTCTGTTTCTCTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1024 GACCTTTCTGTTTCTCTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083
QY 1081 GAAACCCCATCTCCCTTAAAGCAGAGACTCAGAGAGTCCCTTGGCTGTTTAACTGGG 1140
DB 1084 GAAACCCCATCTCCCTTAAAGCAGAGACTCAGAGAGTCCCTTGGCTGTTTAACTGGG 1143
QY 1141 ACTGCATCCCAAAACCACTAATCAATCCCACTGAGTGAACCTCTGTGATCAAAAGCC 1200
DB 1144 ACTGCATCCCAAAACCACTAATCAATCCCACTGAGTGAACCTCTGTGATCAAAAGCC 1203
QY 1201 TCTCTCTGAGTGAAGTGTGCTTGAAGTCAATGCTGAGGAGTGAAGAGAGAGAGAGAGAGAG 1260
DB 1204 TCTCTCTGAGTGAAGTGTGCTTGAAGTCAATGCTGAGGAGTGAAGAGAGAGAGAGAGAGAG 1263
QY 1261 TTTTGTGGGATGCTCTAATCACTTCTCAAGCTTCCCTCAAGAACTGATTTGGCC 1320
DB 1264 TTTTGTGGGATGCTCTAATCACTTCTCAAGCTTCCCTCAAGAACTGATTTGGCC 1323
QY 1321 TGGAACTTCATCCCACTCTTGTATGATCTCAAGTGTCAAGTGAATTTGTGATGAA 1380
DB 1324 TGGAACTTCATCCCACTCTTGTATGATCTCAAGTGTCAAGTGAATTTGTGATGAA 1383
QY 1381 CTGAATTAATAAACAATCTAGAGTATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
DB 1384 CTGAATTAATAAACAATCTAGAGTATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1443
QY 1441 CAGGAAGGAGCTGGAGCAATTTAAAAAATA 1472
DB 1444 CAGGAAGGAGCTGGAGCAATTTAAAAAATA 1475

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RESULT 15

AAF92097
ID AAF92097 standard; cDNA; 1475 BP.

AAF92097;

15-MAY-2001 (first entry)

Human PRO1356 cDNA.

Human; PRO protein; mapping; ss.

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XX OS Homo sapiens.
XX PN MO200116318-A2.
XX PD 08-MAR-2001.
XX PF 24-AUG-2000; 2000MO-US023328.
XX PR 01-SEP-1999; 99MO-US020111.
XX PR 15-SEP-1999; 99MO-US021090.
XX PR 07-DEC-1999; 99US-0169495P.
XX PR 09-DEC-1999; 99US-0170262P.
XX PR 11-JAN-2000; 2000US-0175481P.
XX PR 18-FEB-2000; 2000MO-US004342.
XX PR 18-FEB-2000; 2000MO-US004342.
XX PR 22-FEB-2000; 2000MO-US004414.
XX PR 01-MAR-2000; 2000MO-US005601.
XX PR 03-MAR-2000; 2000US-0187202P.
XX PR 21-MAR-2000; 2000US-0191007P.
XX PR 30-MAR-2000; 2000MO-US008439.
XX PR 25-APR-2000; 2000US-0199397P.
XX PR 05-MAY-2000; 2000MO-US014042.
XX PR 05-JUN-2000; 2000US-0209832P.
XX PA (GETH ) GENENTECH INC.
XX PI Baton DL, Flvaroff B, Gerritson ME, Goddard A, Godowski PJ;
XX PI Grimaldi CJ, Gurney AL, Matanabe CK, Wood WI;
XX DR WPI; 2001-183260/18.
XX DR P-PSDB; AAB87565.
XX PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
XX PT biology, including use as hybridization probes, and in chromosome and
XX PT gene mapping.
XX PS Claim 2; Fig 79; 278bp; English.
XX CC The present sequence is the coding sequence for a human PRO polypeptide
XX CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
XX CC antagonists or anti-PRO antibodies are useful for preparation of a
XX CC medicament useful in the treatment of a condition which is responsive to
XX CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
XX CC protein may also be employed as molecular weight markers for protein
XX CC electrophoresis. The PRO coding sequence has applications in molecular
XX CC biology, including use as hybridisation probes, and in chromosome and
XX CC gene mapping.
XX SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
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XX Query Match 53.7%; Score 1472; DB 4; Length 1475;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Q	361	GGCCATGATGTGTGACATCAGTGTGCAATCCCTCCCTGGCCGTGCANTATCTGTGTGTGG	420
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Job time : 1852 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 13:46:50 : Search time 292 Seconds

(without alignments)
6674.600 Million cell updates/sec

Title: US-09-787-677a-7

Perfect score: 2742

Sequence: 1 agaaagtcacgcctgcagcagaga.....ggatcatcaatcgtcagc 2742

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1453.4	53.0	1524	4	US-09-663-600A-45
3	1393.6	50.8	1400	4	US-09-663-600A-139
4	144.6	5.3	1253	4	US-09-673-395A-71
5	140.8	5.1	1705	4	US-09-205-258-106
6	140.6	5.1	1665	4	US-09-300-958A-22
7	135.2	4.9	1554	4	US-09-895-652A-14
8	134.2	4.9	708	4	US-09-620-312D-986
9	118.4	4.3	3443	4	US-09-886-683A-3
10	118.4	4.3	3483	4	US-09-130-491-3
11	111.2	4.1	1722	4	US-09-489-847-93
12	90.8	3.3	1380	4	US-09-489-847-125
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14	76.8	2.8	363	2	US-08-966-316-8
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C	32	37.6	1.4	3651	3	US-09-738-894A-3	Sequence 3, Appl
C	33	37.6	1.4	3651	3	US-09-964-469-3	Sequence 3, Appl
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C	35	36.8	1.3	474	4	US-09-621-976-18033	Sequence 18033, A
C	36	36.8	1.3	4269	4	US-09-799-451-363	Sequence 363, App
C	37	36.6	1.3	364	4	US-09-621-976-17202	Sequence 17202, A
C	38	36.4	1.3	4897	6	5196516-7	Patent No. 5196516
C	39	35.4	1.3	44848	4	US-09-435-739-42	Sequence 42, Appl
C	40	35.4	1.3	44848	4	US-09-988-113-42	Sequence 42, Appl
C	41	35.2	1.3	208	4	US-09-603-552-10	Sequence 10, Appl
C	42	35.2	1.3	1312	4	US-09-610-906-5	Sequence 5, Appl
C	43	35.2	1.3	1312	4	US-09-976-594-346	Sequence 346, App
C	44	35.2	1.3	1354	4	US-09-610-906-2	Sequence 2, Appl
C	45	34.8	1.3	25603	4	US-09-819-607-3	Sequence 3, Appl

ALIGNMENTS

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: Sequence 491, Application US/10140002							
: Patent No. 6725730							
: GENERAL INFORMATION:							
: APPLICANT: Baker, Kevin P.							
: APPLICANT: Beresini, Maureen							
: APPLICANT: DeForge, Laura							
: APPLICANT: Desnoyers, Luc							
: APPLICANT: Filvaroff, Ellen							
: APPLICANT: Gao, Wei-Qiang							
: APPLICANT: Gerritsen, Mary B.							
: APPLICANT: Goddard, Audrey							
: APPLICANT: Godowski, Paul J.							
: APPLICANT: Gurney, Austin L.							
: APPLICANT: Sherwood, Steven							
: APPLICANT: Smith, Victoria							
: APPLICANT: Stewart, Timothy A.							
: APPLICANT: Tumas, Daniel							
: APPLICANT: Watanabe, Colin K							
: APPLICANT: Wood, William							
: APPLICANT: Zhang, Zemin							
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC							
: FILE REFERENCE: P3330R1C59							
: CURRENT APPLICATION NUMBER: US/10/140,002							
: CURRENT FILING DATE: 2002-05-06							
: Prior Application removed - See Palm or File Wrapper							
: NUMBER OF SEQ ID NOS: 550							
: SEQ ID NO 491							
: LENGTH: 1475							
: TYPE: DNA							
: ORGANISM: Homo Saplen							
US-10-140-002-491							
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Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
53.7%; Score 1472; DB 4; Length 1475;							
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OTHER INFORMATION: homology
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OTHER INFORMATION: est
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OTHER INFORMATION: id: A116709
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US-09-663-600A-45

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Best Local Similarity 98.1%; Pred. No. 0;
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RESULT 3

US-09-663-600A-139
Sequence 139, Application US/09663600A
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclercq, Aymeric
APPLICANT: Bouguerelet, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31.053.CIP
CURRENT APPLICATION NUMBER: US/09/663, 600A
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/191, 997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066, 677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069, 957
PRIOR FILING DATE: 1997-12-17

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1  PRIOR APPLICATION NUMBER: 60/074,121
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3  PRIOR APPLICATION NUMBER: 60/081,563
4  PRIOR FILING DATE: 1998-04-13
5  PRIOR APPLICATION NUMBER: 60/096,116
6  PRIOR FILING DATE: 1998-08-10
7  PRIOR APPLICATION NUMBER: 60/099,273
8  PRIOR FILING DATE: 1998-09-04
9  NUMBER OF SEQ ID NOS: 229
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11 SEQ ID NO 139
12 LENGTH: 1400
13 TYPE: DNA
14 ORGANISM: Homo sapiens
15 FEATURE:
16 NAME/KEY: sig_peptide
17 LOCATION: 36..107
18 OTHER INFORMATION: von Heijne matrix
19 OTHER INFORMATION: score 5.69999860926514
20 OTHER INFORMATION: seq ILGLGLGLGLTVVA/ML
21 NAME/KEY: polyA_signal
22 LOCATION: 1302..1307
23 NAME/KEY: polyA_site
24 LOCATION: 1389..1400
25 US-09-663-600A-139

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Db	421	GCCCTCGTGGGATTCATTTCTGTGTGCTGGAAATCTTATGAGGATCCTACAGGGACTTCTACT	480
QY	564	CACCACTGATGCTGACAGCATGGAATTTGAGATTGGAGAGGCTCTTTACTTGGGCAATTA	623
Db	481	CACCACTGATGCTGACAGCATGGAATTTGAGATTGGAGAGGCTCTTTACTTGGGCAATTA	540
QY	624	TTTCTTCCCTGTCTTCCCTGATAGCTGGAATCATCTCTGCTTTTCTGTCTCATCCAGA	683
Db	541	TTTCTTCCCTGTCTTCCCTGATAGCTGGAATCATCTCTGCTTTTCTGTCTCATCCAGA	600
QY	684	GAATTCGTCAACTACTACAGATGCTTACCAAGGCCAACCCTTGGCCACAAGGAGCTCTC	743
Db	601	GAATTCGTCAACTACTACAGATGCTTACCAAGGCCAACCCTTGGCCACAAGGAGCTCTC	660

Oy	744	CAAGGCTGTGCAACCTCCCAAGTCAAGATGAGTTCATTCTTCAAGCTTACAGGGT	803
Db	661	CAAGGCTGTGCAACCTCCCAAGTCAAGATGAGTTCATTCTTCAAGCTTACAGGGT	720
Oy	804	ATGTGTAAAGAACCAAGGGGCGAAGCTGGGGGGGTGCTGGGTCTGTGAAAAACAATGAGAC	863
Db	721	ATGTGTAAAGAACCAAGGGGCGAAGCTGGGGGGGTGCTGGGTCTGTGAAAAACAATGAGAC	780
Oy	864	AGCAACCCCGAAGGGCGAAGGTGAGGGGCACTAACACTGATCGGTGTGAGAAAGGAGCTGCT	923
Db	781	AGCAACCCCGAAGGGCGAAGGTGAGGGGCACTAACACTGATCGGTGTGAGAAAGGAGCTGCT	840
Oy	924	GAGGATAGACTGACTTTTGGCCATTGGATTGATGAGCAAAAGCGAATAAGGGGCTAGTGTAC	983
Db	841	GAGGATAGACTGACTTTTGGCCATTGGATTGATGAGCAAAAGCGAATAAGGGGCTAGTGTAC	900
Oy	984	AGCATGCAAGGTGTAATTTGCCAAGGATGCTGGCCATGCGACGCTTTCTGTTTCTCACT	1043
Db	901	AGCATGCAAGGTGTAATTTGCCAAGGATGCTGGCCATGCGACGCTTTCTGTTTCTCACT	960
Oy	1044	TGCGTCTCCCTGGCCCTAAGTCCCAACCCCTCAACTTGAACCCCATTTCCCTTAAGCAG	1103
Db	961	TGCGTCTCCCTGGCCCTAAGTCCCAACCCCTCAACTTGAACCCCATTTCCCTTAAGCAG	1020
Oy	1104	GACTCAGAGGATGCCCTTTGGCCCTCTGTGTTTACCTGGGACTGCATCCCAACCCCACTAAT	1163
Db	1021	GACTCAGAGGATGCCCTTTGGCCCTCTGTGTTTACCTGGGACTGCATCCCAACCCCACTAAT	1080
Oy	1164	CACATGCCACTGACTGACCTCTTGTGTATCAAAACCTCTCTCTGTGTGAGTTGGCTCT	1223
Db	1081	CACATGCCACTGACTGACCTCTTGTGTATCAAAACCTCTCTCTGTGTGAGTTGGCTCT	1140
Oy	1224	TAGTCAATGTGGGGGATGAGGAAGAGAACAGATGGCTTTTGTGGGACTGACTTAACT	1283
Db	1141	TAGTCAATGTGGGGGATGAGGAAGAGAACAGATGGCTTTTGTGGGACTGACTTAACT	1200
Oy	1284	ACTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCCTGGAACCTTCATCCACTCTTGT	1343
Db	1201	ACTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCCTGGAACCTTCATCCACTCTTGT	1260
Oy	1344	TATATCTCCACAGTGTCCACACTTAATTTGTGCATGAACTGAAATTAACAATCCTACGGT	1403
Db	1261	TATATCTCCACAGTGTCCACACTTAATTTGTGCATGAACTGAAATTAACAATCCTACGGT	1320
Oy	1404	ATCCAGGGAACAGAAAGCAGATGACAGATGGAGGACAGAAAGCGACTGGGACATTT	1463
Db	1321	ATCCAGGGAACAGAAAGCAGATGACAGATGGAGGACAGAAAGCGACTGGGACATTT	1380
Oy	1464	AAAAAAAAATGAAAAA 1483	
Db	1381	AAAAAAAAATGAAAAA 1400	
RESULT 4			
US-09-673-395A-71			
; Sequence 71, Application US/09673395A			
; Patent No. 6620923			
; GENERAL INFORMATION:			
; APPLICANT: SPECHT, THOMAS			
; APPLICANT: HINZMANN, BERND			
; APPLICANT: SCHMITT, ARMIN			
; APPLICANT: PILARSKY, CHRISTIAN			
; APPLICANT: DAHL, EDGAR			
; APPLICANT: ROSENTHAL, ANDRE			
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE			
; FILE REFERENCE: ALBRE-12			
; CURRENT APPLICATION NUMBER: US/09/673.395A			
; NUMBER OF SEQ ID NOS: 637			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 71			
; LENGTH: 1253			

TYPE: DNA
ORGANISM: Homo sapiens
US-09-673-395A-71

Query Match 5.3%; Score 144.6; DB 4; Length 1253;
Best Local Similarity 54.7%; Pred. No. 9.5e-35;
Matches 310; Conservative 0; Mismatches 254; Indels 3; Gaps 1;

QY 109 GAGGTGCGCATGAGCTCTCTGTTGCTCCCACTGTTGGGCTACATCTTACGCTTGGG 168
DB 336 GAGGGCGGAATGCGCAATTCGGGCTGCGAGTCTGCTGCTTCCATGAGCCCTGCTGG 355
QY 169 GCTTTTGGGACACTGTTGCCATGCTGCTCCCGAGCTGAAAACAAGTTCTTATGTCG 228
DB 396 CTGGGTGGTCTGTGGCTGCTGACCGCCATCCCGAGTGGAGATGAGTCTCTATGCGGG 455
QY 229 TGCAGCATTTGTGACAGCACTGCTTCTCCAGGGCTCTGATGATGAAATGTGCAACA 288
DB 456 TGAACATCATCATCGGCCCAAGGCAATGTAAGGGGCTGTGATGACTGCGTCAAGCA 515
QY 289 CAGCAGGAGCATCAACCAAGTGTGATCTATAGCACCCTTCTGGGCTGCGCGTGCAT 348
DB 516 GAGCAGGGGATGATGAGCTGCAAAATGTAAGTCTGCTGCTGCTGCTGCTGCTGCTG 575
QY 349 CAGGCTGCCAGGCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 408
DB 576 GCGAGCCACTGAGCCCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 635
QY 409 CTCTGTGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 465
DB 636 GGCACAGATGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 695
QY 466 AGTGGGGTGTGAGTGGGATGATGATGATGATGATGATGATGATGATGATGATGAT 525
DB 696 TATAGCATGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 755
QY 526 TGCTTGATCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 585
DB 756 CTCTGTGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 815
QY 586 GAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 645
DB 816 TAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 875
QY 646 AGCTGATCATCTCTGCTTTCTG 672
DB 876 GGGAGGTGACTGCTCTCTGTTCTG 902

RESULT 5
US-09-205-258-106
Sequence 106, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
EARLIER FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 106
LENGTH: 1705
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:

NAME/KEY: SITE
LOCATION: (724)
OTHER INFORMATION: n equals a,t,g, or c
US-09-205-258-106

Query Match 5.1%; Score 140.8; DB 4; Length 1705;
Best Local Similarity 50.7%; Pred. No. 1.9e-33;
Matches 334; Conservative 1; Mismatches 324; Indels 0; Gaps 0;

82 AGCAGTCCCTGAAGACGCTTCTACTAGAGGTGAGGCTCCATGAGGCTCTCTGAGCTCCAACT 141
172 AGCTTTCAGAGTCTCTCACTCCGCGAGACGCTGAACATAGCTTCCATGAGGCTCAAGGT 231
142 TGTGGGTACATCTAGAGCTCTTCTGAGGCTTTTGGGCACTGTGTGCTCC 201
232 AATGGGATGCGCTGCGCTCCCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 291
202 CAGCTGAAAAAAGATTCTTATGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 261
292 CAGTGGGCGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 351
262 GGGCTCTGATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 321
352 GGGCTCTGATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 411
322 CAGCTTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 381
412 CTGGCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 471
382 TGCATCT 441
472 CATCTGCT 531
442 CAGGATCCCGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 501
532 GAGGATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 591
502 AGGCTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 561
592 CGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 651
562 CTCACTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 621
652 CAGTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 711
622 TATTTCT 681
712 GGGCTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 771
682 GAGGATCCCGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 740
772 CAGGATCCCGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 830

RESULT 6
US-09-300-958A-22
Sequence 22, Application US/09300958A
Patent No. 6495319

GENERAL INFORMATION:
APPLICANT: McCrelland, Michael
APPLICANT: Weissh, John
TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
FILE REFERENCE: P-PH 3457
CURRENT APPLICATION NUMBER: US/09/300,958A
CURRENT FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/083,331
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/098,070
PRIOR FILING DATE: 1998-08-27
PRIOR APPLICATION NUMBER: 60/118,624
PRIOR FILING DATE: 1999-02-04

NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 1665
TYPE: DNA
ORGANISM: Homo sapiens
US-09-300-958A-22

Query Match 5.1%; Score 140.6; DB 4; Length 1665;
Best Local Similarity 50.8%; Pred. No. 2.1e-33;
Matches 335; Conservative 0; Mismatches 324; Indels 0; Gaps 0;

82 AGCAGTCCCTGAAGACGCTTCTACTAGAGGTGAGGCTCCATGAGGCTCTCTGAGCTCCAACT 141
146 AGCTTTCAGAGTCTCTCACTCCGCGAGACGCTGAACATAGCTTCCATGAGGCTCAAGGT 205
142 TGTGGGTACATCTAGAGCTCTTCTGAGGCTTTTGGGCACTGTGTGCTCC 201
206 AATGGGATGCGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 265
202 CAGCTGAAAAAAGATTCTTATGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 261
266 CATGTGGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 325
262 GGGCTCTGATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 321
326 GGGCTCTGATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 385
322 CAGCTTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 381
386 CTGGCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 445
382 TGCATCT 441
446 CATCTGCT 505
442 CAGGATCCCGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 501
506 GAGGATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 565
502 AGGCTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 561
566 CGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 625
562 CTCACTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 621
626 CAGTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 685
622 TATTTCT 681
686 GGGCTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 745
682 GAGGATCCCGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 740
746 CAGGATCCCGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 804

RESULT 7
US-09-895-652A-14
Sequence 14, Application US/09895652A
Patent No. 6774223

GENERAL INFORMATION:
APPLICANT: Macina, Roberta
APPLICANT: Pillai, Rageswari
TITLE OF INVENTION: Method of Diagnosing, Monitoring, Staging, Imaging and
FILE REFERENCE: DEX-0211
CURRENT APPLICATION NUMBER: US/09/895,652A
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: 60/214,515
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 14
LENGTH: 1554
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (1544)
US-09-895-652A-14

Query Match
Best Local Similarity 54.8%; Score 135.2; DB 4; Length 1554;
Pred. No. 1e-31;
Matches 311; Conservative 0; Mismatches 253; Indels 4; Gaps 2;

109 GAGGTGCGCATGGCCCTCTGCTGCTCCCACTGTTGGGGCTAATCTTAGG-CCTTTGG 167
424 GAGGGCGGAATGGCCCAATTCGGCCCTGCACTGCTTCTCCATGGCCCTGCTGG 483
168 GGGCTTTGGGACACTGGTTGCCATGCTGCTCCCACTGGGAAACAAATTCTTATGTCG 227
484 GCTGGGTGGGTCTGGTGGCCCTGACCGCCATCCCGCAGTGGCAGATGAGCTCTATGCGG 543
228 GTGCCAGCATTTGACAGCAGTTGGCTTTCACAGGGCTCTGGATGGAAATGTCACAC 287
544 GTGCAACATCATCACGCCGCCAGGCCATGTACAAGGGGCTGTGATGAGCTGCTCACGC 603
288 ACAACAGGAGCATCACCCAGTGTGACATCTATAGCACCCCTTGGGGCTGGCCGCTGACA 347
604 AGAGCAGGGAGATGATAGCTGCAAAATGTACAGCTGGTCTGCTGCTGCTGCTGCTGCT 663
348 TCCAGCTGCGCCAGGCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 407
664 TGACAGGCGATCGAGCCCTAATGATGATGATGATGATGATGATGATGATGATGATGAT 723
408 TCTCTGTGGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 464
724 TGCGCAGATGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 783
465 GAGTGGGGTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 524
784 GTATAGCATGGTGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 843
525 TTGGCTGGAATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 584
844 GCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 903
585 TGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 644
904 TTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 963
645 TAGCTGGAATCTTCTGCTTTTCTG 672
964 TGGAGGTGACATGCTCTCTCTGTTCTG 991

RESULT 8

US-09-620-312D-986
Sequence 986; Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Abundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Zhou, Jian-Rui
APPLICANT: Wang, Yunding
APPLICANT: Ma, Yunding
APPLICANT: Wang, Dunru

APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghaast
APPLICANT: Demanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP28
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pc FL_genes Version 1.0
SEQ ID NO 986
LENGTH: 708
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (46)..
US-09-620-312D-986

Query Match
Best Local Similarity 50.7%; Score 134.2; DB 4; Length 708;
Pred. No. 1.2e-31;
Matches 322; Conservative 0; Mismatches 313; Indels 0; Gaps 0;

116 GCCATGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 175
43 GCCATGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 102
176 GGCACATGGTGTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 235
103 AATGGCTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 162
236 ATTGTGACAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 235
163 ATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 222
296 GGCATCACCAAGTGTGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 355
223 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 282
356 GCCATGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 415
283 GCACTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 342
416 GTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 475
343 GCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 402
476 GCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 535
403 ACCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 462
536 CTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 595
463 GCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 522
596 ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 655
523 CTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 582
656 ATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 715
583 TTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 642
716 GCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 750
643 TACTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 677

RESULT 9

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US-09-886-683A-3
; Sequence 3, Application US/0988683A
; Patent No. 6627439
; GENERAL INFORMATION:
; APPLICANT: Hoevel, Thorsten
; APPLICANT: Koch, Stefan
; APPLICANT: Kubbies, Manfred
; APPLICANT: Mundigl, Olaf
; APPLICANT: Rueger, Petra
; TITLE OF INVENTION: Antibodies against SEMPL (p23)
; FILE REFERENCE: Case 20692
; CURRENT APPLICATION NUMBER: US/09/886,683A
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: EP00113344.6
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: EP01107799.7
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3443
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (221)..(853)
; US-09-886-683A-3
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Query Match      4.3%; Score 118.4; DB 4; Length 3443;
Best Local Similarity 52.0%; Pred. No. 3,6e-26;
Matches 291; Conservative 0; Mismatches 266; Indels 3; Gaps 1;
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QY 116 GCCATGCGCTCTCTTGGCTTCCACACTTGTGGCTACATCTAGGCTTCTGGGCTTTTG 175
DB 218 GTCATGGCCCAACGGGGGCTGACGCTGTGGCTTCACTTCGCGCTTCGGATGATC 277
QY 176 GGCACACTGTTGCCATGCTGCTCCCGACGTGAAAACAAATTCTATGTCGGCCAGC 235
DB 278 GGGGCCATCTCAGCACTGCGCCGCGCCAGTGGAGATTTACTCTATGCGCGGACMAC 337
QY 236 ATTGTGACAGCAAGTGGCTTCTCCAAAGGGCTCGATGATGAAATGTCACACAGCACA 295
DB 338 ATGTGACCGCCCAAGCCATGATGAGAGGGCTGTGATGTCTGCGTGTGACAGAGCACC 397
QY 296 GGCATCACCCAGTGTGACATCTATAGCACTTCTGGGCTGCGCGCTGACATCCAGGCT 355
DB 398 GGGCAGATTCAGTGAAGAAAGCTTTGACTCTTGCTGATCTGAGACAGACATGGCAAGCA 457
QY 356 GCCCAGGCCATGATGTGACATCAGTGAATCTCTCCCTGCGCTGCAATTATCTGTG 415
DB 458 ACCCGGCTTGTATGTGTGGATCTCTCTGGAGTGAATGCAATCTTTGTGGCCACC 517
QY 416 GTGGGATGAGATGACAGTCTTCTGCGCAGAAATCCGAG--CCAAAGACAGATGGCG 472
DB 518 GTTGGCATGAAAGTATGAAGTCTTGGAAAGCATAGATGACAAAGATGAGATGGCT 577
QY 473 GTAGCAGGTGAGTCTTTTCACTCTTGAAGGCTCTCTGGAAATTCCTGTTGCTG 532
DB 578 GTCAATGGGGGTGAGATATTTCTTGGAGGCTGCTATTTTATGTGCAACAGATGG 637
QY 533 AATCTTCATGGATCTTACGGGACTTACTACCACTGTGCTGACAGACATGAATTT 592
DB 638 TATGGCAATGAATCTTCAAGAAATCTATGACCTTATGACCCAGATCAATGCGAGTAC 697
QY 593 GAGATTGAGAGGCTTTTACTTGGGCAATATTTCTTCCCTGTTCTCCGATAGCTGGA 652
DB 698 GAATTTGGTGAAGGCTCTTCACTGCGGTGGGCTGCTGCTTCTCTGCGCTTCTGGAGGT 757
QY 653 ATCATCTCTGCTTTTCTG 672
DB 758 GCCCTACTTTGCTGTTCTG 777
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RESULT 10
US-09-130-491-3
; Sequence 3, Application US/09130491
; Patent No. 6416974
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodheart, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/09/130,491
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: US 60/058,108
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: US 60/054,961
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 3483
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (240)...(872)
; US-09-130-491-3
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Query Match      4.3%; Score 118.4; DB 4; Length 3483;
Best Local Similarity 52.0%; Pred. No. 3,7e-26;
Matches 291; Conservative 0; Mismatches 266; Indels 3; Gaps 1;
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QY 116 GCCATGCGCTCTTGGCTTCCACACTTGTGGCTACATCTAGGCTTCTGGGCTTTTG 175
DB 237 GTCATGGCCCAACGGGGGCTGACGCTGTGGCTTCACTTCGCGCTTCGGATGATC 296
QY 176 GGCACACTGTTGCCATGCTGCTCCCGACGTGAAAACAAATTCTATGTCGGCCAGC 235
DB 297 GGGGCCATCTCAGCACTGCGCCGCGCCAGTGGAGATTTACTCTATGCGCGGACMAC 356
QY 236 ATTGTGACAGCAAGTGGCTTCTCCAAAGGGCTCTGATGAAATGTCACACAGCACA 295
DB 357 ATGTGACCGCCCAAGCCATGATGAGAGGGCTGTGATGTCTGCGTGTGACAGAGCACC 416
QY 296 GGCATCACCCAGTGTGACATCTATAGCACTTCTGGGCTGCGCGCTGACATCCAGGCT 355
DB 417 GGGCAGATTCAGTGAAGAAAGCTTTGACTCTTGCTGATCTGACAGACATGGCAAGCA 476
QY 356 GCCCAGGCCATGATGTGACATCAGTGAATCTCTCCCTGCGCTGCAATTATCTGTG 415
DB 477 ACCCGGCTTGTATGTGTGGATCTCTCTGGAGTGAATGCAATCTTTGTGGCCACC 536
QY 416 GTGGGATGAGATGACAGTCTTCTGCGCAGAAATCCGAG--CCAAAGACAGATGGCG 472
DB 537 GTTGGCATGAAAGTATGAAGTCTTGGAAAGCATAGATGACAAAGATGAGATGGCT 596
QY 473 GTAGCAGGTGAGTCTTTTCACTCTTGAAGGCTCTCTGGAAATTCCTGTTGCTG 532
DB 597 GTCAATGGGGGTGAGATATTTCTTGGAGGCTGCTATTTTATGTGCAACAGATGG 656
QY 533 AATCTTCATGGATCTTACGGGACTTACTACCACTGTGCTGACAGACATGAATTT 592
DB 657 TATGGCAATGAATCTTCAAGAAATCTATGACCTTATGACCCAGATCAATGCGAGTAC 716
QY 593 GAGATTGAGAGGCTTTTACTTGGGCAATATTTCTTCCCTGTTCTCCGATAGCTGGA 652
DB 717 GAATTTGGTGAAGGCTCTTCACTGCGGTGGGCTGCTGCTTCTCTGCGCTTCTGGAGGT 776
QY 653 ATCATCTCTGCTTTTCTG 672
DB 777 GCCCTACTTTGCTGTTCTG 796
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RESULT 11
US-09-489-847-93
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/ Sequence 93, Application US/09489847
/ Patent No. 6476195
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al
/ TITLE OF INVENTION: 98 Human Secreted Proteins
/ FILE REFERENCE: P2031P1
/ CURRENT APPLICATION NUMBER: US/09/489,847
/ CURRENT FILING DATE: 2000-01-24
/ EARLIER APPLICATION NUMBER: PCT/US99/17130
/ EARLIER FILING DATE: 1999-07-29
/ EARLIER APPLICATION NUMBER: 60/094,657
/ EARLIER FILING DATE: 1998-07-30
/ EARLIER APPLICATION NUMBER: 60/095,486
/ EARLIER FILING DATE: 1998-08-05
/ EARLIER APPLICATION NUMBER: 60/096,319
/ EARLIER FILING DATE: 1998-08-12
/ EARLIER APPLICATION NUMBER: 60/095,454
/ EARLIER FILING DATE: 1998-08-06
/ EARLIER APPLICATION NUMBER: 60/095,455
/ EARLIER FILING DATE: 1998-08-06
/ NUMBER OF SEQ ID NOS: 376
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 93
/ LENGTH: 1722
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-489-847-93

Query Match 4.1%; Score 111.2; DB 4; Length 1722;
Best Local Similarity 50.0%; Pred. No. 4,1e-24;
Matches 275; Conservative 1; Mismatches 274; Indels 0; Gaps 0;
QY 116 GCCATGGCCCTCTCTGCTCCCACTTGTGGCTACATCTTAGCCCTTTCGGGCTTTG 175
DB 458 GCCATGGGCTCCGACGGTGGAGATCTTGGCTGTGGCTGTGGGCTGGGG 517
QY 176 GGCACTGTTGTCATGCTGCTCCCACTGGAAGAAAGTTCTTATGTCGGTCCAGC 235
DB 518 GGTCTGATCTGCGTGGGGGCTGCCATGTGGAGTGAACCGCTTCTGGAACCAAC 577
QY 236 ATTGTGACAGCAAGTTGGCTTCTCCAGGGGCTCTGATGAAATGTGCACACAGACA 295
DB 578 ATGTGACGGCGAGACCACTGGAAGGGCTGTGATGTCTGTGTCGTGACAGAC 637
QY 296 GGCATCAACCAAGTGAATCTATAGCAACCTTGTGGGCTGCGCGGTGACATCCAGCT 355
DB 638 GGGCACATGACGTGCAAGTGAAGTACACTGGTGTGCTGTGACACCGAGGTGACGGC 697
QY 356 GCCCAGGCCATGATGTGACATCCAGTGAATCTCTCCCTGCGCTGCATTATCTGTG 415
DB 698 GCGGGGGCGTCAACCGTAGGCGCGTGTGCTGCTGCTGCTGCTTCTGTACCTTG 757
QY 416 GTGGGACATGAGATGACAGTCTTGTGCAAGAAATCCGAGCCAAAGACAGAGTGGCGTA 475
DB 758 GCGGGCGCGAGTGCACCACTGTGAGCCCGGCGCCGAGCGGCGGTGTGCGCTC 817
QY 476 GCAAGTGAAGTCTTTTCACTTGTGAGGCTCTCTGGGATTCATCTCTGTGCTGGAAT 535
DB 818 ACCGGAAGCGTGTCTACTCTGTTTGTGGGGTGTGTGCGCTGTGCACTCTGTGTTTC 877
QY 536 CTTCATGGATCTTACAGGGAATCTTACTACCACTGTGGCTGTGACAGATGAATTTGAG 595
DB 878 GCCAATTTGTCTCCGAGTTTACGACCCGCTGTGTGCGGTGTGCGAGAAATACAG 937
QY 596 ATTGAGAGGCTCTTTTACTTGTGGCATTAATTTCTTCTGTCTCTCCATGATCTGGAATC 655
DB 938 CTGGGGCGAGCGGTGATCATGCTGTGGCGGCGACCGGCGTGTCTATGTAGAGGGCTGC 997
QY 656 ATCTCTGCT 665
DB 998 CTCTGTGCT 1007

RESULT 12
US-09-489-847-125
/ Sequence 125, Application US/09489847
/ Patent No. 6476195
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al
/ TITLE OF INVENTION: 98 Human Secreted Proteins
/ FILE REFERENCE: P2031P1
/ CURRENT APPLICATION NUMBER: US/09/489,847
/ CURRENT FILING DATE: 2000-01-24
/ EARLIER APPLICATION NUMBER: PCT/US99/17130
/ EARLIER FILING DATE: 1999-07-29
/ EARLIER APPLICATION NUMBER: 60/094,657
/ EARLIER FILING DATE: 1998-07-30
/ EARLIER APPLICATION NUMBER: 60/095,486
/ EARLIER FILING DATE: 1998-08-05
/ EARLIER APPLICATION NUMBER: 60/096,319
/ EARLIER FILING DATE: 1998-08-12
/ EARLIER APPLICATION NUMBER: 60/095,454
/ EARLIER FILING DATE: 1998-08-06
/ EARLIER APPLICATION NUMBER: 60/095,455
/ EARLIER FILING DATE: 1998-08-06
/ NUMBER OF SEQ ID NOS: 376
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 125
/ LENGTH: 1380
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-489-847-125

Query Match 3.3%; Score 90.8; DB 4; Length 1380;
Best Local Similarity 50.2%; Pred. No. 9,6e-18;
Matches 276; Conservative 0; Mismatches 272; Indels 2; Gaps 2;
QY 116 GCCATGGCCCTCTCTGCTCCCACTTGTGGCTACATCTTAGCCCTTTCGGGCTTTG 175
DB 132 GCCATGGGCTCCGACGGTGGAGATCTTGGCTGTGGCTGTGGGCTGGGG 191
QY 176 GGCACTGTTGTCATGCTGCTCCCACTGGAAGAAAGTTCTTATGTCGGTCCAGC 235
DB 192 GGTCTGATCTGCGTGGGGGCTGCCATGTGGAGTGAACCGCTTCTGGAACCAAC 251
QY 236 ATTGTGACAGCAAGTTGGCTTCTCCAGGGGCTCTGATGAAATGTGCACACAGACA 295
DB 252 ATGTGACGGCGAGACCACTGGAAGGGCTGTGATGTCTGTGTCGTGACAGAC 311
QY 296 GGCATCAACCAAGTGAATCTATAGCAACCTTGTGGGCTGCGCGGTGACATCCAGCT 355
DB 312 GGCA-CATGAGTGAAGTGAAGTACACTGGTGTGCTGTGACACCGAGGTGACGGCG 370
QY 356 GCCCAGGCCATGATGTGACATCCAGTGAATCTCTCCCTGCGCTGCATTATCTGTG 415
DB 371 GCGGGGGCGTCAACCGTAGGCGCGTGTGCTGCTGCTGCTGCTTCTGTGACCTG 430
QY 416 GTGGGACATGAGATGACAGTCTTGTGCAAGAAATCCGAGCCAAAGACAGAGTGGCGTA 475
DB 431 GCGGGCGCGAGTGCACCACTGTGAGCCCGGCGCCGAGCGGCGGTGTGCGCTC 490
QY 476 GCAAGTGAAGTCTTTTCACTTGTGAGGCTCTCTGGGATTCATCTCTGTGCTGGAAT 535
DB 491 ACCGGAAGCGTGTCTACTCTGTTTGTGGGGTGTGTGCGCTGTGCACTCTGTGTTTC 550
QY 536 CTTCATGGATCTTACAGGGAATCTTACTACCACTGTGTGCTGTGACAGATGAATTTGAG 595
DB 551 GCCAATTTGTCTCCGAGTTTACGACCCGCTGTGTGCGGTGTGCGAGAAATACAG 610
QY 596 ATTGAGAGGCTCTTTTACTTGTGGCATTAATTTCTTCTGTCTCTCCATGATCTGGAATC 655
DB 611 CTGGGGCGA-CGCTGTGATCGGCTGTGGGGCGCACCGGCGTGTCTATGTAGAGGGCTGC 669
QY 656 ATCTCTGCT 665
DB 670 CTCTGTGCT 679

RESULT 13
US-09-621-976-1835
; Sequence 1835, Application US/09621976
; Patent No. 663063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 1835
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 173..511
; NAME/KEY: sig.peptide
; LOCATION: 173..409
; OTHER INFORMATION: Von Heljne matrix
; OTHER INFORMATION: score 4.30000019073486
; OTHER INFORMATION: seq YDSILALSPDLQA/AR
US-09-621-976-1835

Query Match 3.0%; Score 81.8; DB 4; Length 615;
Best Local Similarity 51.6%; Pred. No. 3.7e-15;
Matches 209; Conservative 1; Mismatches 193; Indels 2; Gaps 1;

QY 119 ATGGCCCTCTTGGGCTCCAACTGTGGGCTACATCTAGGCTTGGGCTTTGGG 178
DB 173 ATGGCAACCATGCTTGAAGATGCTGGGCTTTTGGGCTTGGGATGGTGGC 232
QY 179 ACACTGGTTCCTGCTGCTCCGCTGAGAAACAAGTTCTTATGCTGCCAGATT 238
DB 233 ACATGGCTGTCACTGTGCTGCTGAGAGATGCTGGGCTTCAATGAAACAATC 292
QY 239 GTGACGACATTTGGCTTCTCCAGGGCTCTGATGGAATGTGCAACACAGACAGC 298
DB 293 GTGCTTTTAAACCTTCTGGGAAGACTGTGATGTAATGCTGAGGAGGCTTAATC 352
QY 299 ATACCCAGTGTGACATCTATAGCACTTCTGGGCTTGGCCGCTGACATCCAGGCTGCC 358
DB 353 AGATGACAGTGAATAATCTATGATTCCTGCTGCTTTTCTCGGACCTACAGGAGCC 412
QY 359 CAGGACATGATGTGACATCAATGATCTCTGCTGCTGCTGATTAATCTGTGTG 418
DB 413 AGAGCATGATGTGTGCTGCTGCTGATGCTTCTTGGCTTCAATGATGGCATCTT 472
QY 419 GGCATGATGACACAGCTTCTGCGAGAAATCCGA--GCCAAGACAGAGTGGCGTAG 476
DB 473 GGCATGAAATGACAGGCTGACGCGGAGCAATGAAAGGAGGCTCACATCTGCTGA 532
QY 477 CAGGTGAGTCTTTTCTATCTTGAAGGCTCTGCGGATCATTC 521
DB 533 CGGCTGAAATCATCTTATCATCGCGGACATGATGCTGCTATCC 577

RESULT 14
US-08-966-316-8
; Sequence 8, Application US/08966316
; Patent No. 5932445
; GENERAL INFORMATION:
; APPLICANT: Lai, Preeti
; APPLICANT: Au-Young, Janice
; APPLICANT: Reddy, Roopa
; APPLICANT: Murty, Lynn B.
; APPLICANT: Mathur, Preeti

TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,316
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0424 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: HMT3AZT01
CLONE: 2417676
US-08-966-316-8

Query Match 2.8%; Score 76.8; DB 2; Length 363;
Best Local Similarity 55.7%; Pred. No. 9.5e-14;
Matches 147; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 116 GCCATGCTCTCTTGGCTCCAACTGTGGGCTACATCTAGGCTTGGGCTTTGG 175
DB 45 GCATGCTGCTCTGCGGAATGACATCTGAGAGTGTCTGACATGCTGGGCTGGGTG 104
QY 176 GGCACACTGTTGCCATGCTGCTCCGCTGAGAAACAAGTTCTTATGCTGGTGCAGC 235
DB 105 AATGCTGCTCTCTGCTGCTGCTGCTGATGGAAGTACCGCTTCAATCGGCAACG 164
QY 236 ATGTGACAGCAATTTGCTTCTCAAGGCTCTGATGGAATGTGCCACACACACACA 295
DB 165 ATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 224
QY 296 GGCATCAACCAATGTGACATCTATAGCACTTCTGCGGCTGCTGCTGCTGCTGCT 355
DB 225 GGCATGACAGTGAAGTGTGACATCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 284
QY 356 GCCCAGGACATGATGTGACATCC 379
DB 285 GCACGTGCTCTGTGTCAATCGCC 308

RESULT 15
US-09-404-879A-104
; Sequence 104, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.

```

? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
? TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
? FILE REFERENCE: 210121.462C2
? CURRENT APPLICATION NUMBER: US/09/404,879A
? CURRENT FILING DATE: 1999-09-24
? NUMBER OF SEQ ID NOS: 393
? SOFTWARE: FASTSEQ for Windows Version 3.0
? SEQ ID NO 104
? LENGTH: 441
? TYPE: DNA
? ORGANISM: Homo sapien
? US-09-404-879A-104

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Query Match	2.7%	Score 75.4	DB 4	length 441
Best Local Similarity	53.6%	Pred. No. 3e-13		
Matches 157, Conservative	0	Mismatches 136	Indels 0	Gaps 0

QY	82	AGCAGTCCCTGAAAGACGCTTCTACTAGAGAGTCTGCATAGCCCTCTCTTGGCCTCCAACT	141
Db	146	AGCCTTCCAGAGTCTCTCAACTCCCGGTGAGAGCTGAACAAATGGCCTCCATGGGGGTTACAGGT	205
QY	142	TGTGGGCTACATCTTAGGCGCTTCTGTGGGCGCTTTTGGGCACTGTGTTCATGCTGCTCCC	201
Db	206	AATGGGCATTCGGCGTGGCCGCTCTGGGCTGAGCGCCGCTCATCTGTGCTGCGCGCTGCC	265
QY	202	CAGCTGGAAGAAACAAGTCTTATGTGGGTGCACAGATTGTGACAGCAAGTGGCTTCTCCAA	261
Db	266	CATGTGGGCGCGTACAGGCGCTTTCATGTGGGACAGCAATTGTTCACCTCGACAGCAATCTGGGA	325
QY	262	GGGCGCTCTGAGATGGAATGTGCACACACAGCAACGCGCATCACCCAGTGTGTACATCTTAG	321
Db	326	GGGCGCTTATGAGATGAACGTGGTGGTGAAGACACCGGCGAGATGCAAGTGAAGGTATGCA	385
QY	322	CACCTTTCTGGGCGTCCCGCTGACATCCAGGCTGCCAGGCGCATATAGTGTGA	374
Db	386	CTGCGTGTGCTGACATCGCCGACAGAACTGTGACAGGGGCGGCCGCGCTCTGTATCA	438

Search completed: October 30, 2004, 09:12:15
Job time : 295 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 13:46:35 ; Search time 12494 Seconds

(without alignments)
7997.258 Million cell updates/sec

Title: US-09-787-677A-7

Perfect score: 2742

Sequence: 1 agagagcagcgtcgscagaga.....ggtgatcaatcctgtagc 2742

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST: *
1: gb_esc1: *
2: gb_esc2: *
3: gb_esc3: *
4: gb_esc4: *
5: gb_esc5: *
6: gb_esc6: *
7: gb_esc7: *
8: gb_esc8: *
9: gb_esc9: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1043	38.0	2829	3 AK004990	Mus muscu
2	728	26.5	822	4 BG386074	602455248
3	693	25.3	693	9 AY400251	Homo sapi
4	686.8	25.0	945	2 BE513091	601171545
5	676.4	24.7	693	9 AY400252	Pan trogl
6	643	23.5	680	2 BE304667	601105783
7	639	23.3	662	4 BM791379	K-BST0071
8	637.4	23.2	728	4 BG325755	602424466
9	617	22.5	978	4 BG164062	602341087
10	614.6	22.4	652	7 CR628947	DKF2P469L
11	614.4	22.4	786	8 BZ215522	CH230-416
12	613.6	22.4	650	7 CR546700	DKF2P470L
13	606	22.1	643	4 BG328625	602427889
14	592	21.6	761	5 BP445902	BP445902
15	590.4	21.5	729	7 CN793010	4127966 B
16	582.4	21.2	707	7 CR836649	4061487 B
17	582.2	21.2	589	5 BU071883	im35d1.Y
18	577	21.0	676	2 AM385836	CM3-LT004
19	575.6	20.7	630	2 AM837727	CM1-LT004
20	566.6	20.7	1043	4 BG164241	602341250
21	561	20.5	685	7 CR975368	4106492 B
22	555.4	20.3	623	2 AM837724	CM1-LT004
23	555	20.2	555	5 BU073403	im35d1.x
24	551.6	20.1	727	4 B1101652	602887470

25	551.2	20.1	777	4 B1102100	B1102100 602887847
26	550.6	20.1	693	9 AY400253	Mus muscu
27	544.4	19.9	752	4 CB952500	AGENCOURT
28	543.4	19.8	557	4 BG399901	602441435
29	543	19.8	810	4 BG427780	602497154
30	531	19.4	884	6 CA469620	AGENCOURT
31	526.6	19.2	648	7 CN788131	4122426 B
32	522.2	19.0	750	2 AM475316	un64d02.Y
33	521.4	19.0	758	2 B1102679	B1102679 602888236
34	521	19.0	724	4 B1100253	602885716
35	513	18.7	848	6 CA469366	AGENCOURT
36	512.8	18.7	758	6 CB999779	AGENCOURT
37	509.4	18.6	818	6 CA469360	AGENCOURT
38	508.8	18.6	570	7 CR628828	DKF2P469B
39	508.2	18.5	856	2 BP541534	602067905
40	507.6	18.5	886	2 BP032123	601559727
41	504.8	18.4	846	2 BF789255	602105156
42	504.8	18.4	1114	2 BF789836	602105395
43	503	18.3	511	1 AM006504	wf05e05.x
44	502.4	18.3	546	2 BF819923	MRI-RT002
45	501.2	18.3	774	7 CK031415	AGENCOURT

ALIGNMENTS

RESULT 1	AK004990	2829 bp	MRNA	linear	HTC 03-APR-2004
LOCUS	AK004990	Mus musculus adult male liver cDNA, RIKEN full-length enriched library, clone:1300013G06 product:claudin 2, full insert sequence.			
DEFINITION	AK004990	AK004990.1 GI:12836594			
ACCESSION	AK004990	AK004990.1 GI:12836594			
VERSION	AK004990	AK004990.1 GI:12836594			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kohno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kohno, H., Akiyama, J., Nishii, K., Kikunai, T., Tashiro, H., Itoh, A., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishise, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
PUBMED	11076861				
REFERENCE	4				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409, 685-690 (2001)				
MEDLINE	5				
PUBMED	11076861				
REFERENCE	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.				

Db 1110 GATCCTCTGTGCTTGAATGCTCAACCCAAAGCCCAATCCATCTGCACTTTAG 1169
 Qy 1100 CAGAGTCAAGAGATCCCTTGGCCCTGTGGTTACCTGGGATCTCAATCCCAACAC 1159
 Db 1170 GCTATGCCAGAGGCTCTCTGCTGCTTGGTTTACTGAGATCTGTCCCAACCA 1229
 Qy 1160 TAAATCAATCCCACTGATGATGATGATGATGATGATGATGATGATGATGATG 1219
 Db 1230 TCAATCTGTGATCAATCACTGTGATCAAAAGACCTCTGCTGCTGATGATG 1289
 Qy 1220 CTCTTACTCA-----TTGCTGGGATGGAGAGAGAGAGAGAGAGAGAGAGAG 1274
 Db 1290 CTCTTAACTCAATTAATTAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1349
 Qy 1275 CTCTTAACTCAATTAATTAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1323
 Db 1350 TTCTAGTCTCTCTCAAAATCTCAAGCCAAAGAGAGAGAGAGAGAGAGAGAGAG 1409
 Qy 1324 AACCTCATCCCACTCTTGTATGATCTCAAGTGTCAAGTCAATTTGTGATGATG 1383
 Db 1410 AGCTTCTCTTCAAGTTTGTGATGATGATGATGATGATGATGATGATGATGATG 1469
 Qy 1384 AAATTAATCAATCTCAAGTATCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1443
 Db 1470 AAGGAAGTATCTCATGGATCCA-GAAGATACAGCTGGGATGAGAGAGAGAG 1521
 Qy 1444 GAAGGAGCTGGAGATCTTAAATTAATTAATTAATTAATTAATTAATTAATTA 1503
 Db 1522 --AGGCAACCTGGATCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1579
 Qy 1504 CAGGCACTTTCAGATTTCTCATATTTGTGGGCTGGAGTCAAGCTGTGAGCTGAG 1563
 Db 1580 CAGGCACTTCTCATATTTCTCATATTTGTGGGCTGGAGTCAAGCTGTGAGCTGAG 1627
 Qy 1564 AAGCAAG 1623
 Db 1628 CACTGTCAAG 1685
 Qy 1624 CCACTGAG 1683
 Db 1686 CCAAG 1745
 Qy 1684 CTAGGAG 1743
 Db 1746 CTGGGAG 1804
 Qy 1744 TTCTTGAAG 1803
 Db 1805 TTCTTGAAG 1864
 Qy 1804 TG-----GAGCTGTGGGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1851
 Db 1865 GAGCTTAAAG 1924
 Qy 1852 AGAAG 1911
 Db 1925 AAG 1961
 Qy 1912 CAGGCTTGAAG 1971
 Db 1982 GAGAGCTTCAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2040
 Qy 1972 CAG 2030
 Db 2041 -----AGCACTACAGAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2083
 Qy 2031 CTTTCAAGATTTCCCACTGTGATGATGATGATGATGATGATGATGATGATGATG 2090
 Db 2084 TTCTTCACTTTTCACTTGAAGATGATGATGATGATGATGATGATGATGATGATG 2143
 Qy 2091 GAGCTCAG 2150
 Db 2144 GTCTCCAGTGTGAG 2203

Qy 2151 ACTGCTCCTGGAGATTCAGATGAGTGGAG--TGAGAGATGATGATGATGATGATG 2208
 Db 2204 ACTTCTCCTGGAGATTCAGATGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 2263
 Qy 2209 TCACTCTTGAAGTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2268
 Db 2264 TTATTTTCAAGAGGCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2323
 Qy 2269 CCAAGGATTTTCCCTCAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 2328
 Db 2324 GAGAGATTTCCCAAG 2383
 Qy 2329 CTCTGAGAGCTGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2382
 Db 2384 CTATCAAAAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2443
 Qy 2383 TTTCATATTCACCTTCTGAG--CATGTCAGAGTGTCTTCCAACTGAGAGAGAG 2441
 Db 2444 TTTCATATTCACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2502
 Qy 2442 CCGCTTGAAGAGTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2501
 Db 2503 CTTTAACTTGAAGTCAATCCCAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 2547
 Qy 2502 GCGTCTCTGATCACTGATCCCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2561
 Db 2548 GCGTCTCTGAG 2607
 Qy 2562 ATTGCTTCTGATGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 2618
 Db 2608 ATTGCTTCTGATGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 2664

RESULT 2
 B386074
 LOCUS
 DEFINITION
 mRNA sequence.
 B386074 822 bp mRNA linear EST 12-MAR-2001
 602455248F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4583675 5',
 mRNA sequence.
 B386074
 B386074.1 GI:13279520
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 822)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: gsa@bbs.fda.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: NIH Intramural Sequencing Center
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LCM307 row: P column: 12
 High quality sequence stop: 746.
 Location/Qualifiers
 1..822
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4583675"
 /issue="type="adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_15"
 /note="Organ: colon; Vector: pOT7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'

FEATURES

SOURCE

ORIGIN

adaptor: GGCACAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies) "

Query Match 26.5%; Score 728; DB 4; Length 822;
Best Local Similarity 96.3%; Pred. No. 3.8e-197;
Matches 778; Conservative 0; Mismatches 25; Indels 5; Gaps 3;

1 AGAAGTCAGCCTGGCAGAGAGACTCTGAATGAGGATTAAGAGGTTTCAAGAGCAAGA 60
9 AGAAGTCAGCCTGGCAGAGAGACTCTGAATGAGGATTAAGAGGTTTCAAGAGCAAGA 68
61 GCTTCAGCCGGAAGCAAG 120
69 GCTTCAGCCGGAAGCAAG 128
121 GGCCTCTTGGCCTCCAACTGTGGGCTACATCTAGAGGCTTCTGGGGCTTTTGGGCAC 180
129 GGCCTCTTGGCCTCCAACTGTGGGCTACATCTAGAGGCTTCTGGGGCTTTTGGGCAC 188
181 ACTGTTGCAATGCTGCTCCAGCTGGAAGCAAGTTTATGTGGTGGCAGCATTTGT 240
189 ACTGTTGCAATGCTGCTCCAGCTGGAAGCAAGTTTATGTGGTGGCAGCATTTGT 248
241 GAG 300
249 GAG 308
301 CACCAAGTGAACATCTATAGCAACCTTCTGGGCTGCGGCTGACATCCAGGCTGCCA 360
309 CACCAAGTGAACATCTATAGCAACCTTCTGGGCTGCGGCTGACATCCAGGCTGCCA 368
361 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
369 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 428
421 CATGAGATGACAGTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
429 CATGAGATGACAGTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 488
481 TGAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 540
489 TGAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 548
541 TGGGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 600
549 TGGGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 608
601 AGAGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 660
609 AGAGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 668
661 CTGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 720
669 CTGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 727
721 ACCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 780
728 CTC---TTGACAAAGAGAGCTCTCCAGGCTGGTCAATCCCAAAAGTCAAGAGTGA 784
781 CAATCTCTAAGAGCTGACAGGATATG 808
785 CCAAT-CTACAGCTGACGGGATG 811

RESULT 3
AY400251 693 bp DNA linear GSS 15-DEC-2003
LOCUS Homo sapiens CLDN2 gene, VIRUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.

ACCESSION AY400251 GI:39756240
VERSION AY400251.1
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
1 (bases 1 to 693)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)

TITLE
JOURNAL
PUBMED
14671302
2 (bases 1 to 693)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

COMMENT
FEATURES
source
1..693
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>693
/gene="CLDN2"
/locus_tag="HOMO495"

ORIGIN
Query Match 25.3%; Score 693; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 4.2e-187;
Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

119 ATGGCTCTTGGGCTTCCAACTTGGGCTAATCTAGGCTTGGGGCTTTGGGC 178
1 ATGGCTCTTGGGCTTCCAACTTGGGCTAATCTAGGCTTGGGGCTTTGGGC 60
179 ACACTGTTCCATGCTGCTCCAGCTGGAAGCAAGTTCTTATGCGGTGCAGATT 238
61 ACACTGTTCCATGCTGCTCCAGCTGGAAGCAAGTTCTTATGCGGTGCAGATT 120
239 GTGACAGAGTGGCTTCTCCAGAGGCTCTGATGATGATGATGATGATGATGATGATG 298
121 GTGACAGAGTGGCTTCTCCAGAGGCTCTGATGATGATGATGATGATGATGATGATG 180
299 ATCAACCAAGTGTGACATCTATAGCAACCTTCTGGGCTGCGGCTGACATCCAGGCTGCC 358
181 ATCAACCAAGTGTGACATCTATAGCAACCTTCTGGGCTGCGGCTGACATCCAGGCTGCC 240
359 CAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 418
241 CAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
419 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 478
301 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
479 GGTGAGTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 538
361 GGTGAGTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 420
539 CATGAGTCTTACAGGAGCTTCTAACAAGCTGATGATGATGATGATGATGATGATGATG 598
421 CATGAGTCTTACAGGAGCTTCTAACAAGCTGATGATGATGATGATGATGATGATGATG 480
599 GAGAGAGCTCTTACTTGGGATTAATTTCTTCCCTGTTCTCCCTGATGATGATGATGATG 658

Db 481 GGAGAGCTCTTACTGAGGATATTTCTTCCTGTTCCCTGATAGCTGAATCATC 540
 Qy 659 CTCTGCTTTTCCCTGCTATATCCAGAGAAATGCTTCCAACTACTACATGCTTACCAAGCC 718
 Db 541 CTCTGCTTTTCCCTGCTATATCCAGAGAAATGCTTCCAACTACTACATGCTTACCAAGCC 600
 Qy 719 CAACCTCTTCCCAAGAGAGCTTCCAGAGGCTGCTGAACCTCCCAAGTCAAGAGTGA 778
 Db 601 CAACCTTTTCCCAAGAGAGCTTCCAGAGGCTGCTGAACCTCCCAAGTCAAGAGTGA 660
 Qy 779 TTCAATTCCTACAGCCTGACAGGGTATGTGA 811
 Db 661 TTCAATTCCTACAGCCTGACAGGGTATGTGA 693

RESULT 4
 BE513091 945 bp mRNA linear EST 07-AUG-2000
 LOCUS 601171545F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3545171 5',
 DEFINITION mRNA sequence.
 ACCESSION BE513091
 VERSION BE513091.1 GI:9720302
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 945)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: egabbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 Cloning Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
 Plate: LNCM241 row: 1 column: 12
 High quality sequence start: 36
 High quality sequence stop: 782.
 Location/Qualifiers
 1. 945
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3545171"
 /issue_type="adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_15"
 /note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAAGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN
 Query Match 25.0%; Score 686.8; DB 2; Length 945;
 Best Local Similarity 94.0%; Pred. No. 2.8e-185;
 Matches 758; Conservative 0; Mismatches 42; Indels 6; Gaps 4;

Qy 1 AGAAGTCAAGCTGAGAGAGAGCTGTAATGAGAGGATTTAGAGGTTTCAAGAGAGAGA 60
 Db 69 AGAAGTCAAGCTGAGAGAGAGAGCTGTAATGAGAGGATTTAGAGGTTTCAAGAGAGAGA 128
 Qy 61 GCTTCAAGCTGAGAGAGAGAGAGCTGTAATGAGAGGATTTTCAAGAGAGGTTGCTCAT 120
 Db 129 GCTTCAAGCTGAGAGAGAGAGAGCTGTAATGAGAGGATTTTCAAGAGAGGTTGCTCAT 188

Qy 121 GGCCTCTTGGGCTCCAACTTGTGGGCTACATCTAGGCTTCTGGGGCTTTTGGGAC 180
 Db 189 GGCCTCTTGGGCTCCAACTTGTGGGCTACATCTAGGCTTCTGGGGCTTTTGGGAC 248
 Qy 181 ACTGTTGCCATGCTGCTCCAGCTGAGAAACAACTTTATATGCTGGTCCAGCATTTGT 240
 Db 249 ACTGTTGCCATGCTGCTCCAGCTGAGAAACAACTTTATATGCTGGTCCAGCATTTGT 308
 Qy 241 GACAGAGTTGGCTTCTCCAAAGGCTCTGGAATGGAATGTCACACAGCACAAGGCAT 300
 Db 309 GACAGAGTTGGCTTCTCCAAAGGCTCTGGAATGGAATGTCACACAGCACAAGGCAT 368
 Qy 301 CACCAAGTGAATCTATATGACACCTTCTGGGCTGCGCGTGAATTCACAGGCTCCCA 360
 Db 369 CACCAAGTGAATCTATATGACACCTTCTGGGCTGCGCGTGAATTCACAGGCTCCCA 428
 Qy 361 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 Db 429 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 488
 Qy 421 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
 Db 489 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 548
 Qy 481 TGGAGTCTTTTTCATCTGAGAGGCTCTGGGATTCATCTGCTGCTGCTGATCTTCA 540
 Db 549 TGGAGTCTTTTTCATCTGAGAGGCTCTGGGATTCATCTGCTGCTGCTGATCTTCA 607
 Qy 541 TGGAGTCTTCAAGGAGCTTCTACTACACATGATGCTGACAGCATGAATTTGA--GATT 588
 Db 608 TGGAGTCTTCAAGGAGCTTCTACTACACATGATGCTGACAGCATGAATTTGAAGATTG 667
 Qy 599 GAGAGGCTTTTACTTGGGCTATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 657
 Db 668 GAGAGGCTTTTACTTGGGCTATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 727
 Qy 658 CCTGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 717
 Db 728 CCTGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 787
 Qy 718 CCAACTCTTTCACCAAGAGCTTCCCAAGGCTGCTCAACTCCCAAGTCAAGAGTGA 777
 Db 788 CGCACCTCTTTCACCAAGAGAGCTTCCCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 845
 Qy 778 GTTCAATTCCTACAGCTGACAGGCT 803
 Db 846 GTTCAATTCCTACAGCTGACAGGCT 871

RESULT 5
 AY400252 693 bp DNA linear GSS 15-DEC-2003
 LOCUS Pan troglodytes CLDN2 gene, VIRUAL TRANSCRIPT, partial sequence,
 DEFINITION genomic survey sequence.
 AY400252
 ACCESSION AY400252.1 GI:39756241
 VERSION GSS.
 KEYWORDS Pan troglodytes (chimpanzee)
 SOURCE Pan troglodytes
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 REFERENCE 1 (bases 1 to 693)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
 Fierliera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 693)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,

Todd, M.A., Tanenbaum, D.M., Civejlo, D.R., Lu, F., Murphy, B.,
Fertigler, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.J.,
Adams, M.D., and Cargill, M.
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES
source
1..693
Location/Qualifiers

gene
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>693
/gene="CLDN2"
/locus_tag="HOMO495"

ORIGIN

Query Match 24.7%; Score 676.4; DB 9; Length 693;
Best Local Similarity 97.7%; Pred. No. 2.5e-182;
Matches 677; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

119 ATGGCCCTCTTGGCCCTCAACTTGTGGCTACATCTAGAGCTTCTGGGGCTTTGGGC 178
1 ATGGCCCTCTTGGCCCTCAACTTGTGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 60
179 ACATGCTTGCATGCTGCTCTCCAGCTGGAACAACTTCTTATGTGCTGCGACAT 238
61 ACNNTGTTGCCATGCTGCTCTCCAGCTGGAACAACTTCTTATGTGCTGCGACAT 120
239 GTGACAGCACTTGGCTTCTCCAGGGCTCTGATGGAATGTGCACACACAGCAGGC 238
121 GTACAGCACTTGGCTTCTCCAGGGCTCTGATGGAATGTGCACACACAGCAGGC 180
299 ATACCCAGGTGACATCTATAGACCTCTGGGCTCTGCCGCTGACATCCAGGCTGCC 358
181 ATACCCAGGTGACATCTATAGACCTCTGGGCTCTGCCGCTGACATCCAGGCTGCC 240
359 CAGGCCATGATGATGATCAGTCAATCTCTCTGCTGCTGATCTCTGCTGCTG 418
241 CAGGCCATGATGATGATCAGTCAATCTCTCTGCTGCTGATCTCTGCTGCTG 300
419 GGCATGATGATGATGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 478
301 GGCATGATGATGATGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
479 GGTGAGCTCTTTTCACTTGTGAGGCTCTGGGATTCATTCCTGTTGCTGGAATCT 538
361 GGTGAGCTCTTTTCACTTGTGAGGCTCTGGGATTCATTCCTGTTGCTGGAATCT 420
539 CATGGATCTTCAAGGACTTCTACCTCACTGGTGCCTGACAGCATGAATTTGAGATT 598
421 CATGGATCTTCAAGGACTTCTACCTCACTGGTGCCTGACAGCATGAATTTGAGATT 480
599 GGAAGGCTCTTTTCACTTGGGCAATTTCTTCTCTGTTCTGCTGATAGCTGATCATC 658
481 GGAAGGCTCTTTTCACTTGGGCAATTTCTTCTCTGTTCTGCTGATAGCTGATCATC 540
659 CTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 718
541 CTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
719 CAACCTTCTGCAAGAGCTCTCCAGGCTGTGCAACTCCCAAGTCAAGAGTGA 778
601 CAACCTTCTGCAAGAGCTCTCCAGGCTGTGCAACTCCCAAGTCAAGAGTGA 660
779 TTCAATCTCAAGCTGACAGGGTATGTGA 811
661 TTCAATCTCAAGCTGACAGGGTATGTGA 693

RESULT 6
BE304667

LOCUS BE304667 680 bp mRNA linear EST 13-JUL-2000
DEFINITION 60105783F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988309 5',
mRNA sequence.
ACCESSION BE304667
VERSION BE304667.1 GI:9176036
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL 1 (bases 1 to 680)
COMMENT NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L10M77 row: f column: 22
High quality sequence start: 27
High quality sequence stop: 680.

FEATURES
source
1..680
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2988309"
/issue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 15"
/note="Organ: colon; Vector: pORF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dt priming. Directionality
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACGAG (g). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN

Query Match 23.5%; Score 643; DB 2; Length 680;
Best Local Similarity 100.0%; Pred. No. 9.7e-173;
Matches 643; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

224 GTTGTCGACAGCATTTGTGACAGCATTTGGCTTCTCCAGGCTCTGATGGAATGTGCC 283
38 GTGCGTGCACAGCATTTGTGACAGCATTTGGCTTCTCCAGGCTCTGATGGAATGTGCC 97
284 ACACACAGCAGCAGCATCCAGGCTGACATCTATAGCACCCTTGGGCTGCCGCT 343
98 ACACACAGCAGCAGCATCCAGGCTGACATCTATAGCACCCTTGGGCTGCCGCT 157
344 GACATCAGGCTGCCAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 403
158 GACATCAGGCTGCCAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 217
404 ATTATCTCTGTGTGGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 463
218 ATTATCTCTGTGTGGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 277
464 AGAGTGGGGTGGAGGTGAGTCTTTTCACTTGTGAGGCTCTGGGATTCATTCCT 523
278 AGAGTGGGGTGGAGGTGAGTCTTTTCACTTGTGAGGCTCTGGGATTCATTCCT 337
524 GTTGCTGGAATCTTATGAGATCTCTACCGGATCTTCTACTCACTGCTGCTGACAGC 583
338 GTTGCTGGAATCTTATGAGATCTCTACCGGATCTTCTACTCACTGCTGCTGACAGC 397
584 ATGAATTTGAGATTTGAGAGGCTCTTATCTTGGGCAATTTCTTCCCTGCTCCCTG 643

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DTF
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: L1CM1274 row: d column: 18
 High quality sequence stop: 708.
 Location/Qualifiers

FEATURES

Source

1..728
 /organism="Homo sapiens"
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 /clone="IMAGE:4562273"
 /issue_type="renal cell adenocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NIH_MGC_14"
 /note="Organ: kidney; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; CDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 23.2%; Score 637.4; DB 4; Length 728;
 Best Local Similarity 97.4%; Pred. No. 4e-171;
 Matches 712; Conservative 0; Mismatches 11; Indels 8; Gaps 6;

91 TGAAGAGCTTCACTGAGAGCTGTCAGAGCTCTGCTGCTCAACTGGGGCTA 150
 2 TGAAGAGCTTCACTGAGAGCTGTCAGAGCTCTGCTGCTCAACTGGGGCTA 61
 151 CATCTAGAGCTTCTGGGGCTTTGGGACACTGGTTCAGAGCTGCTCCCACTGGA 210
 62 CATCTAGAGCTTCTGGGGCTTTGGGACACTGGTTCAGAGCTGCTCCCACTGGA 120
 211 AACAGTTCTTATGTCGTCGACAGATTGTGACAGAGTTGGCTTCCAGGGCTCTG 270
 121 AACAGTTCTTATGTCGTCGACAGATTGTGACAGAGTTGGCTTCCAGGGCTCTG 180
 271 GAGGAAATGGCCACACAGACAGAGCATCCCACTGAGATCTATAGCAACCTTCT 330
 181 GATGAAATGGCCACACAGACAGAGCATCCCACTGAGATCTATAGCAACCTTCT 240
 331 GGGCTGCGCCGCTGACATCCAGGCTGCCAGGCGCATGATGATGATCCAGTGAATCTC 390
 241 GGGCTGCGCCGCTGACATCCAGGCTGCCAGGCGCATGATGATGATCCAGTGAATCTC 300
 391 CTCCTGCGCCGCTGATATCTCTGTGGTGGGATGATGACAGTCTTTCAGAGATC 450
 301 CTCCTGCGCCGCTGATATCTCTGTGGTGGGATGATGACAGTCTTTCAGAGATC 360
 451 CCGAGCCAAAGACAGAGTGGCGGAGAGGAGTCTTTTATACCTTGGAGGCTCCCT 510
 361 CCGAGCCAAAGACAGAGTGGCGGAGAGGAGTCTTTTATACCTTGGAGGCTCCCT 420
 511 GGGATTCATTCCTGTTGCTGGAATCTTCATGGGATCTTAAGGGAATCTTACTACCACT 570
 421 GGGATTCATTCCTGTTGCTGGAATCTTCATGGGATCTTAAGGGAATCTTACTACCACT 480
 571 GGTGCTGACAGCATGAATTTGAATTTGAAGAGCTCTTTACTTGGGCTATATTTCTTC 630
 481 GGTGCTGACAGCATGAATTTGAATTTGAAGAGCTCTTTACTTGGGCTATATTTCTTC 540
 631 CCGTTCTGCTGATGCTGGAATCATCTCTGCTTTTCTGCTCAATCCAGGAATCG 690
 541 CCGTTCTGCTGATGCTGGAATCATCTCTGCTTTTCTGCTCAATCCAGGAATCG 600

QY 691 CTCCACTACTACGATGCTTACCAAGCCCACTCTTGGCCACAGAGCTCTTCAAGGCC 750
 DB 601 CTCCACTACTACGATGCTTACCAAGCCCACTCTTGGCCACAGAGCTCTTCAAGGCC 656
 QY 751 TGGTCAACTCTCCAAAGTCAAGGTGATGTTCAATCTTACAGCTTACAGGGTATGTG 810
 DB 657 -TGGTCAACTCTCCAAAGTCAAGGTGATGTTCAATCTTACAGCTTACAGGGTATGTG 713
 QY 811 AAGACACAGGG 821
 DB 714 AAGACACAGGG 724

RESULT 9

BG164062 978 bp mRNA linear EST 06-FEB-2001
 602341087P1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4449212 5',
 mRNA sequence.

LOCUS

BG164062

DEFINITION

mRNA sequence.

ACCESSION

BG164062.1

VERSION

GI:12670765

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

ATTNORS

NIH-MGC <http://mgs.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: L1AM10232 row: m column: 21
 High quality sequence stop: 689.
 Location/Qualifiers

FEATURES

1..978

Source

/organism="Homo sapiens"

mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4449212"

/issue_type="hypernephroma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; cloned unidirectionally; oligo-dT primed.
 Average insert size 1.3 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 22.5%; Score 617; DB 4; Length 978;
 Best Local Similarity 93.9%; Pred. No. 3.3e-165;
 Matches 698; Conservative 0; Mismatches 35; Indels 10; Gaps 5;

QY 95 GAGGCTTCTACTGAGAGTCTGCGATGAGCTCTCTTGGCTTCAACTTGGGCTACATC 154
 DB 1 GAGGCTTCTACTGAGAGTCTGCGATGAGCTCTCTTGGCTTCAACTTGGGCTACATC 60
 QY 155 CTAGAGCTTCTGAGGCTTTTGGGACACAGTGGTGGCCATGCTGCTCCCGCTGGAATAA 214
 DB 61 CTAGAGCTTCTGAGGCTTTTGGGACACAGTGGTGGCCATGCTGCTCCCGCTGGAATAA 119
 QY 215 AGTTCTTATGTCGGTCCAGCATTTGTGACAGAGTGGCTTCTCCAGGGCTCTGATG 274
 DB 120 AGTTCTTATGTCGGTCCAGCATTTGTGACAGAGTGGCTTCTCCAGGGCTCTGATG 179

Db 20 AGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGATTAAGGTCTTCAAGAGCAAGA 79
Qy 61 GCTTCAGCCTGAAAGCAAGGAGAGCTCCCTGAAAGCTTTCTACTGAGAGGTCTGGCAT 120
Db 80 GCTTCAGCCTGAAAGCAAA-GGAGCAGTCCCTGAAAGAGCTTCTACTGAGAGGTCTGGCAT 138
Qy 121 GGGCTCTCTGGGCTCCCACTGTGGGCTCATCTGAGGCTCTGGGGCTTTTGGGAC 180
Db 139 GGGCTCTCTGGGCTCCCACTGTGGGCTCATCTGAGGCTCTGGGGCTTTTGGGAC 198
Qy 181 ACTGTTGCATGCTGCTCCCACTGAGTGAAGCAAGTTCTTATGTCGGTCCAGCATTTGT 240
Db 199 ACTGTTGCATGCTGCTCCCACTGAGTGAAGCAAGTTCTTATGTCGGTCCAGCATTTGT 258
Qy 241 GACAGCAGTTGGCTTCTCCAAAGGGCTCTGGATGGAATGTCACACACAGCAGCAGCAT 300
Db 259 GACAGCAGTTGGCTTCTCCAAAGGGCTCTGGATGGAATGTCACACACAGCAGCAGCAT 318
Qy 301 CACCCAGTGTGACATCTATGACACCTTCTGGGCTGTCGCGCTGACATCCAGGCTGGCCA 360
Db 319 CACCCAGTGTGACATCTATGACACCTTCTGGGCTGTCGCGCTGACATCCAGGCTGGCCA 378
Qy 361 GGGCATGATGATGACATCCAGTGAATCTCTCCCTGAGCTGATATCTCTGTGTGG 420
Db 379 GGGCATGATGATGACATCCAGTGAATCTCTCCCTGAGCTGATATCTCTGTGTGG 438
Qy 421 CATGATGATGACATCTCTCTGCGCAGAAATCCGAGCCAAAGACAGAGTGGCGTGAAG 480
Db 439 CATGATGATGACATCTCTCTGCGCAGAAATCCGAGCCAAAGACAGAGTGGCGTGAAG 498
Qy 481 TGAGATCTTTTCACTCTGAGAGGCTCTGAGGATTAATCTCTGCTGCTGGAATCTTCA 540
Db 499 TGAGATCTTTTCACTCTGAGAGGCTCTGAGGATTAATCTCTGCTGGAATCTTCA 558
Qy 541 TGGGATCTTACGGGACTTCTACTCACCAGTGTGCTGCTGACAGATGAATTTGAGATTGG 600
Db 559 TGGGATCTTACGGGACTTCTACTCACCAGTGTGCTGCTGACAGATGAATTTGAGATTGG 618
Qy 601 AGAGGCTCTTACTTGGGCAATTAATTTCTTCCC 632
Db 619 AGAGGCTCTTACTTGGGCAATTAATTTCTTCCC 650

RESULT 13
BG328625 643 bp mRNA linear EST 27-FEB-2001
LOCUS 602427889P1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4547230 5',
DEFINITION mRNA sequence.
ACCESSION BG328625
VERSION BG328625.1 GI:13135063
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 643)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Straube, Ph.D.
Email: rstraube@nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
http://image.liml.gov
Plate: LIMC1235 row: a column: 23
High quality sequence stop: 641.
Location/Qualifiers
1. 643
/organism="Homo sapiens"

/mol type="mRNA"
/db xref="IMAGE:4547230"
/clone="IMAGE:4547230"
/issue="adenocarcinoma cell line"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 15"
/note="Organ: colon; Vector: pOTB7; Site: 1; XhoI; Site: 2;
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCAAGG(G). Size selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the Laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN
Query Match 22.1%; Score 606; DB 4; Length 643;
Best Local Similarity 99.5%; Pred. No. 4.1e-162;
Matches 639; Conservative 0; Mismatches 0; Indels 3; Gaps 3;
Qy 5 GTACAGCTGGCAGAGAGACTCTGAAATGAGGATTAAGGTCTTCAAGAGCAAGGCTT 64
Db 2 GTACAGCTGGCAGAGAGACTCTGAAATGAGGATTAAGGTCTTCAAGAGCAAGGCTT 61
Qy 65 CAGCTGAAAGCAAGGAGAGAGTCCCTGAAAGAGCTTCTACTGAGAGTCTGCATGGCC 124
Db 62 CAGCTGAAAGCAAGGAGAGAGTCCCTGAAAGAGCTTCTACTGAGAGTCTGCATGGCC 121
Qy 125 TCTCTGGCTCCCACTGTGGCTACATCTAGGCTTCTGGGCTTTTGGGCAACTG 184
Db 122 TCTCTGGCTCCCACTGTGGCTACATCTAGGCTTCTGGGCTTTTGGGCAACTG 181
Qy 185 GTTGGCATGCTGCTCCCACTGAGTGAAGCAAGTCTTATGTCGGTCCAGC ATTGGAC 243
Db 182 GTTGGCATGCTGCTCCCACTGAGTGAAGCAAGTCTTATGTCGGTCCAGCATTGGAC 241
Qy 244 AGCAGTTGGCTTCCCAAGGAGGCTCTGAGTGAATGAGGCA- CACAGCAGGCAATCA 302
Db 242 AGCAGTTGGCTTCCCAAGGAGGCTCTGAGTGAATGAGGCAATGAGGCAATCA 301
Qy 303 CCGAGTGTGACATCTATGAGCACCCTTCTGGGCTGCGCGCTGACATCCAGGCTGCCAGG 362
Db 302 CCGAGTGTGACATCTATGAGCACCCTTCTGGGCTGCGCGCTGACATCCAGGCTGCCAGG 361
Qy 363 CCATGATGTGACATCCAGTGCATCTCTCTGCGCTGCA- TTATCTTGTGTGGGC 421
Db 362 CCATGATGTGACATCCAGTGCATCTCTCTGCGCTGCAATTTCTTGTGTGGGC 421
Qy 422 ATGAGATGACAGATCTTCTGCGCAGGAATCCGAGCCAAAGACAGAGTGGCGTAGCAGT 481
Db 422 ATGAGATGACAGATCTTCTGCGCAGGAATCCGAGCCAAAGACAGAGTGGCGTAGCAGT 481
Qy 482 GGAATCTTTTCACTCTTGGAGGCTCTCTGGGATTCATTTCTGTGCTGGAATCTTTCAT 541
Db 482 GGAATCTTTTCACTCTTGGAGGCTCTCTGGGATTCATTTCTGTGCTGGAATCTTTCAT 541
Qy 542 GGAATCTTACGGGACTTCTACTCACCAGTGTGCTGACAGCATGAATTTGAGATTGGA 601
Db 542 GGAATCTTACGGGACTTCTACTCACCAGTGTGCTGACAGCATGAATTTGAGATTGGA 601
Qy 602 GAGGCTCTTACTTGGGCAATTAATTTCTGCTGCTGCTGCTG 643
Db 602 GAGGCTCTTACTTGGGCAATTAATTTCTGCTGCTGCTGCTGCTG 643

RESULT 14
BP445902 761 bp mRNA linear EST 30-DEC-2003
LOCUS BP445902 full-length enriched swine cDNA library, adult liver Sus
DEFINITION scrofa cDNA clone LVRO10047F07 5', mRNA sequence.
ACCESSION BP445902
VERSION BP445902.1 GI:40435969
KEYWORDS EST.

SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 REFERENCE 1 (bases 1 to 761)
 AUTHORS Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
 Okumura,N., Hamashima,N. and Awata,T.
 TITLE PEDE (Pig EST Data Explorer): construction of a database for ESTs
 derived from porcine full-length cDNA libraries
 JOURNAL Nucleic Acids Res. 32 (1), D484-D488 (2004)
 COMMENT Contact: Hirohide Uenishi
 Animal Genome Laboratory, Genome Research Department
 National Institute of Agrobiological Sciences
 2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
 Tel: +81-29-838-8627
 Fax: +81-29-838-8627
 Email: huenishi@affrc.go.jp
 EST project with full-length enriched cDNA libraries carried out in
 Animal Genome Research Program (Japan) by National Institute of
 Agrobiological Sciences and STAP-Institute
 Single pass sequencing of clones derived from oligo-capped cDNA
 library
 Vector sequences were eliminated by RepeatMasker version 2002/07/13
 and crossmatch version 0.990319
 Low quality bases were trimmed based on the quality values.
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 Best Local Similarity 88.1%; Pred. No. 4.6e-158;
 Matches 657; Conservative 0; Mismatches 85; Indels 4; Gaps 1;
 QY 1 AGAAGTCAGCTGCGAGAGACCTCGAATGAGGAGTTAGAGTGC---TTCAAGAGC 56
 DB 16 AGAGGTGCGCTGCGAGACACTGTCAATGAGGAGTTAGAGGCGAGATCCAAAGAGC 75
 QY 57 AAGAGCTTCAGCCTGAAGACAAGGAGCACTCCCTGAAGACGCTTCTACTGAGAGCTCG 116
 DB 76 AAGTGTCAACGCCGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 135
 QY 117 CCATGCGCTCTCTGCGCTCAACTGTGAGGCTTCAATCTTCTGAGGCTTTTGG 176
 DB 136 CCATGCGCTCTCTGCGCTCAACTGTGAGGCTTCAATCTTCTGAGGCTTTTGG 195
 QY 177 GCACATGCTGTCAGTCTGCTCCCAAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 236
 DB 196 GCACCTGCTGTCAGTCTGCTCCCAAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 255
 QY 237 TTGTGACAGAGTGTGCTTCTCCAAAGGAGCTTGTGATGATGATGATGATGATGATGATG 296
 DB 256 TGTGACAGAGTGTGCTTCTCCAAAGGAGCTTGTGATGATGATGATGATGATGATGATG 315
 QY 297 GCATCACCAAGTGTGATCTATAGCACTTCTGAGGCTGCGGCTGATCATCAGGCTG 356
 DB 316 GCATCACCAAGTGTGATCTATAGCACTTCTGAGGCTGCGGCTGATCATCAGGCTG 375
 QY 357 CCCAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 416
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 DB 436 TGGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 495

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 DB 496 TGGGTGAGTCTTTTTCATCTCTGAGGAGCTCTGAGGATTCATCTGTTGCTGGAATC 555
 QY 537 TTGATGAGATCCCAAGGAGCTTACTCAACACTGAGTGTGACAGATGAATTGAGA 596
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 QY 597 TTGAGAGGCTCTTTTACTTGGGATTAATTTCTCCCTGTTCTCCGATAGCTGGAATCA 656
 DB 616 TGGAGAGGCTCTTCTACTTGGGATTAATTTCTCCCTGTTCTCCGATAGCTGGAATCA 675
 QY 657 TCTCTGCTTTTCTGCTATCCCAAGAAATGCTTCAACTACTGATGCTTACCAAG 716
 DB 676 TCTCTGCTTTTCTGCTATCCCAAGAAATGCTTCAACTACTGATGCTTACCAAG 735
 QY 717 CCCAGCTCTGCGCAGAGAGCTCT 742
 DB 736 CCCAGCTCTGCGCAGAGAGCTCT 761
 RESULT 15
 CN793010 729 bp mRNA linear EST 26-MAY-2004
 LOCUS 4127966 BARC 8BOV Bos taurus cDNA clone 8BOV_46D02 5', mRNA
 DEFINITION sequence.
 ACCESSION CN793010
 VERSION CN793010.1 GI:47688990
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 REFERENCE 1 (bases 1 to 729)
 AUTHORS Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassel,C.P. and
 Matukumalli,L.K.
 TITLE Construction and Analysis of a cDNA Library Generated From
 Intestinal Muscle and Epithelial Tissues of Holstein Cattle
 JOURNAL Unpublished (2004)
 COMMENT Contact: Richard G. Baumann
 Bovine Functional Genomics Lab
 ANRI
 BUDG 162: BARC-EAST, Beltsville, MD 20705, USA
 Tel: 3015048604
 Fax: 3015048744
 Email: rbaumann@anri.barc.usda.gov
 Single pass sequencing. Bases called and trimmed with phred
 0.000925 using options -trimalt "" -trim faaltvector identified by
 cross_match using options -mismatch 12 -minscore 12
 Plate: 46 row: D column: 02
 Seq primer: CCATTTAGGTGACACTATATGAAAC
 High quality sequence stop: 729.
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 /organism="Bos taurus"
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 /strain="Holstein"
 /db_xref="taxon:9913"
 /clone="8BOV_46D02"
 /sex="Female"
 /tissue_type="Epithelial, Muscle"
 /dev_stage="Lactating, Neonatal"
 /lab_host="DH10B TONa"
 /clone_lib="BARC 8BOV"
 /note="Organ: Intestine; Vector: pCMVSPORT6.1; Site 1:
 NCI; Site 2: EcoRI; Normalized cow cDNA intestinal
 library in pCMVSPORT6.1, constructed from equimolar mRNA
 pools derived from 5 sources, 4 lactating intestinal, 1
 neonatal intestinal 4/5 lactating, proximal duodenum,
 jejunum, distal ileum, colon, 1/5 neonatal, proximal
 duodenum, jejunum, distal ileum"

ORIGIN

Query Match	21.5%	Score 590.4;	DB 7;	Length 729;
Best Local Similarity	90.1%;	Pred. No. 1.3e-157;		
Matches 644;	Conservative 0;	Mismatches 67;	Indels 4;	Gaps 1;

Oy	1	AGAACTACAGCCTGGCAGAGAGA	CTCGAATATGAGGATTAAGAGTGG	-----TTCAAGAGC	56
Db	15	AGAACTACAGCCTGGCAGAGACA	CTGTGAATATGAGGATTAAGAGTGG	-----TTCAAGAGC	74
Oy	57	AAGAGCTTCAAGCCTGTAAGA	CAAGGAGCAGTCCCTTAAGA	CAGCTTCTACTGAGAGTCTG	116
Db	75	CAAGAGCTACAGCAGAGAGCA	CAAGGAGCAGTCCCTTAAGA	CAGCTTCTACTGAGAGTCTA	134
Oy	117	CCATGGCCTCTCTTGGCCTTCCA	CTTGTGGGCTACATCTCAAGCCTTCTTGGGCTTTGG		176
Db	135	CCATGGCCTCTCTTGGCCTTCCA	CTTGTGGGCTACATCTCAAGCCTTCTTGGGCTTTGG		194
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Db	195	GCACCGTATTTCCANCTGCTG	CCCCCAGCTGGAACCAAGCTCT	TTATGTGTGCGCAGCA	254
Oy	237	TTGTGACAGCAGTGGCTTCTTCCA	AGAGGCTCTGTAGATGAAATGTGCA	CACACAGCAG	296
Db	255	TTGTGACTGCGGTTGGCTTCTTCCA	AGAGGCTCTGTGATGAGTGTGCA	CACACAGCAG	314
Oy	297	GCATCACCCAGTGTGACATCTA	TATAGCACCCCTTCTGGGCTG	CCCGCTGCATCCAGGCTG	356
Db	315	GCATCACCCAGTGTGACATCTA	CACAGCACCATGTAAAGCTG	CGCCGCTGCATCCAGGCTG	374
Oy	357	CCCAGGCCATGATGTTGATCAT	CCATCCAGTGCAATCTCTCC	TCCGCTGCTGATTAATCTCTGTGG	416
Db	375	CCCAGGCCATGATGTTGATCAT	CCAGTGCAATCTCTCTCTTGGATGAT	TGTCTCTGTGG	434
Oy	417	TGGGATGATGAGCA	CAGTCTTCTG	CAGAGAAACCGAAGCAAGAGTGGCGGTAG	476
Db	435	TGGGATGATGAGCA	CAGTCTTCTTCCAGGAGTCTG	AGCAAGAGCAGAGTGGCGGTG	494
Oy	477	CAGGTGAGTCTTTTTCATCTCTG	AGAGGCTCTCTGGGATTCAT	TCTCTGTGCTGCGATC	536
Db	495	TGGGAGGAGTCTTCTTTCATCTCTG	AGAGGCTCTCTGGGCTTCAT	TCTCTGTGCTGCGATC	554
Oy	537	TTCATGGAGTCTTACCGGAG	CTTCTACTCACACTGTGTG	CTGACAGATGAATTTGAGA	596
Db	555	TTCATGGAGTCTTACCGGAG	CTTCTACTTCCCGCTGTGG	CTGACAGATGAATTTTGA	614
Oy	597	TTGAGAGAGCTCTTTA	ACTTGGGATTAATTTCTTCC	TGTCTCCCTGATAGCTGGAATCA	656
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Oy	657	TTCTCTGCTTTTCCGTCAT	CCCAAGAAATGGCTTCCA	ACTACTAGATGCCCA	711
Db	675	TTCTCTGCTTTTCCGTCAT	CCCAAGAAATGGCTTCCA	ACTACTAGATGCCCA	729

Search completed: October 30, 2004, 09:07:18
Job time : 12501 secs

QY 2101 TGGCATATCCATGCCCCAGGCTGCTGTGTCCATGATCTGAGTGAATAGTGCATGCTGCTT 2160
DB 2101 TGGCATATCCATGCCCCAGGCTGCTGTGTCCATGATCTGAGTGAATAGTGCATGCTGCTT 2160
QY 2161 GGGATTCGACCTGAGGTGGAGTGGAGAAATGCTTCCAGAGAACAGTTCACCTCTTAA 2220
DB 2161 GGGATTCGACCTGAGGTGGAGTGGAGAAATGCTTCCAGAGAACAGTTCACCTCTTAA 2220
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DB 2221 GTCCGAATAATGTTCCCTTTACCTCGAGTGGAGTGGAGGAGTCAACCAAGATTTT 2280
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QY 2461 TCAGGCTTGGAGAACTCTCTCAGGCTCAGCTCTTCAATGAGCCTTCTGATCACTCCA 2520
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QY 2581 CATTCACAAATTTTGAATGATGCTTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2640
DB 2581 CATTCACAAATTTTGAATGATGCTTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2640
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DB 2641 GTAAACCTCTCGGTGGTGGGAGCATATCTGATCTCTGATCTCTGATCTCTGATCTCTGAT 2700
QY 2701 GTAAACGTCGACGACACAGAGGTGATCAATAATTTGTTAGC 2742
DB 2701 GTAAACGTCGACGACACAGAGGTGATCAATAATTTGTTAGC 2742

RESULT 2
AK075405 2959 bp mRNA linear PRI 03-SEP-2002
LOCUS Homo sapiens cDNA PSEC0096 f18, clone NT2RP2002060, highly similar
DEFINITION To Homo sapiens clone sp82 claudin 2 mRNA.
ACCESSION AK075405
VERSION AK075405.1 GI:22761472
KEYWORDS oligo capping; f18 (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1
Oca,T., Nishikawa,T., Suzuki,Y., Kawai,Hio,Y., Hayashi,K.,
Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T.,
Nakamura,Y., Nagahari,K., Sugano,S. and Isegai,T.
HRI human cDNA sequencing project
Unpublished
2 (bases 1 to 2959)
Isegai,T. and Yamamoto,J.
Direct Submission
Submitted (20-MAR-2002) Takao Isegai, Helix Research Institute,
Genomics Laboratory, 1532-3 Yana, Kisesazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass
sequencing, clone selection and full insert sequencing; Helix
Research Institute (supported by Japan Key Technology Center etc.);

CDNA library construction: Institute of Medical Science, University
of Tokyo, Laboratory of Genome Structure, Human Genome Center.
Location/Qualifiers
1.2959
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP2002060"
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/note="cloning vector: pHE18F1-mRNA from NT2 neuronal
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induction"

ORIGIN
Query Match 99.1%; Score 2717; DB 9; Length 2959;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 2717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAGCCTGGCAGAGAGACTTGAATGAGGATTAGAGGTTCAAGAGCAAGA 60
DB 209 AGAAGTCAGCCTGGCAGAGAGACTTGAATGAGGATTAGAGGTTCAAGAGCAAGA 268
QY 61 GCTTCAGCCTGAAG 120
DB 269 GCTTCAGCCTGAAG 328
QY 121 GGCCTCTCTTGGGCTTCAACTTGTGGGCTTCACTTGAAGCTTCTGGGGCTTTTGGG 180
DB 329 GGCCTCTCTTGGGCTTCAACTTGTGGGCTTCACTTGAAGCTTCTGGGGCTTTTGGG 388
QY 181 ACTGTTGACAGCTGCTCCCGCAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 389 ACTGTTGACAGCTGCTCCCGCAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAG 448
QY 241 GACAG 300
DB 449 GACAG 508
QY 301 CACCCAGTGTGACATCTATAGACAGCTTGTGGGCTTGGGCTTGGGCTTGGGCTTGG 360
DB 509 CACCCAGTGTGACATCTATAGACAGCTTGTGGGCTTGGGCTTGGGCTTGGGCTTGG 568
QY 361 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 569 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 628
QY 421 CATGAGATGACAGCTTCTGACAGAGATCCGAGCAAGAGAGAGAGAGAGAGAGAGAG 480
DB 629 CATGAGATGACAGCTTCTGACAGAGATCCGAGCAAGAGAGAGAGAGAGAGAGAG 688
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DB 689 TGGAGTCTTTTTCATCTTGGAGGCTCTGGAGATTCATCTGTTGCTGGAATCTTCA 748
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DB 809 AGAGGCTCTTATCTTGGGCTTATTTCTTCCCTGTTCTCCCTGATAGTGAATCTCT 868
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RESULT 3
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 DEFINITION
 Human DNA sequence from clone RPL-75H8 on chromosome Xq22.3-23
 Containing the CLDN2 gene for claudin 2, the gene for a novel protein
 similar to KIAA0136, a eukaryotic translation elongation factor 1
 alpha 1 (EEF1A1) pseudogene and a CpG island, complete sequence.
 ACCESSION
 AL158821
 VERSION
 HTG; claudin; CLDN2; CpG island; EEF1A1; KIAA0136.
 KEYWORDS
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.


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Matches 2717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	GCTTCAGCTGGAAGACAAAGGAGAGCTCCCTGAAGAGCTTCTAAGAGAGCTGGCAT	120
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QY	121	GGCCTCTCTGGCCTCAACTGTGGGCTAATCTAAGCCTCTGGGGCTTTTGGGAC	180
DB	5021	GGCCTCTCTGGCCTCAACTGTGGGCTAATCTAAGCCTCTGGGGCTTTTGGGAC	5080
QY	181	ACTGGTTCATGCTGCTCCCGAGCTGGAAAACAAGTTCTATGTGGTCCAGCATTT	240
DB	5081	ACTGGTTCATGCTGCTCCCGAGCTGGAAAACAAGTTCTATGTGGTCCAGCATTT	5140
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DB	5261	GGCCATGATGTGATCCAGTGAATCTCTCTGCTGGCTGATTAATCTCTGTGGGG	5320
QY	421	CATGATGATGACAGTCTTTCGCCAGGAATCCGAGCAAAAGACAGATGGCGGTACAG	480
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DEFINITION Sequence 51 from Patent EP1067182.
ACCESSION AX136129
VERSION AX136129.1 GI:14272537
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and
Hayashi, K.
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VERSION	BD123517.1	GI:23218462				
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SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
AUTHORS	Ota, T., Iisogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and Hayashi, K.					
TITLE	Secretory protein or membrane protein					
JOURNAL	Patent: JP 2002017376-A 26 22-JAN-2002;					
COMMENT	HEPIX RESEARCH INSTITUTE OS Homo sapiens (human) PN JP 2002017376-A/26 PD 22-JAN-2002 PF 07-UUL-2000 JP 2000253173 PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,TOMOYASU PI SUGIYAMA, PI KOJI HAYASHI PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,PC C12P21/02,C12Q1/68//C12P21/08,C12N15/00,C12N5/00 CC Secretory protein or membrane protein FH Key Location/Qualifiers FT CDS Location/Qualifiers					
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ORIGIN						
Query Match	91.6%; Score 2513; DB 6; Length 2863;					
Best Local Similarity	99.9%; Pred. No. 0;					
Matches 2713; Conservative	0; Mismatches 4; Indels 0; Gaps 0;					
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Db		173	GCTTCAGAGCTGAAG	232		
OY		121	GAGCTCTCTGGGCTCCAACTTGTGGGCTCATCTTAGAGGCTTCTGGGGCTTTTGGGCA	180		
Db		233	GAGCTCTCTGGGCTCCAACTTGTGGGCTCATCTTAGAGGCTTCTGGGGCTTTTGGGCA	292		
OY		181	ACTGGTTCAGTGTCTCTCCAGCTGAAAACAGTTCTTATGTGGGTCCAGCATTTGT	240		
Db		293	ACTGGTTCAGTGTCTCTCCAGCTGAAAACAGTTCTTATGTGGGTCCAGCATTTGT	352		
OY		241	GACAGAGATTGGCTTCTCAAGAGGCTCTGAGTGAATGTGCACACACACAGAGAT	300		
Db		353	GACAGAGATTGGCTTCTCAAGAGGCTCTGAGTGAATGTGCACACACACAGAGAT	412		
OY		301	CACCAAGTGAATATATAGAACCTCTGGGGCTGCGCGTGATCTCAGAGCTGCCA	360		
Db		413	CACCAAGTGAATATATAGAACCTCTGGGGCTGCGCGTGATCTCAGAGCTGCCA	472		
OY		361	GGCCATGATGTGATATCCAGATGATCTCTCCCTGGAGCTGATATCTGTGTGGG	420		
Db		473	GGCCATGATGTGATATCCAGATGATCTCTCCCTGGAGCTGATATCTGTGTGTGGG	532		
OY		421	CATGAGATGACAGTCTTCTGCCAGGAATCCGAGCCAAAGACAGAGTGGGGTGCAG	480		
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RESULT 6
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LOCUS
DEFINITION
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to Mus musculus claudin-2 mRNA.
ACCESSION
AK075371
VERSION
AK075371.1 GI:22761413
KEYWORDS
oligo capping; fls (full insert sequence).
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
AUTHORS
Ota, T., Nishikawa, T., Suzuki, Y., Kawai-Hio, Y., Hayashi, K.,
Ishii, S., Saito, K., Yamamoto, J., Wakamatsu, A., Nagai, T.,
Nakamura, Y., Nagahara, K., Sugano, S. and Isogai, T.
HRI human cDNA sequencing project
Unpublished
2 (bases 1 to 2863)

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Submitted (20-WAR-2002) Takeo Isogai, Helix Research Institute,
Genomics Laboratory, 1533-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass
sequencing, clone selection and full insert sequencing; Helix
Research Institute (supported by Japan Key Technology Center etc.);
cDNA library construction; Institute of Medical Science, University
of Tokyo, Laboratory of Genome Structure, Human Genome Center.
Location/Qualifiers
1. 2863

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CDS

ORIGIN

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Query Match 91.6%; Score 2513; DB 9; Length 2863;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2713; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB 113 AGAAGTCAGCTGGCAGAGAGACTGTAATAGGGGATTAGAGTGTTCAGAGGACAGA 172
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ACCESSION AX092348
VERSION AX092348.1 GI:13444488
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Eaton,D.L., Filvaroff,E., Gerritsen,M.F., Goddard,A.,
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
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Patent: WO 0116318-A 79 08-MAR-2001,
JOURNAL Genentech, Inc. (US)
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ORIGIN

Query Match 53.7%; Score 1472; DB 6; Length 1475;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db		1324	TGGAACCTCCATCCCACTCTTGTATGACCTCCACAGTGTCCAGACTAAATTTGTGATGA	1383
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LOCUS				PAT 26-NOV-2001
DEFINITION		Sequence 1 from Patent WO0166740.		
ACCESSION		AX299996		
VERSION		AX299996.1		GI:17129473
KEYWORDS				
SOURCE		Homo sapiens (human)		
ORGANISM		Homo sapiens		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE		Bacon, D.L., Fong, S., Goddard, A., Godowski, P.J., Grimaldi, C.J.,		
JOURNAL		Gurney, A.L., Tunas, D., Watanabe, C.K., Wood, W.I. and Zhang, Z.		
FEATURES		Compositions and methods for the treatment of immune related		
SOURCE		diseases		
ORIGIN		Patent: WO 0166740-A 1 13-SEP-2001;		
		Genentech, Inc. (US)		
		Location/Qualifiers		
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Best Local Similarity		100.0%; Pred. No. 0; Indels 0; Gaps		
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Db	304	CACCCAGTGTGACATCTAATAGCAACCTTCTGGGCTGCTCCGCTGACATCCAGGCTGCCA	363
OY	361	GGCCATGATGTGTGACATCCAGTGCAAATCTCTCCCTGGCTGTGATTATCTCTGTGTGGG	420
Db	364	GGCCATGATGTGTGACATCCAGTGCAAATCTCTCCCTGGCTGTGATTATCTCTGTGTGGG	423
OY	421	CATGAGATGCAACATCTTTCGCGCAGGAATCCGAGCCAAAGACAGAGTGGCGGTAGCAGG	480
Db	424	CATGAGATGCAACATCTTTCGCGCAGGAATCCGAGCCAAAGACAGAGTGGCGGTAGCAGG	483
OY	481	TGAGATCTTTTTCATCCCTTGGAGGGCTCTCGGATTCATTTCTGTGGCTCGGAATCTTCA	540
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QY 1261 TTTTGGGCGATTGCTCTAATCTTCTCAAGCTTCCCTCCAAAGAACTGATTTGGCCC 1320
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DB 1444 CAGAAAGGCGCTGGGACATTTAAAAATA 1475

RESULT 9
AX395213 1475 bp DNA linear PAT 18-MAY-2002
LOCUS Sequence 1 from Patent WO216429.
DEFINITION AX395213
ACCESSION AX395213
VERSION AX395213.1 GI:21066244
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Goddard, A., Goddard, P.J., Gurney, A.L., Hillan, K.J., Polakis, P.,
AUTHORS Smith, V., Wood, W.I., Wu, T.D. and Zhang, Z.
TITLE Compositions and methods for the diagnosis and treatment of tumor
JOURNAL Patent: WO 0216429-A 1 28-FEB-2002;
Genentech, Inc. (US)
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source location/Qualifiers
1.1475
/organism="Homo sapiens"
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ORIGIN
Query Match 53.7%; Score 1472; DB 6; Length 1475;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1444 CAGAAAGGCGCTGGGACATTTAAAAATA 1475

RESULT 10
AX454606 1475 bp DNA linear PAT 06-JUL-2002
LOCUS
DEFINITION Sequence 191 from Patent WO0208284.
ACCESSION AX454606
VERSION AX454606.1 GI:21713927
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.B., Goddard,A.,
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Pooni,N.P., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Je,W.
TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0208284-A 191 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary B. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scott A. (US) ; Pan, James (US)
; Pooni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)
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Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 11
AX464358 1475 bp DNA linear PAT 16-JUL-2002
LOCUS
DEFINITION Sequence 491 from Patent WO0140466.
ACCESSION AX464358
VERSION AX464358.1 GI:21899195
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E.,
Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Guney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tamas, D., Wetanabe, C.K.,
Wood, W.L., and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
same
JOURNAL Patent: WO 0140466-A 491 07-JUN-2001;
Genentech Inc. (US)
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Location/Qualifiers
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ORIGIN
Query Match 53.7%; Score 1472; DB 6; Length 1475;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 484 TGAAGTCTTCTTCACTTGTGAGAGCTTGTGGAGCTTGTGGAGCTTGTGGAGCTTGT 543
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QY 1441 CAG 1472
DB 1444 CAG 1475
RESULT 12
AX491084 1475 bp DNA linear PAT 16-AUG-2002
LOCUS AX491084
DEFINITION Sequence 191 from Patent WO0200690.
ACCESSION AX491084
VERSION AX491084.1 GI:22323879
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Baker, K.P., Ferrara, N., Gerlitz, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Guney, A.L., Hillan, K.J., Mayers, S.A., Pan, J.,
Pao, N.F., Stephan, J.P., Wetanabe, C.K., Williams, P.M., Wood, W.L.
and Ye, W.
TITLE Competitions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0200690-A 191 03-JAN-2002;
Genentech, Inc. (US)
FEATURES
Source 1.1475
Location/Qualifiers

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/mol_type="unassigned DNA"
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ORIGIN

Query Match	Score	DB	Length
53.7%	1472	6	1475

Best Local Similarity: 100.0%; Pred. No. 0;
 Matches 1472: Conservative 0: Mismatches

[illegible]

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QY	61	GCTTCAGCCTGAAGAACAAGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGCTCCCAT	120
Db	64	GCTTCAGCCTGAAGAACAAGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGCTCCCAT	123
QY	121	GGCCTCTTGTGGCCTCCAACTTTGTGGGCTACATCTTAGGCTTCTTGGGGCTTTTGGGAC	180
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QY	181	ACTGGTTGGCAAGTCGTGCTCCCGAGCTGAAAAACAAGTTCTTAATGCGGGTCCAGCATGTT	240
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QY	241	GACAGCAGTTGGCTTCTCCAAAGGGCTCTGAGTGAATGTGCCACACACAGCACAGGCAT	300
Db	244	GACAGCAGTTGGCTTCTCCAAAGGGCTCTGAGTGAATGTGCCACACACAGCACAGGCAT	303
QY	301	CACCCAGTGTGACATCTATAGCACCTTCTGGGGCTGCCCGCTGACATCCAGGCTGCCCA	360
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QY	361	GGCCATATATGATGACATCAGTGCAAATCTCCCTCCGCGCTGCATTAATCTGTGATGGG	420
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QY	421	CATGAGATGACACAGTCTTCTGCGCAAGAAATCCGAGCCAAAGACAGAGTGGCGGTAGCAGG	480
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QY	541	TGGATTCCTAAGGGACTTCTACTACACATGGTGTGCTGACAGCATGAATTTGAAATTGG	600
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QY	661	CTGCTTTTCTGCTCATCTCCAGAGAAATGCTCCAACTTACATGATGCTTACCAAGCCCA	720
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QY	721	ACCTCTTGGCAAGAGAGCTCTCCAAAGGCTGTGTAACCTCCCAAGTCAAGAGTAGTT	780
Db	724	ACCTCTTGGCAAGAGAGCTCTCCAAAGGCTGTGTAACCTCCCAAGTCAAGAGTAGTT	783
QY	781	CAATTCTCTACAGCCTGACAGGGTATGTGTGAAGAACAGAGGGCCAGAGCTGGGGGGTGGC	840
Db	784	CAATTCTCTACAGCCTGACAGGGTATGTGTGAAGAACAGAGGGCCAGAGCTGGGGGGTGGC	843
QY	841	TGGGCTCTGTAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAAGGACCTTACACT	900
Db	844	TGGGCTCTGTAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAAGGACCTTACACT	903
QY	901	GGATCTGTACGAAGGTGTGTGAGATGACATCTTTGGCCATTTGACATTTGACCAAG	960
Db	904	GGATCTGTACGAAGGTGTGTGAGATGACATCTTTGGCCATTTGACATTTGACCAAG	963

Qy	961	GCAGAAATGGGGGCTAGCTGTAACAGCATGAGAGTTGAAATTGGCCAAAGATGCTGCCATGC	1020
Db	964	GCAGAAATGGGGGCTAGCTGTAACAGCATGAGTTGAAATTGGCCAAAGATGCTGCCATGC	1023
Qy	1021	CAGCCTTCTGTTTCTCCACCTTGCTGCTCCCTGGCCTTAAGTCCCAACCTTCACCTT	1080
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Qy	1081	GAAACCCCATTTCCCTTAAGCCAGAGCTCAAGAGATCCCTTTGGCCTTGCGTTTAACTTGGG	1140
Db	1084	GAAACCCCATTTCCCTTAAGCCAGAGCTCAAGAGATCCCTTTGGCCTTGCGTTTAACTTGGG	1143
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Qy	1381	CTGAAATTAACCACTCTTAAGGATTCAGAGGAAACAGAAACAGAGATCCAGATGGGAGGA	1440
Db	1384	CTGAAATTAACCACTCTTAAGGATTCAGAGGAAACAGAAACAGAGATCCAGATGGGAGGA	1443
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RESULT 13
AX697065

LOCUS	AX697065	1475 bp	DNA	linear	PAT 02-APR-2003
DEFINITION	Sequence 133 from Patent WO0078961.				
ACCESSION	AX697065				
VERSION	AX697065.1	GI:29498042			
KEYWORDS					
SOURCE	Homo sapiens (human)				

ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE	1
AUTHORS	Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Denoyers,L., Edon,D.L., Gao,W.Q., Pan,J., Boltstein,D., Fong,S., Goddard,A., Gadowski,P.J., Guney,A.L., Smith,V., Tumes,D., Wood,W.I., Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Maranabe,C.K. Secreted and transmembrane polypeptides and nucleic acids encoding the same
TITLE	
JOURNAL	Patent: WO 0078961-A 133 28-DEC-2000;
	Genentech Inc. (US)

FEATURES	location/Qualifiers
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ORIGIN	

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Best Local Similarity	100.0%	Pred. No. 0		
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Qy	1	AGAAGTCAGCCTGGCAGAGAGACTCTAAATGAGGGATTAGAGGTGTTCAAGAGCAGA	60	
Db	4	AGAAGTCAGCCTGGCAGAGAGACTCTAAATGAGGGATTAGAGGTGTTCAAGAGCAGA	63	
Oy	61	GCTTCAGCCTGAMAGCAGGGAGCAGTTCCTGAAGACGCTTACTAGAGAGCTTGCAT	120	

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RESULT 14
AY358474 1475 bp mRNA linear PRI 03-OCT-2003
LOCUS
DEFINITION Homo sapiens clone DNA64886 Claudin-2 (UNQ705) mRNA, complete cds.
ACCESSION AY358474
VERSION AY358474.1 GI:37182070
KEYWORDS P11_CDN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brub, J., Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.B., Heidens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seebagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wiand, D., Woods, K., Xie, M.H., Yasutake, Y., Yl, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
JOURNAL
PUBMED 12975309
REFERENCE 2 (bases 1 to 1475)
AUTHORS Clark, H.F.
TITLE Direct Submission
JOURNAL Submitted (01-NOV-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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ORIGIN

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Query Match 53.7%; Score 1472; DB 9; Length 1475;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 GGCCTCTCTGGCTCCCACTTGTGGGCTACATCTAGAGCTTCTGGGGCTTTTGGGAC 180

DB 124 GGCCTCTCTGGCTCCCACTTGTGGGCTACATCTAGAGCTTCTGGGGCTTTTGGGAC 183

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DB 1384 CTGAAATTAACATCTTACGATTCAGAGGACAGAAAGCAGAGTGGAGGA 1443

QY 1441 CAGAAAGCAGCTGGGACATTTAAAAATA 1472

DB 1444 CAGAAAGCAGCTGGGACATTTAAAAATA 1475

RESULT 15

BC014424 1506 bp mRNA linear PRI 29-JUN-2004

LOCUS BC014424

DEFINITION Homo sapiens claudin 2, mRNA (cDNA clone MGC:20191 IMAGE:4645075), complete cds.

ACCESSION BC014424

VERSION BC014424.1 GI:15680158

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

1 Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G., Klapper, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.P., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheltz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Lonnell, N.A., Peters, G.J., Abramson, R.D., Mullen, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Hale, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hu, X., Gibbs, R.A., Vallalath, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J.J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whilton, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalske, U., Small, D.B., Scherch, A., Schein, J.E., Jones, S.J., Jones, S.J., and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16699-16903 (2002)

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

12477932

2 (bases 1 to 1506)

Strausberg, R.

Direct Submission

JOURNAL

Submitted (17-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca

Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim Macdonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Lissa Prabh, Parvaneh Saeedi, JR Santos, Angeliq Scherch, Ursula Skalska, Duane Smalrus, Jeff Stolt, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.

FEATURES

source

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAL Plate: 29 Row: m Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9966780.
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SEFNSVSLTYV"

gene

CDS

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
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Search completed: October 28, 2004, 20:47:32
Job time : 18354 secs

PT proliferative associated disorders e.g. cancer, rheumatoid arthritis and
 PT Alzheimer's disease.

PS Claim 9; Page 79-80; 84pp; English.

XX The present sequence encodes a human membrane associated organizational
 CC protein (HUNCT). HUNCT is used for the diagnosis, treatment and
 CC prevention of cell proliferative disorders including cancer and
 CC autoimmune/inflammatory, neurological, developmental, vesicle
 CC trafficking, reproductive, gastrointestinal and renal disorders. These
 CC disorders may include atherosclerosis, leukemia, allergies, rheumatoid
 CC arthritis, Alzheimer's disease, anxiety, diabetes, ovulatory defects,
 CC renal failure and irritable bowel syndrome. A vector expressing HUNCT,
 CC and an agonist of HUNCT can be used to treat or prevent a disorder
 CC associated with decreased expression or activity of HUNCT. An antagonist
 CC of HUNCT or a vector expressing the complement of a polynucleotide
 CC encoding HUNCT can be used to treat or prevent a disorder associated with
 CC increased expression or activity of HUNCT. Antibodies which bind HUNCT
 CC can be used for diagnosis of disorders associated with HUNCT expression
 CC or to monitor patients being treated with HUNCT, agonists, antagonists or
 CC inhibitors of HUNCT. Assays are preferably carried out on body fluids
 CC from a patient using radioimmunoassay, enzyme linked immunosorbent assays
 CC or fluorescent activated cell sorting assays. Polynucleotides encoding
 CC HUNCT are also used in hybridisation assays to determine absence,
 CC presence or excess expression of HUNCT and to monitor regulation of HUNCT
 CC levels during disease therapy

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 Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 2

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ID AAFP3769 standard; cDNA; 2863 BP.
AC AAFP3769;
DT 23-MAY-2001 (first entry)
XX Human cDNA encoding a membrane or secretory protein clone PSEC059.
XX Human; secretory protein; membrane protein; vaccine; gene therapy;
XX rheumatoid arthritis; diabetes; ss.
OS Homo sapiens.
PN EP1067182-A2.
PD 10-JAN-2001.
PF 07-JUL-2000; 2000BP-00114090.
XX 08-JUL-1999; 994P-00194179.
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XX (HELI-) HELIX RBS INST.
PA
PI Oca T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
XX WPI; 2001-093989/11.
DR P-PSDB; AAB88342.
XX
PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
XX gene therapy or as candidate target molecules in drug development.
XX
PS Claim 1; SEQ ID NO 51; 609pp + Sequence listing; English.
CC This invention relates to nucleic acid sequences AAFP3744 - AAFP3916
CC which encode human secretory or membrane proteins represented by AAB88317
CC - AAB88419. Included in the invention are primers AAFP3917 - AAFP4295 and
CC AAFP6232 - AAFP6235 which are used to isolate the cDNA sequences of the
CC invention. The invention also includes methods for the production of
CC antibodies directed against the proteins, and cDNA sequences, which can
CC be used in vaccines. The polynucleotide sequences can be used in gene
CC therapy. The polynucleotide sequences and the proteins they encode may be
CC used in the prevention, treatment and diagnosis of diseases associated
CC with inappropriate secretory protein/membrane protein expression. The
CC nucleic acids and complementary sequences may also be used as DNA probes
CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
CC and quantitate the presence of similar nucleic acid sequences in samples.
CC They may also be used to study the expression and function of secretory
CC proteins/membrane polypeptides and their role in metabolism. The
CC polypeptides may be used as antigens in the production of antibodies
CC against them and in assays to identify modulators (agonists and
CC antagonists) of expression and activity. The antibodies and antagonists
CC may also be used as therapeutic agents to down regulate expression and
CC activity. The antibodies may also be used as diagnostic agents for
CC detecting the presence of the polypeptides in samples (e.g. by enzyme
CC linked immunosorbent assay (ELISA)). Examples of diseases which may be
CC treated include rheumatoid arthritis and diabetes
XX
XX Sequence 2863 BP; 670 A; 794 C; 711 G; 688 T; 0 U; 0 Other;
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Db 953 TGGGCTGTGAAACAGTGGACAGCACCCGAGAGGCTCAAGGTGAGGACATCAACT 1012
QY 901 GGAATCGTGAAGAGGCTGTGAGGATGAAGTGAATTTGGCATTTGGATTGAGCAAG 960
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QY 1321 TGGAACTTCATCCCACTCTTGTATAGTCCAGATGTCCAGACTTAATTTGTGATGA 1380
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Db 2473 TGGCATATCATGCCCCAGAGGTGCTGCTGATGATCTAGTATGCTGACTGCTGCT 2532
Qy 2161 GGGATTCAGCTGAGGTGGAGTGAAGATGGTTCACAGAAAGACAGTTCCACTTAAAG 2220
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Qy 2221 GTCCGAAAATGTTTCCCTTTAACTTGAAGTGAAGTGAAGGGGCTATACCAAGATATT 2280
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Db 2653 TCCCTCAGCAGTCTAGGAGTGAAGTGGCTTCTGAAAAATTCAGACACACTCTCGAACT 2712
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Db 2953 CATTCACAATTTTGAATTAATGTTATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3012
Qy 2641 GTAAACCTTTCGGTGGGTGGGGGCAATCTAGACTCTCTGTATCCCCAGACTATCT 2700
Db 3013 GTAAACCTTTCGGTGGGTGGGGGCAATCTAGACTCTCTGTATCCCCAGACTATCT 3072
Qy 2701 GTAAACGTCAGAGGCA 2717
Db 3073 GTAAACGTCAGAGGCA 3089

RESULT 4
AB271540
ID AB271540 standard; DNA; 3126 BP.
XX
XX AB271540;

DT 03-APR-2003 (first entry)
 XX
 DE Secreted protein gene 168 genomic fragment HTP1H83, SEQ ID NO:650.
 XX
 KW Human; secreted protein; digestive disorder; gastrointestinal disorder;
 KW mouth; oesophagus; stomach; small intestine; large intestine; liver;
 KW biliary tract; pancreas; cancer; tumour; hyperproliferative disorder;
 KW immune disorder; inflammation; infection; wound healing; drug screening;
 KW chromosome identification; chromosome mapping; cytostatic; gene therapy;
 KW antiinflammatory; immunosuppressive; valnerary; chromosome Xq22.3-23;
 KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN W020027648-A1.
 XX
 PD 03-OCT-2002.
 XX
 PF 19-MAR-2002; 2002MO-US008276.
 XX
 PR 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI; 2003-023900/02.
 XX
 PT New human secreted proteins and nucleic acids, useful for detecting,
 PT preventing, diagnosing, prognosticating, treating and/or ameliorating,
 PT e.g. gastrointestinal diseases and disorders, or cancers.
 XX
 PS Disclosure; Page 1211-1212; 1216pp; English.
 XX
 CC AB271190-AB271478 represent cDNAs corresponding to 178 human secreted
 CC protein genes, and ABP00011-ABP00299 represent the proteins they encode.
 CC AB271479-AB271540 represent human secreted protein genomic fragments. The
 CC invention also encompasses antibodies specific for the secreted proteins.
 CC the use of the secreted proteins in drug screening, and recombinant
 CC vectors and host cells comprising a nucleic acid of the invention. The
 CC secreted proteins, nucleic acids encoding them, antibodies or antibody
 CC fragments specific for the secreted proteins, and modulators of protein
 CC activity are useful for diagnosing, treating, ameliorating or preventing
 CC digestive disorders. Such conditions include disorders of the mouth,
 CC oesophagus, stomach, small intestine, large intestine, liver, biliary,
 CC tract and pancreas, and include cancers of these organs and tissues. The
 CC secreted proteins and their nucleic acids may also be used in the
 CC treatment of immune disorders, inflammation, infection,
 CC hyperproliferative disorders, and to promote wound healing. Nucleic acids
 CC of the invention may be used for chromosome identification, chromosome
 CC mapping, in gene therapy, for identifying individuals from minute
 CC biological samples, as hybridisation probes, and as molecular weight
 CC markers. The present sequence represents a human secreted protein genomic
 CC fragment referred to in the disclosure of the invention
 XX
 SQ Sequence 3126 BP; 739 A; 848 C; 761 G; 778 T; 0 U; 0 Other;

Query Match 91.6%; Score 2513; DB 8; Length 3126;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2713; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGAAGTCAAGCTGCGAAGAGACTCTGAATGAGGATTAGAGTGTTCAGAGCAAGA 60
 DB 373 AGAAGTCAAGCTGCGAAGAGACTCTGAATGAGGATTAGAGTGTTCAGAGCAAGA 432

QY 61 GCTTACAGCTGAAGCAAGGAGAGTCCCTGAAGAGCTTCTAATGAGGTCTGACAT 120
 DB 433 GCTTACAGCTGAAGCAAGGAGAGTCCCTGAAGAGCTTCTAATGAGGTCTGACAT 492

QY 121 GGCCTCTCTGGCTCCAACTTGTGGCTACATCTAGAGGCTTCTGGGGCTTTTGGGAC 180

DB 493 GGCCTCTCTGGCTCCAACTTGTGGCTACATCTAGAGGCTTCTGGGGCTTTTGGGAC 552

QY 181 ACTGTTGCAATGCTGCTCCAGCTGAGAAAACAAGTTCTTATGCGGTCCAGCATTTGT 240

DB 553 ACTGTTGCAATGCTGCTCCAGCTGAGAAAACAAGTTCTTATGCGGTCCAGCATTTGT 612

QY 241 GACAGCAAGTTGGCTTCTCAAGGGGCTCTGGAATGGAATGCAACACAGCAGAGCAT 300

DB 613 GACAGCAAGTTGGCTTCTCAAGGGGCTCTGGAATGGAATGCAACACAGCAGAGCAT 672

QY 301 CACCCAGTGTGACATCTATATGACACCTTCTGGGCTGCGCGCTGACATCCAGGCTCCCA 360

DB 673 CACCCAGTGTGACATCTATATGACACCTTCTGGGCTGCGCGCTGACATCCAGGCTCCCA 732

QY 361 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420

DB 733 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 792

QY 421 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480

DB 793 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 852

QY 481 TGAAGTCTTTTCAATCTTGAAGGCTCTGGGATTCATCTGTTGCTTGAATCTTCA 540

DB 853 TGAAGTCTTTTCAATCTTGAAGGCTCTGGGATTCATCTGTTGCTTGAATCTTCA 912

QY 541 TGGGATCTTACGAGGACTTCTACATCACAATGAGGCTGAGCAGATGAAATTTAGATTGG 600

DB 913 TGGGATCTTACGAGGACTTCTACATCACAATGAGGCTGAGCAGATGAAATTTAGATTGG 972

QY 601 AGAGGCTCTTACTTGGGCTTATTTCTTCTGTTCTCCCTGATGATGATGATGATGATG 660

DB 973 AGAGGCTCTTACTTGGGCTTATTTCTTCTGTTCTCCCTGATGATGATGATGATGATG 1032

QY 661 CTGCTTTTCTGCTCATTCCTCAAGAAATGCTCTCAACTACTGATGATGATGATGATG 720

DB 1033 CTGCTTTTCTGCTCATTCCTCAAGAAATGCTCTCAACTACTGATGATGATGATGATG 1092

QY 721 ACTCTTTCACAAAGAGCTCTCAAGGCTGCTCAAGCTTCTCAAGTCAAGTGAATG 780

DB 1093 ACTCTTTCACAAAGAGCTCTCAAGGCTGCTCAAGCTTCTCAAGTCAAGTGAATG 1152

QY 781 CAATTCCTCAAGCTCTCAAGGCTGATGATGATGATGATGATGATGATGATGATGATG 840

DB 1153 CAATTCCTCAAGCTCTCAAGGCTGATGATGATGATGATGATGATGATGATGATGATG 1212

QY 841 TGGGCTGTGAAACAGTGAAGACAGACCCCGAGGSCCAAGTGAAGGACACTTACACT 900

DB 1213 TGGGCTGTGAAACAGTGAAGACAGACCCCGAGGSCCAAGTGAAGGACACTTACACT 1272

QY 901 GATTCGTGCAAGAGTGTCTGAGATGATGATGATGATGATGATGATGATGATGATG 960

DB 1273 GATTCGTGCAAGAGTGTCTGAGATGATGATGATGATGATGATGATGATGATGATG 1332

QY 961 GCAAAATGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020

DB 1333 GCAAAATGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1392

QY 1021 CAGCTTTCTGTTTCTCACTTGTCTCTCCCTGCTCAAGTCTTCAAGTCTTCAAGTCT 1080

DB 1393 CAGCTTTCTGTTTCTCACTTGTCTCTCCCTGCTCAAGTCTTCAAGTCTTCAAGTCT 1452

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DB 1453 GAAACCCCATTTCTTAAAGCAGAGTCAAGAGATCTTGTGCTTGTGTTTAACTGGG 1512

QY 1141 ACTTCATCCCAACCACTAATCAATCCCACTGATGATGATGATGATGATGATGATGATG 1200

DB 1513 ACTTCATCCCAACCACTAATCAATCCCACTGATGATGATGATGATGATGATGATGATG 1572

QY 1201 TCTCTCTGAGAGTGTGCTTCTTAACTAATGCTGAGGATGAGGATGAGGATGAGGATG 1260

DB 1573 TCTCTCTGAGAGTGTGCTTCTTAACTAATGCTGAGGATGAGGATGAGGATGAGGATG 1632

CC a pharmaceutical composition for diagnosing or treating diabetes or
CC conditions related to diabetes. The present sequence is that of the human
CC immunoglobulin Fc portion used to generate fusion proteins, increasing
CC the stability of the fused protein as compared to the secreted protein
CC only. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 3126 BP; 739 A; 848 C; 761 G; 778 T; 0 U; 0 Other;

Query Match 91.6%; Score 2513; DB 9; Length 3126;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2713; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 1 AGAAGTCAAGCTGGCAGAGAGACTCTGAATAGAGATTAGAGTGTTCAGAGCAGA 60
DB 373 AGAAGTCAAGCTGGCAGAGAGACTCTGAATAGAGATTAGAGTGTTCAGAGCAGA 432
QY 61 GCTTCAAGCTGAAGACAGAGGAGCAGTCCCTGAAGACGCTTCTAAGAGTCTGCAT 120
DB 433 GCTTCAAGCTGAAGACAGAGGAGCAGTCCCTGAAGACGCTTCTAAGAGTCTGCAT 492
QY 121 GGCCTCTCTGGCTCCAACTGTGGGCTACATCTAGAGCTTCTGGGCTTTTGGGAC 180
DB 493 GGCCTCTCTGGCTCCAACTGTGGGCTACATCTAGAGCTTCTGGGCTTTTGGGAC 552
QY 181 ACTGGTTGCAATGTGTCTCCCAAGCTGGAACAAAGTTCTTATGTCCGTGCCAGATTGT 240
DB 553 ACTGGTTGCAATGTGTCTCCCAAGCTGGAACAAAGTTCTTATGTCCGTGCCAGATTGT 612
QY 241 GACAGCAGTTGGCTTCTCAAGAGGCTCTGGATGGAATGTGCCACACAGCAGAGCAT 300
DB 613 GACAGCAGTTGGCTTCTCAAGAGGCTCTGGATGGAATGTGCCACACAGCAGAGCAT 672
QY 301 CACCCAGTGTGACATCTAATAGACCCCTTCTGGGCTTCCGCTGACATCCAGCTGCCA 360
DB 673 CACCCAGTGTGACATCTAATAGACCCCTTCTGGGCTTCCGCTGACATCCAGCTGCCA 722
QY 361 GGCCTCTCTGGCTCCAACTGTGGGCTACATCTAGAGCTTCTGGGCTTTTGGGAC 420
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DB 793 CATGAGATGACAGTCTTCTGCCAGAACTCCGAGCCAAAGACAGATGGCGGTAGAG 852
QY 481 TGAAGTCTTTTCAATCTTGAAGGCTCTGGGATTCATCTCTGTGCTTGAATCTTCA 540
DB 853 TGAAGTCTTTTCAATCTTGAAGGCTCTGGGATTCATCTCTGTGCTTGAATCTTCA 912
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DB 1333 GCAAAATGGGGCTAGTGTAAACAGATGAGGTTAAATTTGCCAGAGATCTGCCATGC 1392
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QY 1801 GTGTGGAGCTGTGGGGTACTGAGAGAAACACATCTCTTAAGAGGTGTAAAGACCG 1860
DB 2173 GTGTGGAGCTGTGGGGTACTGAGAGAAACACATCTCTTAAGAGGTGTAAAGACCG 2232
QY 1861 GTGAGTGTGTGTGGCTCAAGTGGGTGTCTACTGTGCAAGTGAAGAGGCCCTCT 1920
DB 2233 GTGAGTGTGTGTGGCTCAAGTGGGTGTCTACTGTGCAAGTGAAGAGGCCCTCT 2292
QY 1921 AGAACTCTTCAAGGCTAATGAAATCAAGTCAAAATGAGATCAAGCCCTCCAGGCTCC 1980
DB 2293 AGAACTCTTCAAGGCTAATGAAATCAAGTCAAAATGAGATCAAGCCCTCCAGGCTCC 2352
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QY	1981	ACCACGAGAGACTACAGAGGCTCTGAAAGACCAATAGACCAAGCGAGCCCTTCAATTT	2040
Db	2253	ACCACGAGAGACTACAGAGGCTCTGAAAGACCAATAGACCAAGCGAGCCCTTCAATTT	2412
QY	2041	CCCCCACTGTCCATCGGAGAGTGTCTCCAGATGGCTAGAGGGCATCTAAGGGCTCCAGCA	2100
Db	2413	CCCCCACTGTCCATCGGAGAGTGTCTCCAGATGGCTAGAGGGCATCTAAGGGCTCCAGCA	2472
QY	2101	TGGCATATCCATGCCCCACGGTGTGTGTCTCATATCTGAAGTAAAGCTGTGCATCTGTGCTT	2160
Db	2473	TGGCATATCCATGCCCCACGGTGTGTGTCTCATATCTGAAGTAAAGCTGTGCATCTGTGCTT	2532
QY	2161	GGGAATTGACGTGAGGTGGAGTGGAGATGGTTCCCGAGAAAGACGTTTCCACTCTTAAG	2220
Db	2533	GGGAATTGACGTGAGGTGGAGTGGAGATGGTTCCCGAGAAAGACGTTTCCACTCTTAAG	2592
QY	2221	GTCCGAAATGTTCCCTTTACCTCGAGTGGAGTGAAGGGGTCTATACCAAGATATTT	2280
Db	2593	GTCCGAAATGTTCCCTTTACCTCGAGTGGAGTGAAGGGGTCTATACCAAGATATTT	2652
QY	2281	TCCCTCACCACTCTAAGGCGATGATCTGGCTTTCTGAAAAATTCAGACACACTTCTGAAACT	2340
Db	2653	TCCCTCACCACTCTAAGGCGATGATCTGGCTTTCTGAAAAATTCAGACACACTTCTGAAACT	2712
QY	2341	CATTGTACGACGAGAGGGGCCCATCTGTTGTCTGTAAACAATGCTTTACATGTCACACTTC	2400
Db	2713	CATTGTACGACGAGAGGGGCCCATCTGTTGTCTGTAAACAATGCTTTACATGTCACACTTC	2772
QY	2401	TTGCCATGTTCCAGCTGCTCTCCCAACCTGGAGGGCCGCTCTCCCTTAGCCAAATGCTCC	2460
Db	2773	TTGCCATGTTCCAGCTGCTCTCCCAACCTGGAGGGCCGCTCTCCCTTAGCCAAATGCTCC	2832
QY	2461	TCAGGCTTGGAGAACTTCTCAGGGTCACTTCCTTCAATGAGCTTCTGTGATCACTCCA	2520
Db	2833	TCAGGCTTGGAGAACTTCTCAGGGTCACTTCCTTCAATGAGCTTCTGTGATCACTCCA	2892
QY	2521	TCCCTCTCCATACCCCTCCCTCCCCCAACCCCAATGATATAATGCTCTTGATGCTTAG	2580
Db	2893	TCCCTCTCCATACCCCTCCCTCCCCCAACCCCAATGATATAATGCTCTTGATGCTTAG	2952
QY	2581	CATTACAAATTTTGAATGATCGTATTTATTTGTGTGTGTCCGATCTCAAAATATATTT	2640
Db	2953	CATTACAAATTTTGAATGATCGTATTTATTTGTGTGTGTCCGATCTCAAAATATATTT	3012
QY	2641	GTAACCCCTTGGTGGTGGGGGCGCATATCTTGAACCTCTGTATATCCCGACACTATCT	2700
Db	3013	GTAACCCCTTGGTGGTGGGGGCGCATATCTTGAACCTCTGTATATCCCGACACTATCT	3072
QY	2701	GTAACAGTGCACGAGCAC 2717	
Db	3073	GTAACAGTGCACGAGCAC 3089	
RESULT 6			
ADCT4722			
ID	ADCT4722 standard; DNA; 3126 BP.		
XX			
AC	ADCT4722;		
XX			
DT	01-JAN-2004 (first entry)		
DE	Human secreted protein-related DNA - SEQ ID 1355.		
XX			
KW	antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;		
KW	antidiabetic; immunosuppressive; dermatological; nephrotropic;		
KW	antiparkinsonian; neuroprotective; nootropic; antibacterial; virocidic;		
KW	fungicide; antiparasitic; antiarteriosclerotic; vulnerary; cytostatic;		
KW	haemopoietic; haematologic; anaemia; autoimmune disorder;		
KW	rheumatoid arthritis; inflammation; Grave's disease; diabetes;		
KW	systemic lupus erythematosus; glomerulonephritis; neurodegenerative;		
KW	Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;		
KW	cancer; bacterial; viral; fungal; parasitic infection; gene therapy;		
KW	human; ds.		

OS	Homo sapiens.
XX	
XX	N02003038063-A2.
PN	
XX	
PD	08-MAY-2003.
XX	
PF	19-MAR-2002; 2002MO-US008277.
XX	
PR	21-MAR-2001; 2001US-0277340P.
PR	19-JUL-2001; 2001US-0306171P.
PR	13-NOV-2001; 2001US-0331287P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
PI	Rosen CA, Ruben SM;
DR	WPI; 2003-430516/40.
XX	
PT	New human secreted polypeptide for diagnosing, preventing or treating
PT	hematopoietic or hematologic disorders (e.g. anemia), autoimmune
PT	disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
PT	atherosclerosis).
XX	
PS	Disclosure; SEQ ID NO 1355; 2272bp; English.
XX	
CC	The invention relates to a novel human secreted polypeptide comprising a
CC	defined sequence given in the specification. The polypeptide, nucleic
CC	acid molecule, antibody, agonist or antagonist of the invention may be
CC	useful for preparing a composition for diagnosing or treating a
CC	haemopoietic or haematologic disorder such as anaemia, autoimmune
CC	disorders such as rheumatoid arthritis, inflammation, Grave's disease,
CC	diabetes, systemic lupus erythematosus or glomerulonephritis,
CC	neurodegenerative disorders including Parkinson's disease and Alzheimer's
CC	disease, wounds and hyperproliferative disorders including
CC	atherosclerosis or cancer, as well as bacterial, viral, fungal or
CC	parasitic infections. The polypeptide may also be used during gene
CC	therapy procedures and for identifying a binding partner by contacting
CC	the polypeptide with a binding partner and determining whether the
CC	binding partner increases or decreases the activity of the polypeptide.
CC	The current sequence is that of the human secreted protein-related DNA of
CC	the invention.
XX	
SQ	Sequence 3126 BP; 739 A; 848 C; 761 G; 778 T; 0 U; 0 Other;
	Query March 91.6%; Score 2513; DB 10; Length 3126;
	Best Local Similarity 99.9%; Pred. No. 0;
	Matches 2713; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	1 AGAAGTCAGCCTGGCAGAGAAGACTCTGAATGAGGAGTTAGAGGTGTTCAAGACAGA 60
DB	373 AGAAGTCAGCCTGGCAGAGAAGACTCTGAATGAGGAGTTAGAGGTGTTCAAGACAGA 412
YY	61 GCCTTCAAGCTTGAAACAAGGAGAGATGCCCTGGAAGAGCTTCTAATAAGAGTGCAT 120
DB	433 GCCTTCAAGCTTGAAACAAGGAGAGATGCCCTGGAAGAGCTTCTAATAAGAGTGCAT 492
QY	121 GGCTCTCTTGGGCTCCAATTGTGGGCTCATCTTAGGCGCTTTGGGGCTTTTGGCAC 180
DB	493 GGCTCTCTTGGGCTCCAATTGTGGGCTCATCTTAGGCGCTTTGGGGCTTTTGGCAC 552
QY	181 ACTGTTGCCATGCTGTCCTCCCAAGCTGGAATAACAAGTTCTTAATGCTGGTCCAGCAT 240
DB	553 ACTGTTGCCATGCTGTCCTCCCAAGCTGGAATAACAAGTTCTTAATGCTGGTCCAGCAT 612
QY	241 GACAGCAGTTGGCTTCTCCAAAGGGCCCTGGAATGGAAATGGCCACACAGCACAAGGAT 300
DB	613 GACAGCAGTTGGCTTCTCCAAAGGGCCCTGGAATGGAAATGGCCACACAGCACAAGGAT 672
QY	301 CACCAGATGACATCTATAGCAACCTTCTGGGCGCTGCCGCTGACATCCAGGCTGCCCA 360
DB	673 CACCAGATGACATCTATAGCAACCTTCTGGGCGCTGCCGCTGACATCCAGGCTGCCCA 732

Qy 361 GGCCATGATGATGATCATCATGATGATCTCTCCCTGAGCTGATATCTCTGTGTGG 420
Db 733 GGCCATGATGATGATCATCATGATGATCTCTCCCTGAGCTGATATCTCTGTGTGG 792
Qy 421 CATGATGATGATGATCTCTCTGAGGAAATCCGAGCCAAAGACAGATGCGGTAGCAG 480
Db 793 CATGATGATGATGATCTCTCTGAGGAAATCCGAGCCAAAGACAGATGCGGTAGCAG 852
Qy 481 TGGAGTCTTTTCACTCTGAGGAGCTCTGAGGATGATCTCTGAGTCTGAGATCTTCA 540
Db 853 TGGAGTCTTTTCACTCTGAGGAGCTCTGAGGATGATCTCTGAGTCTGAGATCTTCA 912
Qy 541 TGGAGTCTTACGAGGATCTTCTACTCACTGATGCTGAGAGATGAGATTTGAGATGG 600
Db 913 TGGAGTCTTACGAGGATCTTCTACTCACTGATGCTGAGAGATGAGATTTGAGATGG 972
Qy 601 AGAGGCTCTTTACTTGGGATTTATTTCTCTGTTCTCCCTGATGCTGAGATGATCT 660
Db 973 AGAGGCTCTTTACTTGGGATTTATTTCTCTGTTCTCCCTGATGCTGAGATGATCT 1032
Qy 661 CTGCTTTCTCTGATCTCCAGAGAAATGCTCCAACTAGATGCTCCAAAGCCCA 720
Db 1033 CTGCTTTCTCTGATCTCCAGAGAAATGCTCCAACTAGATGCTCCAAAGCCCA 1092
Qy 721 ACCCTTGGCAAGAGATCTCTCAAGGCTGATCACTCCCAAGTCAAGAGTGAAT 780
Db 1093 ACCCTTGGCAAGAGATCTCTCAAGGCTGATCACTCCCAAGTCAAGAGTGAAT 1152
Qy 781 CAATTCCTACAGCTGACAGGGATGATGTAAGAAACAGGGGCAAGCTGGGGGATGGC 840
Db 1153 CAATTCCTACAGCTGACAGGGATGATGTAAGAAACAGGGGCAAGCTGGGGGATGGC 1212
Qy 841 TGGGCTCTGTAAAAACAGTGAACAGACCCGAGGGGCAAGGATGAGGACATCACT 900
Db 1213 TGGGCTCTGTAAAAACAGTGAACAGACCCGAGGGGCAAGGATGAGGACATCACT 1272
Qy 901 GGATCTGTGAGAGATGCTGCTGAGGATGATGATCTTTGGCAATTTGAGCAAG 960
Db 1273 GGATCTGTGAGAGATGCTGCTGAGGATGATGATCTTTGGCAATTTGAGCAAG 1332
Qy 961 GCAGAAATGGGGGCTAGTGTAAACAGATGACAGTGTAAATGCAAGAGATGCTGCCATGC 1020
Db 1333 GCAGAAATGGGGGCTAGTGTAAACAGATGACAGTGTAAATGCAAGAGATGCTGCCATGC 1392
Qy 1021 CAGGCTTCTGTCTTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
Db 1393 CAGGCTTCTGTCTTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1452
Qy 1081 GAAACCCCATTCCTTAAGCAGAGATCAGAGATCCTTGGCTGCTGCTGCTGCTGCTGCT 1140
Db 1453 GAAACCCCATTCCTTAAGCAGAGATCAGAGATCCTTGGCTGCTGCTGCTGCTGCTGCT 1512
Qy 1141 ACTTCATCCCAAAACCACTAATCAATCCCACTGATGACCTCTGTGATCAAAAGACC 1200
Db 1513 ACTTCATCCCAAAACCACTAATCAATCCCACTGATGACCTCTGTGATCAAAAGACC 1572
Qy 1201 TCTCTGCTGAGTGGTGGCTCTTAAGCTCATTTGCTGGGATGGAAGAGAGATGGC 1260
Db 1573 TCTCTGCTGAGTGGTGGCTCTTAAGCTCATTTGCTGGGATGGAAGAGAGATGGC 1632
Qy 1261 TTTTGTGGGATGCTCTAATCTTAAGCTCTCAAGCTCCCTCAAGAAACGATTTGGCC 1320
Db 1633 TTTTGTGGGATGCTCTAATCTTAAGCTCTCAAGCTCCCTCAAGAAACGATTTGGCC 1692
Qy 1321 TGGAACTCCATCCCACTCTGTATGATCTCAAGTGTCCAGATTAATTTGTGATGAA 1380
Db 1693 TGGAACTCCATCCCACTCTGTATGATCTCAAGTGTCCAGATTAATTTGTGATGAA 1752
Qy 1381 CTGAAATTAACATCTCTACGATTCAGAGGAAACAGAAAGAGATGAGATGGAGGA 1440
Db 1753 CTGAAATTAACATCTCTACGATTCAGAGGAAACAGAAAGAGATGAGATGGAGGA 1812
Qy 1441 CAGGAAGGAGCTGGGATTTAAAAAATAAAAAATAAAAAATCCCAAGCCCATTT 1500

Db 1813 CAGGAAGGAGCTCTGGAGATTTAAAAAATAAAAAATAAAAAATCCCAAGCCCATTT 1872
Qy 1501 TCTCAGGGGATTTTCAAGAAATCTCTCATTTTGTGGGCTGGGATGATGAGCTGAGCTTG 1560
Db 1873 TCTCAGGGGATTTTCAAGAAATCTCTCATTTTGTGGGCTGGGATGATGAGCTGAGCTTG 1932
Qy 1561 AGGAAGGCAAGAGAAAGAAAGAAATGCTGTGAAACCTCAGTGGAGCGGATCTTG 1620
Db 1933 AGGAAGGCAAGAGAAAGAAAGAAATGCTGTGAAACCTCAGTGGAGCGGATCTTG 1992
Qy 1621 ACTCACTAAGAACTGCTCAGAGCTGAGATCAACAATTTGGCTGAAAGCCCTGCTC 1680
Db 1993 ACTCACTAAGAACTGCTCAGAGCTGAGATCAACAATTTGGCTGAAAGCCCTGCTC 2052
Qy 1681 ACTCTAGGAGCCTGACCTGAGCTCTTGGCTTAACCAACAAGGATAGGCTATAGCAAT 1740
Db 2053 ACTCTAGGAGCCTGACCTGAGCTCTTGGCTTAACCAACAAGGCTATAGCAAT 2112
Qy 1741 GGTTCCTTAGAAGATGAACAGATTTTCTAGGATGAGCCCTTGGCTGGGGATGACA 1800
Db 2113 GGTTCCTTAGAAGATGAACAGATTTTCTAGGATGAGCCCTTGGCTGGGGATGACA 2172
Qy 1801 GTGTGGAGCTGTGGGATCTAGAGAAACACCATTTCTTGAAGTGTCTAAGAACCAAG 1860
Db 2173 GTGTGGAGCTGTGGGATCTAGAGAAACACCATTTCTTGAAGTGTCTAAGAACCAAG 2232
Qy 1861 GTGTAGT 1920
Db 2233 GTGTAGT 2292
Qy 1921 AGAACTCTTACAGGCGTAATGAAATACGCTCAATAGATGATGAGCCCTTGGGATGC 1980
Db 2293 AGAACTCTTACAGGCGTAATGAAATACGCTCAATAGATGATGAGCCCTTGGGATGC 2352
Qy 1981 ACCCAAGAGCACTAAGAGCTCTTGAAGAACATAGACCAAGCCGCTTCAAGATT 2040
Db 2353 ACCCAAGAGCACTAAGAGCTCTTGAAGAACATAGACCAAGCCGCTTCAAGATT 2412
Qy 2041 CCCCCATGCTCTTGGGAGATGCTCAAGATGCTGAGAGGATCTTAAAGGCTCCAGCA 2100
Db 2413 CCCCCATGCTCTTGGGAGATGCTCAAGATGCTGAGAGGATCTTAAAGGCTCCAGCA 2472
Qy 2101 TGGCATATCCATGCAAGGCTGCTGTGATGATGATGATGATGATGATGATGATGATGAT 2160
Db 2473 TGGCATATCCATGCAAGGCTGCTGTGATGATGATGATGATGATGATGATGATGATGAT 2532
Qy 2161 GGGATTCAGCTGAGTGGAGTGGAGATGATGATGATGATGATGATGATGATGATGATGAT 2220
Db 2533 GGGATTCAGCTGAGTGGAGTGGAGATGATGATGATGATGATGATGATGATGATGATGAT 2592
Qy 2221 GTCCGAATATGTTCCCTTTACCTTGAAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 2280
Db 2593 GTCCGAATATGTTCCCTTTACCTTGAAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 2652
Qy 2281 TCCCTCAAGCTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340
Db 2653 TCCCTCAAGCTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2712
Qy 2341 CATTTGTCAGAGAGAGGAGCCCATGCTGTGTGTGATGATGATGATGATGATGATGATGAT 2400
Db 2713 CATTTGTCAGAGAGAGGAGCCCATGCTGTGTGTGATGATGATGATGATGATGATGATGAT 2772
Qy 2401 TTGCAATGTTCAAGCTGCTCTCCCAACCTGGAAGGCGCTCTCCCTTGAAGAGTCTCC 2460
Db 2773 TTGCAATGTTCAAGCTGCTCTCCCAACCTGGAAGGCGCTCTCCCTTGAAGAGTCTCC 2832
Qy 2461 TCAAGCTTGGAGAACTTCTCAGAGTCACTCTTGAATGAGGCTCTGATCACTCA 2520
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Qy 2521 TCCCTCTCAAGCCCTCTCCCTCCCAACCTCAATGATTAATTTGCTTGAAGTCTTGA 2580

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Db 2893 TCCCTCTCTACCCCTCCCTCCCAACCTCAATGTAATAATGCTTCTTGTAG 2952
Qy 2581 CATTACAAATTTTGGATGATCGTTATTTGTTGTCGATCCAGTCAAGATATAT 2640
Db 2953 CATTACAAATTTTGGATGATCGTTATTTGTTGTCGATCCAGTCAAGATATAT 3012
Qy 2641 GTAAACCTTGGTGGGTGGGGCCATATCTTAACCTCTCTGTATCCCCAGCTATCT 2700
Db 3013 GTAAACCTTGGTGGGTGGGGCCATATCTTAACCTCTCTGTATCCCCAGCTATCT 3072
Qy 2701 GTAAACCTTGGTGGGTGGGGCCAGC 2717
Db 3073 GTAAACCTTGGTGGGTGGGGCCAGC 3089

RESULT 7
AAA37060
ID AAA37060 standard; cDNA; 1475 BP.
AC. AAA37060;
DT 08-AUG-2000 (first entry)
XX
DE Human PRO1356 (UNQ705) cDNA sequence SEQ ID NO:133.
KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KM transmembrane; secretion; immunohesion; pharmaceutical; screening; ss.
XX Homo sapiens.
XX
PN W0200012708-A2.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WC-US020111.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
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PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
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PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
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PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
XX
XX (GETH) GENENTECH INC.
XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
XX WPI; 2000-237871/20.
XX P-PSDB; AAY99378.
XX
XX New mammalian DNA sequences encoding transmembrane, receptor or secreted
XX PT PRO polypeptides, useful for screening of potential peptide or small
XX PT molecule inhibitors of the relevant receptor/ligand interactions.
XX
XX Claim 2; Fig 77; 773pp; English.
XX
XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
XX receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
XX transmembrane and receptor PRO proteins can be used for screening of
XX potential peptide or small molecule inhibitors of the relevant
XX receptor/ligand interactions. The polypeptides and nucleotide sequences
XX encoding them have various industrial applications, including uses as
XX pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
XX primers and hybridization probes used in the isolation of the PRO
XX polypeptides from the present invention
XX
XX Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
XX
XX
XX Query Match 53.7%; Score 1472; DB 3; Length 1475;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGAAGTCAGCTGGCAGAGAGACTCTGAATGAGGATTTAGAGTTTCAAGAGCAGA 60
DB 4 AGAAGTCAGCTGGCAGAGAGACTCTGAATGAGGATTTAGAGTTTCAAGAGCAGA 63
QY 61 GCTTCAAGCTGGAAGCAAGGAGAGAGTCCCTGAAGCGCTTCTAAGAGGTTGCAAT 120
DB 64 GCTTCAAGCTGGAAGCAAGGAGAGAGTCCCTGAAGCGCTTCTAAGAGGTTGCAAT 123
QY 121 GGCCTCTCTGGCTCCCACTTGGGGTACATCTAGAGCTTCTGGGGCTTTGGGCAC 180
DB 124 GGCCTCTCTGGCTCCCACTTGGGGTACATCTAGAGCTTCTGGGGCTTTGGGCAC 183
QY 181 ACTGGTGGCAATGCTGCTCCCACTGGAAGAAAGTTCTATGTCGGTGCACATTTGT 240
DB 184 ACTGGTGGCAATGCTGCTCCCACTGGAAGAAAGTTCTATGTCGGTGCACATTTGT 243
QY 241 GACAGCAGTTGGCTTCTCAAGGGCTCTGAGTGAATGTGCCACACACAGCAGGCAAT 300
DB 244 GACAGCAGTTGGCTTCTCAAGGGCTCTGAGTGAATGTGCCACACACAGCAGGCAAT 303
QY 301 CACCCAGTGTGACATCTATAGACACCTTTTGGGGCTGCGCTGACATCCAGGCTGCCCA 360
DB 304 CACCCAGTGTGACATCTATAGACACCTTTTGGGGCTGCGCTGACATCCAGGCTGCCCA 363
QY 361 GGCAGATGATGTGACATCTAGTGAATCTCTCCCTGGCTGTCAATTTATCTGTGTGGG 420
DB 364 GGCAGATGATGTGACATCTAGTGAATCTCTCCCTGGCTGTCAATTTATCTGTGTGGG 423
QY 421 CATGAGATGCAAGTCTTCTGCGCAGGAATCCGAGCCAAAGACAGAGTGGCGGTAGCAGG 480
DB 424 CATGAGATGCAAGTCTTCTGCGCAGGAATCCGAGCCAAAGACAGAGTGGCGGTAGCAGG 483

QY 481 TGGAGTCTTTTTCATCTCTGAGAGGCTCTGAGATTCATCTCTGCTGGAATCTTCA 540
DB 484 TGGAGTCTTTTTCATCTCTGAGAGGCTCTGAGATTCATCTCTGCTGGAATCTTCA 543
QY 541 TGGAGTCTTACGGGACTTCTACCTACCACTGCTGCTGACAGCATGAATTTAGATTGG 600
DB 544 TGGAGTCTTACGGGACTTCTACCTACCACTGCTGCTGACAGCATGAATTTAGATTGG 603
QY 601 AGAGGCTTTTACTTGGGCAATTTTCTCCCGTCTCTCCGATAGCTGGAATCAATCT 660
DB 604 AGAGGCTTTTACTTGGGCAATTTTCTCCCGTCTCTCCGATAGCTGGAATCAATCT 663
QY 661 CTGCTTTCTGCTCATCCAGAGAAATGCTCCAACTACTAGATGCTTACCAAGCCCA 720
DB 664 CTGCTTTCTGCTCATCCAGAGAAATGCTCCAACTACTAGATGCTTACCAAGCCCA 723
QY 721 ACCTTTGCAAGAGAGCTCTCAAGGCTGCTCAACCTTCCCAAGTCAAGATGATT 780
DB 724 ACCTTTGCAAGAGAGCTCTCAAGGCTGCTCAACCTTCCCAAGTCAAGATGATT 783
QY 781 CAATTCTACAGCTGACAGGATTTGTGTGAAGAACCAAGGAGGCAAGCTGGGGTGGC 840
DB 784 CAATTCTACAGCTGACAGGATTTGTGTGAAGAACCAAGGAGGCAAGCTGGGGTGGC 843
QY 841 TGGGCTGTGAAGAAACAGTGAAGACACCCGAGGGCCAGGTTGAGGACATCACT 900
DB 844 TGGGCTGTGAAGAAACAGTGAAGACACCCGAGGGCCAGGTTGAGGACATCACT 903
QY 901 GATTCGTGACAGAGGCTCTGAGAGATTAAGTGAATTTGGCATTTGATTTAGACAAAG 960
DB 904 GATTCGTGACAGAGGCTCTGAGAGATTAAGTGAATTTGGCATTTGATTTAGACAAAG 963
QY 961 GCGAAGATGGGGCTAGTGTGAAGACATGACAGGTTGAATTTGCCAAGATGCTGGCTGC 1020
DB 964 GCGAAGATGGGGCTAGTGTGAAGACATGACAGGTTGAATTTGCCAAGATGCTGGCTGC 1023
QY 1021 CAGGCTTTCTGTTTCTCTGACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1024 CAGGCTTTCTGTTTCTCTGACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083
QY 1081 GAAACCCCATTTCCCTTAAGCAGAGACTCAGAGGATCCCTTTGCTGCTGCTGCTGCTG 1140
DB 1084 GAAACCCCATTTCCCTTAAGCAGAGACTCAGAGGATCCCTTTGCTGCTGCTGCTGCTG 1143
QY 1141 ACTTCATCCCAAAACCACTAATCACTCCCACTGACTGACCTCTGTGTATCAAAAGCC 1200
DB 1144 ACTTCATCCCAAAACCACTAATCACTCCCACTGACTGACCTCTGTGTATCAAAAGCC 1203
QY 1201 TCTCTGCGCTGAGGTTGGCTCTTAAGCTCATTTGCTGGGAAATGGGAAGAGAGAGTGGC 1260
DB 1204 TCTCTGCGCTGAGGTTGGCTCTTAAGCTCATTTGCTGGGAAATGGGAAGAGAGAGTGGC 1263
QY 1261 TTTTGTGGGCAATTTCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAAC 1320
DB 1264 TTTTGTGGGCAATTTCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAAC 1323
QY 1321 TGAACCTCATCTCACTCTTTGTTATGATCTCAAGTGTCAAGATTAATTTGTGATGAA 1380
DB 1324 TGAACCTCATCTCACTCTTTGTTATGATCTCAAGTGTCAAGATTAATTTGTGATGAA 1383
QY 1381 CTGAATTAATAACATCTTAAGGATTCAGAGGAAACAGAAACAGAGATGAGAGGAGGA 1440
DB 1384 CTGAATTAATAACATCTTAAGGATTCAGAGGAAACAGAAACAGAGATGAGAGGAGGA 1443
QY 1441 CAGGAAGCAGCTGGGACATTTAAAAAATA 1472
DB 1444 CAGGAAGCAGCTGGGACATTTAAAAAATA 1475
RESULT 8
AAF54296
ID AAF54296 standard; DNA; 1475 BP.

421 CATGATGACAGCTCTTCTGCGAGGATCCCGCAAGAGAGAGTGGCGGTAGCAGG 480
 424 CATGAGATGACAGCTCTTCTGCGAGGATCCCGCAAGAGAGAGTGGCGGTAGCAGG 483
 481 TGGAGTCTTTTATCTCTGAGGAGGCTCTGAGGATTCATCTCTGTTGCTGGAATCTCA 540
 484 TGGAGTCTTTTATCTCTGAGGAGGCTCTGAGGATTCATCTCTGTTGCTGGAATCTCA 543
 541 TGGAGTCTTACGAGGAGCTTCTACCACTGTGCTGAGAGCATGAAATTTGAGATTGG 600
 544 TGGAGTCTTACGAGGAGCTTCTACCACTGTGCTGAGAGCATGAAATTTGAGATTGG 603
 601 AGAGGCTCTTACTTGGGAGCATTAATTTCTTCTGTTCTCCCTGATAGCTGAATCACTCT 660
 604 AGAGGCTCTTACTTGGGAGCATTAATTTCTTCTGTTCTCCCTGATAGCTGAATCACTCT 663
 661 CTGCTTTCTGCTCATCCAGAGAAATGCTCCAACTACTAGATGCTTACCAAGCCCA 720
 664 CTGCTTTCTGCTCATCCAGAGAAATGCTCCAACTACTAGATGCTTACCAAGCCCA 723
 721 ACCTTTGCGACAGAGAGCTCTCCAGGCTGTGCACTCCCAAGTCAAGAGTGAATT 780
 724 ACCTTTGCGACAGAGAGCTCTCCAGGCTGTGCACTCCCAAGTCAAGAGTGAATT 783
 781 CAATTCCTACAGCTGACAGGGTATGTGTGAAGAACAGGGGCCAGAGCTGGGGGGTGGC 840
 784 CAATTCCTACAGCTGACAGGGTATGTGTGAAGAACAGGGGCCAGAGCTGGGGGGTGGC 843
 841 TGGGCTGTGAAACAGTGGAGACGACCCGAGGGGCGACAGGATGAGGAGCATCACTCACT 900
 844 TGGGCTGTGAAACAGTGGAGACGACCCGAGGGGCGACAGGATGAGGAGCATCACTCACT 903
 901 GGATCTGTGAGAGGTGTGCTGAGAGTATGACTGATTTGGCATTTGATGAGCAAG 960
 904 GGATCTGTGAGAGGTGTGCTGAGAGTATGACTGATTTGGCATTTGATGAGCAAG 963
 961 GCGAAATGGGGGCTAGTGAACAGCATGACAGGTTGAATTTGCCAAGATGCTGCCATGC 1020
 964 GCGAAATGGGGGCTAGTGAACAGCATGACAGGTTGAATTTGCCAAGATGCTGCCATGC 1023
 1021 CAGGCTTTGTTTCTCTCACTTGTGCTGCTCCCTGCGCTTAAGTCCCAAGCCCTCACTT 1080
 1024 CAGGCTTTGTTTCTCTCACTTGTGCTGCTCCCTGCGCTTAAGTCCCAAGCCCTCACTT 1083
 1081 GAAACCCCATTCCTTAAGCCAGAGCATCAGAGATCCCTTTGCTGTTTAACTGTGG 1140
 1084 GAAACCCCATTCCTTAAGCCAGAGCATCAGAGATCCCTTTGCTGTTTAACTGTGG 1143
 1141 ACTTCATCCCAAAACCACTAATCACTCCCACTGACTGACCTCTGTGATCAAAAGACC 1200
 1144 ACTTCATCCCAAAACCACTAATCACTCCCACTGACTGACCTCTGTGATCAAAAGACC 1203
 1201 TCTCTGAGGTAGTGGCTTCTAGCTCATGCTGTGGGAGTGGGAGAGAGAGTGGC 1260
 1204 TCTCTGAGGTAGTGGCTTCTAGCTCATGCTGTGGGAGTGGGAGAGAGAGTGGC 1263
 1261 TTTTGGGAGTGTCTTAACCTTCTCAAGGTTCCCTCAAAAGATGATTTGGCCC 1320
 1264 TTTTGGGAGTGTCTTAACCTTCTCAAGTGTCCCTCAAAAGATGATTTGGCCC 1323
 1321 TGGAACTCCATCCCACTCTTTGTTATGACTGCACAGTGTCCAGACTAATTTGTGCATGAA 1380
 1324 TGGAACTCCATCCCACTCTTTGTTATGACTGCACAGTGTCCAGACTAATTTGTGCATGAA 1383
 1381 CTGAATTAACAATCTCTAGGATCAAGGAGACAGAAACAGAGATGCAAGATGGAGGA 1440
 1384 CTGAATTAACAATCTCTAGGATCAAGGAGACAGAAACAGAGATGCAAGATGGAGGA 1443
 1441 CAGGAAGCAGCCCTGGAGCATTTTAAAAATA 1472
 1444 CAGGAAGCAGCCCTGGAGCATTTTAAAAATA 1475

RESULT 10
 AAS15360
 ID AAS15360 standard; cDNA; 1475 BP.
 XX
 AC AAS15360;
 XX
 DT 16-JAN-2002 (first entry)
 XX
 DE cDNA encoding human PRO1356 polypeptide.
 XX
 KW Human; PRO1356; clone DNA64886-1601; immune-related disorder;
 KW inflammatory disorder; infectious disorder; immunodeficiency disorder;
 KW autoimmune disorder; renal disease; demyelinating disease; skin disease;
 KW neoplasia; transplantation associated disease; gene therapy;
 KW immunosuppressive; anti-inflammatory; antidiabetic; ss.
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 122..814
 FT /tag= a
 FT /product= "PRO1356 polypeptide"
 FT sig_peptide 122..193
 FT /tag= b
 FT mat_peptide 194..811
 FT /tag= c
 XX
 PN MO20016740-A2.
 PD 13-SEP-2001.
 XX
 PE 01-MAR-2001; 2001MO-US006666.
 XX
 PR 03-MAR-2000; 2000US-0187202P.
 PR 21-MAR-2000; 2000US-0191015P.
 PR 30-MAY-2000; 2000MO-US014941.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 24-AUG-2000; 2000MO-US023328.
 PR 01-DEC-2000; 2000MO-US032678.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Etkon DL, Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
 PI Tuma D, Watanabe CK, Wood WI, Zhang Z;
 DR P-PSDB; AAU09178.
 DR WPI; 2001-625876/72.
 PT Nucleic acids encoding PRO polypeptides, useful for detecting and
 PT treating immune related diseases and disorders in mammals including
 PT autoimmune diseases, inflammatory diseases and asthma.
 XX
 PS Claim 2; Fig 1; 122bp; English.
 XX
 CC The present invention relates to the isolation of 9 novel human PRO
 CC polypeptides (AAU09178-AAU09186) and the cDNA sequences encoding them.
 CC The novel PRO polypeptides include PRO1356, PRO1268, PRO1884, PRO3444,
 CC PRO3151, PRO4322, PRO3964, PRO1008 and PRO19598. The cDNA sequences
 CC encoding these PRO polypeptides have been designated as clones DNA64886-
 CC 1601, DNA64903-1553, DNA64318-2520, DNA87997, DNA89273, DNA92223-2567,
 CC DNA96973, DNA101921 and DNA145867 respectively. Compositions (e.g.
 CC vaccines) containing PRO polypeptides and methods of using these
 CC compositions are useful in the treatment and diagnosis of immune-related
 CC disorders. Such disorders include immune-mediated inflammatory disorders (e.g.
 CC (e.g. osteoarthritis), non-immune-mediated inflammatory disorders (e.g.
 CC diabetes mellitus), infectious disorders (e.g. granulomatous hepatitis),
 CC immunodeficiency disorders (e.g. AIDS), autoimmune disorders (e.g.
 CC rheumatoid arthritis), immune-related renal diseases (e.g. cirrhosis),
 CC demyelinating diseases of the peripheral or central nervous system (e.g.
 CC Guillain-Barre syndrome), immune-mediated skin diseases (e.g. contact
 CC dermatitis), neoplasias and transplantation associated diseases. The
 CC polynucleotide sequences of the invention may be used in gene therapy.
 CC AAS15360-AAS15368 represent cDNA sequences encoding for the novel human

PRO polypeptides of the invention

CC Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

XX Query Match 53.7%; Score 1472; DB 4; Length 1475;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAGCTGGGAGAGAGCTGTAATGAGGGATTAGAGTGTTCAGAGAGAGAGA 60
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 4 AGAAGTCAGCTGGGAGAGAGAGCTGTAATGAGGGATTAGAGTGTTCAGAGAGAGAGA 63
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 61 GCTTCAGCTGGAAGACAAAGGAGAGAGCTCCCTGAAGAGCTTCTACTGAGAGAGTGGCAT 120
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 64 GCTTCAGCTGGAAGACAAAGGAGAGAGCTCCCTGAAGAGCTTCTACTGAGAGAGTGGCAT 123
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 121 GGCCTCTCTTGGGCTCCCACTTGTGGGCTACATCTAGGCTTCTGGGGCTTTTGGGAC 180
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 124 GGCCTCTCTTGGGCTCCCACTTGTGGGCTACATCTAGGCTTCTGGGGCTTTTGGGAC 183
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 181 ACTGTTTCCATGCTGCTCCCGAGTGGAAAACAAGTCTTATGTGGTGGCCAGCATTTT 240
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 184 ACTGTTTCCATGCTGCTCCCGAGTGGAAAACAAGTCTTATGTGGTGGCCAGCATTTT 243
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 241 GACAGCAGTTGGCTTCTCAAGGGCTCTGGAATGAATGTCACACACAGCAGAGCAT 300
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 244 GACAGCAGTTGGCTTCTCAAGGGCTCTGGAATGAATGTCACACACAGCAGAGCAT 303
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 301 CACCCAGTGTGACATCTATAGACACCTTCTGGGCTGGCCGCTGACATTCAGGCTGCCA 360
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 304 CACCCAGTGTGACATCTATAGACACCTTCTGGGCTGGCCGCTGACATTCAGGCTGCCA 363
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 361 GGCAGTATGTGATCAGATCCAGTGAATCTCTCCCTGGCTGGCATTAATCTGTGGTGG 420
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 364 GGCAGTATGTGATCAGATCCAGTGAATCTCTCCCTGGCTGGCATTAATCTGTGGTGG 423
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 421 CATGAGATGACAGTCTTCTGCCAGAAATCCGAGCCAGAACAGAGTGGCGGTAGAGAG 480
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 424 CATGAGATGACAGTCTTCTGCCAGAAATCCGAGCCAGAACAGAGTGGCGGTAGAGAG 483
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 481 TGGAGTCTTTTTCATCTTGGAGGCTCTGGGATTTGATTCCTGTGGCTGGAACTTTCA 540
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 484 TGGAGTCTTTTTCATCTTGGAGGCTCTGGGATTTGATTCCTGTGGCTGGAACTTTCA 543
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 541 TGGAGTCTTACGGGACTTCTACTACACATCTGTGTCCTGACAGCATGAATTTGAGATTG 600
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 544 TGGAGTCTTACGGGACTTCTACTACACATCTGTGTCCTGACAGCATGAATTTGAGATTG 603
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 601 AGAGGCTCTTACTTGGGCAATTAATTTCTCCCTGTCTCCCTGATAGCTGGAAATCATCT 660
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 604 AGAGGCTCTTACTTGGGCAATTAATTTCTCCCTGTCTCCCTGATAGCTGGAAATCATCT 663
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 661 CTGCTTTTCTGCTCATCTCCAGAGAAATCGCTCCAACTACTACAGTCCCTACCAAGCCA 720
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 664 CTGCTTTTCTGCTCATCTCCAGAGAAATCGCTCCAACTACTACAGTCCCTACCAAGCCA 723
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 721 ACTCTTTCACAAAGAGCTCTCCAGGCTGTGTCAACCTCCCAAAGTCAAGAGTGTG 780
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 724 ACTCTTTCACAAAGAGAGCTCTCCAGGCTGTGTCAACCTCCCAAAGTCAAGAGTGTG 783
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 781 CAATTCCTACAGCTGACAGGGTATGTGTGAAGAACAGAGGGGCGAGAGCTGGGGGGTGGC 840
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 784 CAATTCCTACAGCTGACAGGGTATGTGTGAAGAACAGAGGGGCGAGAGCTGGGGGGTGGC 843
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 841 TGGGCTGTGAAAAACAGTGGACAGACCCCGAGGGGCGACAGTGGAGGACATTCACACT 900
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 844 TGGGCTGTGAAAAACAGTGGACAGACCCCGAGGGGCGACAGTGGAGGACATTCACACT 903
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 901 GGATGTGTGAGAAAGTGTGTGCTGAGAGATAGACTCTTGGCCATTGGATTGACAAAG 960
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 904 GGATGTGTGAGAAAGTGTGTGCTGAGAGATAGACTCTTGGCCATTGGATTGACAAAG 963
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 961 GCAGAAATGGGGGCTAGTGTACAGCATGACAGTGAATGCCAAGAGATGCTGCCATGC 1020
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 964 GCAGAAATGGGGGCTAGTGTACAGCATGACAGTGAATGGCCAAAGATGCTGCCATGC 1023
 QY 1021 CAGCCTTCTGTTTCTTCTACAGCTTGTGCTCCCTGGCCCTTAAGTCCCAACCTCAACTT 1080
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1024 CAGCCTTCTGTTTCTTCTACAGCTTGTGCTCCCTGGCCCTTAAGTCCCAACCTCAACTT 1083
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1081 GAAACCCCATTCCTTAAAGCAGAGACTCAGAGAGATCCCTTGGCCCTGTGTTTACCTGGG 1140
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1084 GAAACCCCATTCCTTAAAGCAGAGACTCAGAGAGATCCCTTGGCCCTGTGTTTACCTGGG 1143
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1141 ACTCCATCCCAAAACCACTAATCAATCCCACTGACCTCTGTGTATCAAAAGACC 1200
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1144 ACTCCATCCCAAAACCACTAATCAATCCCACTGACCTCTGTGTATCAAAAGACC 1203
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1201 TCTCTGTGCTGAGTGTGCTCTTACCTAATGCTGTTGGGGAATGGGAAGAGACAGTGGC 1260
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1204 TCTCTGTGCTGAGTGTGCTCTTACCTAATGCTGTTGGGGAATGGGAAGAGACAGTGGC 1263
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1261 TTTTGTGGGCAATGCTCTAATCACTTCTCAAGCTTCCCTCCAAAGAACTGATTTGGCCC 1320
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1264 TTTTGTGGGCAATGCTCTAATCACTTCTCAAGCTTCCCTCCAAAGAACTGATTTGGCCC 1323
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1321 TGGAACTTCATCCACTCTTGTATGACTCCAGAGTTCAGAGTCACTTAATTTGTGATGA 1380
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1324 TGGAACTTCATCCACTCTTGTATGACTCCAGAGTTCAGAGTCACTTAATTTGTGATGA 1383
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1381 CTGAATTAATAACATCTTACAGGATATCCAGAGAAACAGAAAGCAGAGATGGAGGA 1440
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1384 CTGAATTAATAACATCTTACAGGATATCCAGAGAAACAGAAAGCAGAGATGGAGGA 1443
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1441 CAGAAAGCAGCTGGGACATTTAAAAAATA 1472
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1444 CAGAAAGCAGCTGGGACATTTAAAAAATA 1475
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 11
 AAF92097
 ID AAF92097 standard; cDNA; 1475 BP.
 XX
 AC AAF92097;
 XX
 DT 15-MAY-2001 (first entry)
 XX
 DE Human PRO1356 cDNA.
 XX
 KW Human; PRO protein; mapping; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200116318-A2.
 XX
 XX 08-MAR-2001.
 PF 24-AUG-2000; 2000MO-US023328.
 XX
 PR 01-SEP-1999; 99MO-US020111.
 PR 15-SEP-1999; 99MO-US021090.
 PR 07-DEC-1999; 99US-0169495P.
 PR 09-DEC-1999; 99US-0170262P.
 PR 11-JAN-2000; 2000US-0175481P.
 PR 18-FEB-2000; 2000MO-US004341.
 PR 18-FEB-2000; 2000MO-US004342.
 PR 22-FEB-2000; 2000MO-US004414.
 PR 01-MAR-2000; 2000MO-US005601.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 30-MAR-2000; 2000MO-US008439.
 PR 25-APR-2000; 2000US-0199397P.
 PR 22-MAY-2000; 2000MO-US014042.
 PR 05-JUN-2000; 2000US-0209832P.
 XX
 PA (GETH) GENENTECH INC.

QY 1 AGAAGTCAAGCTGGCAGAGAGACTCTGAATAGAGGATTAAGGTCTTCAAGAGCAGA 60
DB 4 AGAAGTCAAGCTGGCAGAGAGACTCTGAATAGAGGATTAAGGTCTTCAAGAGCAGA 63
QY 61 GCTTCAGCTGGAAGACAGAGGAGAGTCCCTGAAGAGCTTCTA CTGAGAGGTGCGCAT 120
DB 64 GCTTCAGCTGGAAGACAGAGGAGAGTCCCTGAAGAGCTTCTA CTGAGAGGTGCGCAT 123
QY 121 GGCCTCTCTTGGCTTCGAACCTTGTGGGCTACATCTAGGCTTGTGGGGCTTTTGGGCAC 180
DB 124 GGCCTCTCTTGGCTTCGAACCTTGTGGGCTACATCTAGGCTTGTGGGGCTTTTGGGCAC 183
QY 181 ACTGTTGGCCATGCTGCTCCCGACACTGGAACAAAGTTCTTAATGTCCGTGCGACATTTGT 240
DB 184 ACTGTTGGCCATGCTGCTCCCGACACTGGAACAAAGTTCTTAATGTCCGTGCGACATTTGT 243
QY 241 GACAGCAGTTGGCTTCTCCAAAGGGCTCTGGAATGGAATGTGSCACACACAGCAGAGCAT 300
DB 244 GACAGCAGTTGGCTTCTCCAAAGGGCTCTGGAATGGAATGTGSCACACACAGCAGAGCAT 303
QY 301 CACCCAGTGTGACATCTTAAGCACCCTTCTGGGCTGCGCTGACATCCAGGCTGCGCA 360
DB 304 CACCCAGTGTGACATCTTAAGCACCCTTCTGGGCTGCGCTGACATCCAGGCTGCGCA 363
QY 361 GGCCTATATGTGACATCTCAAGTGAATCTCTCCCTGCGCTGCAATTAATCTGTGTGGG 420
DB 364 GGCCTATATGTGACATCTCAAGTGAATCTCTCCCTGCGCTGCAATTAATCTGTGTGGG 423
QY 421 CATGAGATGACAGTCTTCTGCGCAGGAATCCCGAGCCAAAGACAGATGGCGGTAGCAGG 480
DB 424 CATGAGATGACAGTCTTCTGCGCAGGAATCCCGAGCCAAAGACAGATGGCGGTAGCAGG 483
QY 481 TGAAGTCTTTTTCATCTTGGAGGCTCTGGAATTCATTCCTGTGCTGGAATCTTCA 540
DB 484 TGAAGTCTTTTTCATCTTGGAGGCTCTGGAATTCATTCCTGTGCTGGAATCTTCA 543
QY 541 TGGGATCTTAAGGGAATCTTAACCACTGTGTGCTGAGACAGCATGAATTTGAGATTGG 600
DB 544 TGGGATCTTAAGGGAATCTTAACCACTGTGTGCTGAGACAGCATGAATTTGAGATTGG 603
QY 601 AGAGGCTCTTTAATCTTGGGCAATTAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 604 AGAGGCTCTTTAATCTTGGGCAATTAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
QY 661 CTGCTTCTCTGCTCATCCAGAGAAATGCTCCCACTACGATGCTTACCAAGCCCA 720
DB 664 CTGCTTCTCTGCTCATCCAGAGAAATGCTCCCACTACGATGCTTACCAAGCCCA 723
QY 721 ACCTCTTGGCAAGAGGCTTCTCAAGGCTGTCAACCTTCCCAAATCAAGAGTGAATT 780
DB 724 ACCTCTTGGCAAGAGGCTTCTCAAGGCTGTCAACCTTCCCAAATCAAGAGTGAATT 783
QY 781 CAATTCCTACAGGCTGACAGGCTATGTGTGAAGAACAGAGGGCCAGAGCTGGGGGGTGGC 840
DB 784 CAATTCCTACAGGCTGACAGGCTATGTGTGAAGAACAGAGGGCCAGAGCTGGGGGGTGGC 843
QY 841 TGGGCTCTGTAAAAACAGTGAACAGCACCAGAGGGCCAGAGGTGAAGGCACTACCACT 900
DB 844 TGGGCTCTGTAAAAACAGTGAACAGCACCAGAGGGCCAGAGGTGAAGGCACTACCACT 903
QY 901 GGAATCTGTGACAAAGGCTGTGCTGAGATTAAGTGAATTTGGCCATTGGAATTGACAAAG 960
DB 904 GGAATCTGTGACAAAGGCTGTGCTGAGATTAAGTGAATTTGGCCATTGGAATTGACAAAG 963
QY 961 GCAAAATGGGGGGGTAGTGTAAAGCATGACATGAGGTGAATTTGCCAAGGATGCTGGCAATG 1020
DB 964 GCAAAATGGGGGGGTAGTGTAAAGCATGACATGAGGTGAATTTGCCAAGGATGCTGGCAATG 1023
QY 1021 CAGCCTTCTGTCTTCTCACTTGTGCTGCTCCCTGCTGAAGTCCCAACCTTCACTT 1080
DB 1024 CAGCCTTCTGTCTTCTCACTTGTGCTGCTCCCTGCTGAAGTCCCAACCTTCACTT 1083
QY 1081 GAAACCCCATTCCTTAAGCAGAGACTCAAGAGATCCCTTGTGCTGCTTAACTGAGG 1140

DB 1084 GAAACCCCATTCCTTAAGCAGAGACTCAAGAGATCCCTTGTGCTGCTTAACTGAGG 1143
QY 1141 ACTTCATCCCCAAACCACTAATCAATCCCACTGA CTGACCTCTGTGATCAAGACCC 1200
DB 1144 ACTTCATCCCCAAACCACTAATCAATCCCACTGA CTGACCTCTGTGATCAAGACCC 1203
QY 1201 TCTCTGCTGAGTGGTGGCTCTTAAGTCAATGCTGCGGAGTGGAGAGAGACAGTGGC 1260
DB 1204 TCTCTGCTGAGTGGTGGCTCTTAAGTCAATGCTGCGGAGTGGAGAGAGACAGTGGC 1263
QY 1261 TTTTGGGGGATGTGCTTAACCTTCAACTTCCCTCCAAAGAACTGATTTGGCCC 1320
DB 1264 TTTTGGGGGATGTGCTTAACCTTCAACTTCCCTCCAAAGAACTGATTTGGCCC 1323
QY 1321 TGAACCTCATCCCACTCTTTTATGACTCAAGTGTCAAGTCACTAATTTGCAATGA 1380
DB 1324 TGAACCTCATCCCACTCTTTTATGACTCAAGTGTCAAGTCACTAATTTGCAATGA 1383
QY 1381 CTGAATTAATAACCATCTTACGATATCCAGGGAACAGAAACAGAGATGAGAGGA 1440
DB 1384 CTGAATTAATAACCATCTTACGATATCCAGGGAACAGAAACAGAGATGAGAGGA 1443
QY 1441 CAGGAAGCAGCTGGGACATTTAAAAATA 1472
DB 1444 CAGGAAGCAGCTGGGACATTTAAAAATA 1475

RESULT 13
ABI8167
ID ABI8167 standard; cDNA; 1475 BP.
XX
AC ABI8167;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO1356 cDNA sequence SEQ ID NO:191.
XX
XX Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;
XX vulnereary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;
XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
XX age-related macular degeneration; arterial restenosis; angina;
XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;
XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
XX wound healing; chromosome mapping; gene mapping; gene; ss.
OS Homo sapiens.
XX
XX WO20020690-A2.
XX
PD 03-JAN-2002.
XX
PF 20-JUN-2001; 2001MO-US019692.
XX
XX 23-JUN-2000; 2000US-0213637P.
XX 20-JUL-2000; 2000US-021956P.
XX 25-JUL-2000; 2000US-0220624P.
XX 25-JUL-2000; 2000US-0220664P.
XX 28-JUL-2000; 2000MO-US020710.
XX 02-AUG-2000; 2000US-022895P.
XX 17-AUG-2000; 2000US-00643657.
XX 23-AUG-2000; 2000MO-US023522.
XX 24-AUG-2000; 2000MO-US023328.
XX 07-SEP-2000; 2000US-0230978P.
XX 18-SEP-2000; 2000US-00664610.
XX 18-SEP-2000; 2000US-00665350.
XX 24-OCT-2000; 2000US-0242922P.
XX 08-NOV-2000; 2000US-00709238.
XX 08-NOV-2000; 2000MO-US030952.
XX 10-NOV-2000; 2000MO-US030873.
XX 01-DEC-2000; 2000MO-US032678.
XX 20-DEC-2000; 2000US-00747259.

QY 1381 CTGAAATTAACCATCTCTACGATTCAGGAAACAGAAACAGATGCGAGGA 1440
 DB 1384 CTGAAATTAACCATCTCTACGATTCAGGAAACAGAAACAGATGCGAGGA 1443
 QY 1441 CAGGAAGCGACCTGGACATTTTAAAAATA 1472
 DB 1444 CAGGAAGCGACCTGGACATTTTAAAAATA 1475

RESULT 14
 ABK1089
 ID ABK1089 standard; cDNA; 1475 BP.
 AC ABK1089;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE cDNA encoding tumour-associated antigenic target protein, TAT134.
 XX
 KW TAT134; Tumour-associated Antigenic Target; tumour; breast cancer;
 KW colorectal cancer; lung cancer; ovarian cancer;
 KW central nervous system cancer; liver cancer; bladder cancer; melanoma;
 KW pancreatic cancer; leukaemia; gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 122..814
 FT /tag= a
 FT /product= "TAT134"
 FT /note= "Tumour-associated antigenic target"
 XX
 PN MO200216429-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 22-JUN-2001; 2001WO-US020118.
 XX
 PR 24-AUG-2000; 2000WO-US023328.
 PR 26-SEP-2000; 2000US-0235451P.
 PR 01-DEC-2000; 2000WO-US032578.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Goddard A, Goddard PJ, Gurney AL, Hillan KJ, Polakis P, Smith V,
 PI Wood WI, Wu TD, Zhang Z;
 DR P-PSDB; AAU76534.
 DR WPI; 2002-280917/32.
 XX
 PT Novel isolated tumor-associated antigenic target polypeptides which are
 PT useful as targets for cancer therapy and diagnosis in mammals.
 XX
 PS Claim 1; Fig 1; 121bp; English.
 XX

CC generating either transgenic animals or knockout animals, and in gene
 CC therapy. The TAT polypeptides and nucleic acids may also be used for
 CC tissue typing and the TAT polypeptides are useful for screening compounds
 CC that mimic the TAT polypeptide (agonist) or prevent the effect of TAT
 CC polypeptide (antagonist). The antibody is useful for staging TAT
 CC polypeptide-expressing cancers, purifying or immunoprecipitating TAT
 CC polypeptide from cells, for detection and quantitation of TAT polypeptide
 CC in vitro, e.g., in an enzyme linked immunosorbent assay (ELISA) or
 CC Western blot. The antibodies are also useful for treating a cancer in a
 CC expressing cancer or alleviating one or more symptoms of cancer in a
 CC mammal. The present sequence represents the coding sequence of TAT134
 CC
 XX
 SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
 Query Match 53.7%; Score 1472; DB 6; Length 1475;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAGCTTGGCAGAGAGATCTGAAATGAGGATTTAGAGTTCAGAGAGAGA 60
 DB 4 AGAAGTCAGCTTGGCAGAGAGATCTGAAATGAGGATTTAGAGTTCAGAGAGAGA 63
 QY 61 GCTTCAGCTGAAAG 120
 DB 64 GCTTCAGCTGAAAG 123
 QY 121 GGCCTCTCTTGGCCTTCAACTTGTGGGCTACATCTAGGCTTCTTGGGCTTGGGCA 180
 DB 124 GGCCTCTTGGCCTTCAACTTGTGGGCTACATCTAGGCTTCTTGGGCTTGGGCA 183
 QY 181 ACTGTTGCCATGCTGCTGCCAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 DB 184 ACTGTTGCCATGCTGCTGCCAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
 QY 241 GACAGAGATGCTTCTTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 DB 244 GACAGAGATGCTTCTTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 303
 QY 301 CACCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 DB 304 CACCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 363
 QY 361 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 364 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 423
 QY 421 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 DB 424 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 483
 QY 481 TGAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 540
 DB 484 TGAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 543
 QY 541 TGGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 600
 DB 544 TGGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 603
 QY 601 AGAGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 660
 DB 604 AGAGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 663
 QY 661 CTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 720
 DB 664 CTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 723
 QY 721 ACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 780
 DB 724 ACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 783
 QY 781 CAATTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 840
 DB 784 CAATTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 843

QY 841 TGGGCTGTGAAAAAGTGGAGACAGACCCGAGGGCCACAGGTGAGGACACTACCACT 900
DB 844 TGGGCTGTGAAAAAGTGGAGACAGACCCGAGGGCCACAGGTGAGGACACTACCACT 903
QY 901 GGATCGGTGAGAAAGTGTGCTGAGGAGTAACTGACTTTGGCCATTGGATTGAGCAAG 960
DB 904 GGATCGGTGAGAAAGTGTGCTGAGGAGTAACTGACTTTGGCCATTGGATTGAGCAAG 963
QY 961 GCAGAAATGGGGGCTAGTGTAAACAGCATGCAAGTTGAATTGCCAAGATCTGCCCATGC 1020
DB 964 GCAGAAATGGGGGCTAGTGTAAACAGCATGCAAGTTGAATTGCCAAGATCTGCCCATGC 1023
QY 1021 CAGGCTTTCTGTTTTCTCACTGTGCTGCTCCCTGCGCCTTAAGTCCCAACCTCACTT 1080
DB 1024 CAGGCTTTCTGTTTTCTCACTGTGCTGCTCCCTGCGCCTTAAGTCCCAACCTCACTT 1083
QY 1081 GAAACCCCATTCCTTAAAGCAGAGACTCAGAGATCCCTTGGCTGTGTTAACTGGG 1140
DB 1084 GAAACCCCATTCCTTAAAGCAGAGACTCAGAGATCCCTTGGCTGTGTTAACTGGG 1143
QY 1141 ACTTCATCCCAAAACCACTAATCAATCCCACTGACTGACCTCTGTGATCAAAAGCCC 1200
DB 1144 ACTTCATCCCAAAACCACTAATCAATCCCACTGACTGACCTCTGTGATCAAAAGCCC 1203
QY 1201 TCTCTGCGGCTGAGGTGGGCTTAAAGCTCAATGCTGAGGAGTGGGAGAGAGAGAGTGGC 1260
DB 1204 TCTCTGCGGCTGAGGTGGGCTTAAAGCTCAATGCTGAGGAGTGGGAGAGAGAGTGGC 1263
QY 1261 TTTTGTGGGCTGCTTAACTAATCTCAAGCTTCCCTCAAAAGAACTGATTGGCCC 1320
DB 1264 TTTTGTGGGCTGCTTAACTAATCTCAAGCTTCCCTCAAAAGAACTGATTGGCCC 1323
QY 1321 TGGAACTCCATCCCACTCTTTGTTATGACTGTCACAGTGTCCAGACTAATTTGTCATGAA 1380
DB 1324 TGGAACTCCATCCCACTCTTTGTTATGACTGTCACAGTGTCCAGACTAATTTGTCATGAA 1383
QY 1381 CTGAAATTAATAACCACTCTAGCGTATCCAGGGAAGAGAGAGATCCAGATGGGAGGA 1440
DB 1384 CTGAAATTAATAACCACTCTAGCGTATCCAGGGAAGAGAGATCCAGATGGGAGGA 1443
QY 1441 CAGGAAGCAGCCTGGAGCAATTTAAAAAATA 1472
DB 1444 CAGGAAGCAGCCTGGAGCAATTTAAAAAATA 1475

RESULT 15
ABL95656 standard; cDNA; 1475 BP.

AC ABL95656;
DT 19-JUL-2002 (first entry)
DE Human angiogenesis related cDNA PRO1356 SEQ ID NO: 191.
XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KM atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KM cardiac; cytosolic; antiangiogenic; hypotensive; vulnary;
XX antiarteriosclerotic; gene; ss.
OS Homo sapiens.
XX WO200208284-A2.
PN 31-JAN-2002.
XX 09-JUL-2001; 2001WO-US021735.
XX 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220644P.
PR 28-JUL-2000; 2000WO-US020710.

PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-0064610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US065520.
PR 01-MAR-2001; 2001WO-US066666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00806889.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00834208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
XX (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERE/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODDARD P J.
PA (GORN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANU/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J P.
PA (WATA/) WATAMBE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A, Paoni NF, Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF, Stephan JF, Watamabe CK, Williams PM, Wood WI, Ye W.
XX WPI; 2002-171999/22.
XX P-PSDB; ABB95518.
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
XX Claim 1; Fig 191; 567pp; English.
XX The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention
XX Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

Query Match 53.78; Score 1472; DB 6; Length 1475;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTACGCTGGCAGAGAGACTCTGAATAGAGGATTAGAGGTGTTCAAGAGGAGAGA 60
DB 4 AGAAGTACGCTGGCAGAGAGACTCTGAATAGAGGATTAGAGGTGTTCAAGAGGAGAGA 63
QY 61 GCTTACGCTGGAAGACAAGGAGAGTCCCTGAAGAGCTTCTACTAGAGGTGTCAT 120
DB 64 GCTTACGCTGGAAGACAAGGAGAGTCCCTGAAGAGCTTCTACTAGAGGTGTCAT 123
QY 121 GGCCTCTCTTGGCCTCCAACTTGTGGGCTACATCTAGGCTCTTGAGGCTTTTGGGAC 180
DB 124 GGCCTCTCTTGGCCTCCAACTTGTGGGCTACATCTAGGCTCTTGAGGCTTTTGGGAC 183
QY 181 ACTGTTGGCCATGCTGTCTCCCACTGCTGGAAGGAAAGGTTCTTAATGCTGGTCCAGCAT 240
DB 184 ACTGTTGGCCATGCTGTCTCCCACTGCTGGAAGGAAAGGTTCTTAATGCTGGTCCAGCAT 243
QY 241 GACAGCAGTTGGCTTCTCAAGAGGCTCTGGATGGAATGTCACACACAGCAGGAGAT 300
DB 244 GACAGCAGTTGGCTTCTCAAGAGGCTCTGGATGGAATGTCACACACAGCAGGAGAT 303
QY 301 CACCCAGTGTGACATCTAATAGACCTTCTGGGCTGCGCCGTGACATCCAGGCTGCCA 360
DB 304 CACCCAGTGTGACATCTAATAGACCTTCTGGGCTGCGCCGTGACATCCAGGCTGCCA 363
QY 361 GGCCTATATGTGATCTCCAGTGAATCTCTCCCTGGGCTGATCTTCTGTGGTGGG 420
DB 364 GGCCTATATGTGATCTCCAGTGAATCTCTCCCTGGGCTGATCTTCTGTGGTGGG 423
QY 421 CATGAGATGACAGTCTTCTGCCAGAAATCCGAGCCAAAGACAGATGGCGGTAGAGG 480
DB 424 CATGAGATGACAGTCTTCTGCCAGAAATCCGAGCCAAAGACAGATGGCGGTAGAGG 483
QY 481 TGAAGTCTTTTTCATCTCTGAGAGGCTCTGAGATTCATCTGTTGCTTGAATCTTCA 540
DB 484 TGAAGTCTTTTTCATCTCTGAGAGGCTCTGAGATTCATCTGTTGCTTGAATCTTCA 543
QY 541 TGGGATCTTACGGGACTTCTTACTACCACTGTGTGCTGACAGCATGAAATTTGAGATTGG 600
DB 544 TGGGATCTTACGGGACTTCTTACTACCACTGTGTGCTGACAGCATGAAATTTGAGATTGG 603
QY 601 AGAGGCTCTTTAATCTTGGGCAATTAATTTCTCCCTGTTCTCCCTGATAGCTGGAATCATCT 660
DB 604 AGAGGCTCTTTAATCTTGGGCAATTAATTTCTCCCTGTTCTCCCTGATAGCTGGAATCATCT 663
QY 661 CTGCTTTCTGCTCATCTCCAGAGAAATCGCTCCAACTACTAGATGCTTACCAAGCCCA 720
DB 664 CTGCTTTCTGCTCATCTCCAGAGAAATCGCTCCAACTACTAGATGCTTACCAAGCCCA 723
QY 721 ACTCTTGGCAAGAGAGCTCTCAAGGCTGTGCAACTTCCAAAGTCAAGATGAGTT 780
DB 724 ACTCTTGGCAAGAGAGCTCTCAAGGCTGTGCAACTTCCAAAGTCAAGATGAGTT 783
QY 781 CAATTCCTACAGCTGACAGGGTATGTGTGAAGAACAGGGGGCCAGAGCTGGGGGGTGGC 840
DB 784 CAATTCCTACAGCTGACAGGGTATGTGTGAAGAACAGGGGGCCAGAGCTGGGGGGTGGC 843
QY 841 TGGGTCGTGAAAAAAGTGAAGACACCCGAGGGCCACAGGTGAGGGAACATCACT 900
DB 844 TGGGTCGTGAAAAAAGTGAAGACACCCGAGGGCCACAGGTGAGGGAACATCACT 903
QY 901 GGAATCGTCAAGAGGCTGTGAGATGACTTGGCCATTGGATTGAGCAAG 960
DB 904 GGAATCGTCAAGAGGCTGTGAGATGACTTGGCCATTGGATTGAGCAAG 963
QY 961 GCAGAAATGGGGGCTAGTGTACAGCATGACGTTGAATTGCCAAGGATGCTGCCATGC 1020
DB 964 GCAGAAATGGGGGCTAGTGTACAGCATGACGTTGAATTGCCAAGGATGCTGCCATGC 1023
QY 1021 CAGCCTTCTGTCTTCTCACTTGTGCTGCCCTGCTTAAGTCCCAACCTCACTT 1080

DB 1024 CAGCCTTCTGTCTTCTCACTTGTGCTGCCCTGCTTAAGTCCCAACCTCACTT 1083
QY 1081 GAAACCCATTCCTTAAAGCAGAGACTCAGAGGATCCCTTGGCCCTGTGATTACCTGGG 1140
DB 1084 GAAACCCATTCCTTAAAGCAGAGACTCAGAGGATCCCTTGGCCCTGTGATTACCTGGG 1143
QY 1141 ACTCATCCCAACCCCACTAATCATCCCACTGACCTGCTGTGATCAAGAACCC 1200
DB 1144 ACTCATCCCAACCCCACTAATCATCCCACTGACCTGCTGTGATCAAGAACCC 1203
QY 1201 TCTCTGTGAGTGTGGCTCTTAAGCTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCC 1260
DB 1204 TCTCTGTGAGTGTGGCTCTTAAGCTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCC 1263
QY 1261 TTTTGTGGGATGTCTTAAGCTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCC 1320
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QY 1321 TGGAACTTCATCCCACTCTTGTATGACTCCACAGTGTCCAGACTTAATTTGTGATGAA 1380
DB 1324 TGGAACTTCATCCCACTCTTGTATGACTCCACAGTGTCCAGACTTAATTTGTGATGAA 1383
QY 1381 CTGAATTAAGCACTCTTACGTTATCCAGGAAACAGAAAGCAGATGCAAGATGGAGGA 1440
DB 1384 CTGAATTAAGCACTCTTACGTTATCCAGGAAACAGAAAGCAGATGCAAGATGGAGGA 1443
QY 1441 CAGAAAGCAGCCTGGGACATTTTAAAAATA 1472
DB 1444 CAGAAAGCAGCCTGGGACATTTTAAAAATA 1475

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Job time : 1851 secs

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OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 15:35:31 ; Search time 293 Seconds
(without alignments)
6651.820 Million cell updates/sec

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Perfect score: 2742
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Scoring table: OLIGO_NNC
Gapop 60.0 , Gapext 60.0

Searched: 824507 seqs, 355394441 residues

Word size : 20

Total number of hits satisfying chosen parameters: 9

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
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6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1472	53.7	1475	US-10-140-002-491	Sequence 491, App
2	1291	47.1	1400	US-09-663-600A-139	Sequence 139, App
3	896	32.7	1524	US-09-663-600A-45	Sequence 45, App1
4	20	0.7	1485	US-09-113-000C-1944	Sequence 1944, App
5	20	0.7	13930	US-09-976-594-1011	Sequence 1011, App
6	20	0.7	13933	US-09-220-132-20	Sequence 20, App1
7	20	0.7	14070	US-09-108-006C-2	Sequence 2, App1
8	20	0.7	1664976	US-08-916-421B-1	Sequence 1, App1
9	20	0.7	1664976	US-09-692-570-1	Sequence 1, App1

ALIGNMENTS

RESULT 1
US-10-140-002-491
Sequence 491, Application US/10140002
Patent No. 6725730
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OR INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C59
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 491
LENGTH: 1475
TYPE: DNA
ORGANISM: Homo Sapien
US-10-140-002-491

Query Match 53.7%; Score 1472; DB 4; Length 1475;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 AGAAGTCAGCCTGCAGAGAGACTTGAATAGAGATTAGAGTGTTCAGAGAGAGA 60
4 AGAAGTCAGCCTGCAGAGAGACTTGAATAGAGATTAGAGTGTTCAGAGAGAGA 63
61 GCTTACAGCCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
64 GTTTCAGCCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
121 GGCCTCTTCTGCTTCCCAATTTTGGGCTTCAATCCCTAGAGAGAGAGAGAG 180
124 GGCCTCTTCTGCTTCCCAATTTTGGGCTTCAATCCCTAGAGAGAGAGAGAG 183
181 ACTGTTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
184 ACTGTTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 243
241 GACAGCAGTGGCTTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
244 GACAGCAGTGGCTTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 303
301 CACCCAGTGTGATCTATATGACACCTTCTGAGAGAGAGAGAGAGAGAGAG 360
304 CACCCAGTGTGATCTATATGACACCTTCTGAGAGAGAGAGAGAGAGAGAG 363
361 GGCAGTGTGATCTATATGACACCTTCTGAGAGAGAGAGAGAGAGAGAG 420
364 GGCAGTGTGATCTATATGACACCTTCTGAGAGAGAGAGAGAGAGAGAG 423
421 CATTGATGACAGTCTTCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
424 CATTGATGACAGTCTTCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 483
481 TGAAGCTTTTTCATCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
484 TGAAGCTTTTTCATCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543
541 TGAAGCTTTTTCATCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
544 TGAAGCTTTTTCATCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 603
601 AGAGGCTTTTTCATCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
604 AGAGGCTTTTTCATCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 663
661 CTGCTTTTCTGCTCATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
664 CTGCTTTTCTGCTCATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 723

QY 721 ACCTCTTGCACAGAGCTCTCCAGAGCCCTGTCACCTTCCCAAGTCAAGAGTGT 780
DB 724 ACCTCTTGCACAGAGCTCTCCAGAGCCCTGTCACCTTCCCAAGTCAAGAGTGT 783
QY 781 CAATCTCTACAGCTGACAGGCTATGTGTGAAGAACAGAGGCGCAGAGCTGGGGGGTGGC 840
DB 784 CAATCTCTACAGCTGACAGGCTATGTGTGAAGAACAGAGGCGCAGAGCTGGGGGGTGGC 843
QY 841 TGGGCTGTGAAAAAGTGGACAGACCCCGAGGGCCACAGTGAAGGACATCACTACT 900
DB 844 TGGGCTGTGAAAAAGTGGACAGACCCCGAGGGCCACAGTGAAGGACATCACTACT 903
QY 901 GATCTGTGCAAGAGCTGCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 960
DB 904 GATCTGTGCAAGAGCTGCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 963
QY 961 GCAGAAATGGGGGCTAGTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1020
DB 964 GCAGAAATGGGGGCTAGTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1023
QY 1021 CAGCCTTCTGTTTCTGCTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1024 CAGCCTTCTGTTTCTGCTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083
QY 1081 GAAACCCCATTCCTTAAGCCAGAGCTCAAGAGTCCCTTGGCTTGAAGTCTGAG 1140
DB 1084 GAAACCCCATTCCTTAAGCCAGAGCTCAAGAGTCCCTTGGCTTGAAGTCTGAG 1143
QY 1141 ACTTCATCCCAACCCCACTATCAATCCCACTGACAGTCAAGTCAAGTCAAGTCAAG 1200
DB 1144 ACTTCATCCCAACCCCACTATCAATCCCACTGACAGTCAAGTCAAGTCAAGTCAAG 1203
QY 1201 TCTCTGAGCTGAGTGGCTCTTGAAGTCAATGCTGAGGAGTGAAGAGAGAGAGTGGC 1260
DB 1204 TCTCTGAGCTGAGTGGCTCTTGAAGTCAATGCTGAGGAGTGAAGAGAGAGAGTGGC 1263
QY 1261 TTTTGTGGGAGTTGCTTAACCTTCTCAAGCTTCCCTCAAGAACTGATTTGGCCC 1320
DB 1264 TTTTGTGGGAGTTGCTTAACCTTCTCAAGCTTCCCTCAAGAACTGATTTGGCCC 1323
QY 1321 TGGAACTCCATCCCATCTCTTGTATGATCCAGAGTCCAGAGTCAATTTTGGCAGAA 1380
DB 1324 TGGAACTCCATCCCATCTCTTGTATGATCCAGAGTCCAGAGTCAATTTTGGCAGAA 1383
QY 1381 CTGAATAAATAACATCTTACAGGATCCAGAGAGAGAGAGAGATGAGATGAGAGAG 1440
DB 1384 CTGAATAAATAACATCTTACAGGATCCAGAGAGAGAGAGAGATGAGATGAGAGAG 1443
QY 1441 CAGGAGGAGAGCTTGAAGATTTAAAAATA 1472
DB 1444 CAGGAGGAGAGCTTGAAGATTTAAAAATA 1475

RESULT 2
US-09-663-600A-139
Sequence 139, Application US/09663600A
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31.US3.CIP
CURRENT APPLICATION NUMBER: US/09/663,600A
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121

QY 84 CAATCTCTGAGAGCTTCTTCACTGAGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 143
DB 1 CAATCTCTGAGAGCTTCTTCACTGAGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
QY 144 TGGGCTACATCTCAGAGCTCTTGGGCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 203
DB 61 TGGGCTACATCTCAGAGCTCTTGGGCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 204 GCTGAGAAACAGATTCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 263
DB 121 GCTGAGAAACAGATTCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 264 GCTCTGAGATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 323
DB 181 GCTCTGAGATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 324 CCGTCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 383
DB 241 CCGTCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 384 CAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 443
DB 301 CAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 444 AGGAATCCGAGGCAAG 503
DB 361 AGGAATCCGAGGCAAG 420
QY 504 GCTCTGAGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 563
DB 421 GCTCTGAGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 564 CACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 623
DB 481 CACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 624 TTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 683
DB 541 TTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 684 GAATGCTCTCACTACTAGATGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 743
DB 601 GAATGCTCTCACTACTAGATGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660

Query Match 47.1%; Score 1291; DB 4; Length 1400;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1391; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 744 CAAGCCCTGGTCAACCTCCCAAGTGAAGTGAATTCAATTCTTCAAGCCTGAACAGGGT 803
DB 661 CAAGCCCTGGTCAACCTCCCAAGTGAAGTGAATTCAATTCTTCAAGCCTGAACAGGGT 720
QY 804 ATGTGTGAAGAACAAGGGGCGCAAGCTGGGGGGTGGCTGGTGGTCTGTGTAAACAGTGGAC 863
DB 721 ATGTGTGAAGAACAAGGGGCGCAAGCTGGGGGGTGGCTGGTGGTCTGTGTAAACAGTGGAC 780
QY 864 AGCAGCCCGAGGGGCGCAAGTGAAGGACACTACCACTGATGATGCTGATGAGAGGGTGGCT 923
DB 781 AGCAGCCCGAGGGGCGCAAGTGAAGGACACTACCACTGATGATGCTGATGAGAGGGTGGCT 840
QY 924 GAGGATGAGTCACTTTGGCCATTGATGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 983
DB 841 GAGGATGAGTCACTTTGGCCATTGATGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 900
QY 984 AGCATGCAAGTGAATTGGCCAGAGATGCTGCCATGCCAGCTTTCTGTTTCTTCACT 1043
DB 901 AGCATGCAAGTGAATTGGCCAGAGATGCTGCCATGCCAGCTTTCTGTTTCTTCACT 960
QY 1044 TGCTGCTCCCTGGCCCTAAGTGGCCCAACCCCTCACTTGAACCCCATTTCCCTTAAGCAG 1103
DB 961 TGCTGCTCCCTGGCCCTAAGTGGCCCAACCCCTCACTTGAACCCCATTTCCCTTAAGCAG 1020
QY 1104 GACTCAGAGATCCCTTTGCTGCTGTTTACCTGGGACTCCATCCCAACCCCACTAT 1163
DB 1021 GACTCAGAGATCCCTTTGCTGCTGTTTACCTGGGACTCCATCCCAACCCCACTAT 1080
QY 1164 CACATCCCACTGACTGACCTCTGTGATCAAGAACCTCTCTGCTGAGTGGCTCT 1223
DB 1081 CACATCCCACTGACTGACCTCTGTGATCAAGAACCTCTCTGCTGAGTGGCTCT 1140
QY 1224 TAGCTCATTTGCTGGGATGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1283
DB 1141 TAGCTCATTTGCTGGGATGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY 1284 ACTTCTCAAGCTTCCCTCCCAAGAACTGATTGGCCCTGAGAACCTCCATCCCACTTGT 1343
DB 1201 ACTTCTCAAGCTTCCCTCCCAAGAACTGATTGGCCCTGAGAACCTCCATCCCACTTGT 1260
QY 1344 TATGACTCCACAGTGTCCAGACTAATTGTCATGAACTGAAATTAACCATCTTACGGT 1403
DB 1261 TATGACTCCACAGTGTCCAGACTAATTGTCATGAACTGAAATTAACCATCTTACGGT 1320
QY 1404 ATCCAGGAGACAGAAAGAGATGAGATGGAGAGACAGAAAGGACGCTGGGACATTT 1463
DB 1321 ATCCAGGAGACAGAAAGAGATGAGATGGAGAGACAGAAAGGACGCTGGGACATTT 1380
QY 1464 AAAAAAATTAATA 1476
DB 1381 AAAAAAATTAATA 1393

RESULT 3
US-09-663-600A-45
; Sequence 45, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueterec, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31. US3. CTP
; CURRENT APPLICATION NUMBER: US/09/663.600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09

;; PRIOR APPLICATION NUMBER: 60/081,563
;; PRIOR FILING DATE: 1998-04-13
;; PRIOR APPLICATION NUMBER: 60/096,116
;; PRIOR FILING DATE: 1998-08-10
;; PRIOR APPLICATION NUMBER: 60/099,273
;; PRIOR FILING DATE: 1998-09-04
;; NUMBER OF SEQ ID NOS: 229
;; SOFTWARE: Patent.pm
;; SEQ ID NO 45
;; LENGTH: 1524
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: sig_peptide
;; LOCATION: 160..231
;; OTHER INFORMATION: Von Heijne matrix
;; OTHER INFORMATION: score 5.6999980926514
;; NAME/KEY: polyA_signal
;; LOCATION: 1510..1515
;; NAME/KEY: polyA_site
;; LOCATION: 1506..1519
;; NAME/KEY: misc_feature
;; LOCATION: 1048..1504
;; OTHER INFORMATION: homology
;; OTHER INFORMATION: id: AA552647
;; OTHER INFORMATION: est
;; NAME/KEY: misc_feature
;; LOCATION: 597..846
;; OTHER INFORMATION: homology
;; OTHER INFORMATION: id: AA345449
;; OTHER INFORMATION: est
;; NAME/KEY: misc_feature
;; LOCATION: 39..53
;; OTHER INFORMATION: homology
;; OTHER INFORMATION: id: AA345449
;; OTHER INFORMATION: est
;; NAME/KEY: misc_feature
;; LOCATION: 113..149
;; OTHER INFORMATION: homology
;; OTHER INFORMATION: id: AA345449
;; OTHER INFORMATION: est
;; NAME/KEY: misc_feature
;; LOCATION: 98..400
;; OTHER INFORMATION: homology
;; OTHER INFORMATION: id: T86266
;; OTHER INFORMATION: est
;; NAME/KEY: misc_feature
;; LOCATION: 1210..1489
;; OTHER INFORMATION: homology
;; OTHER INFORMATION: id: T86158
;; OTHER INFORMATION: est
;; NAME/KEY: misc_feature
;; LOCATION: 954..983
;; OTHER INFORMATION: homology
;; OTHER INFORMATION: id: AA116709
;; OTHER INFORMATION: est
;; US-09-663-600A-45

Query Match 32.7%; Score 896; DB 4; Length 1524;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1046; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 57 AAGAGCTTCAAGCTGGAAGACAAAGGAGCACTCCCTGAAGACGCTTCTACTGAGAGCTTG 116
DB 98 AAGAGCTTCAAGCTGGAAGACAAAGGAGCACTCCCTGAAGACGCTTCTACTGAGAGCTTG 157
QY 117 CAATGCGCTCTCTTGGCTCCAACTTGTGGGCTTACATCTTGAAGCTTCTTGGGCTTTTGG 176
DB 158 CAATGCGCTCTCTTGGCTCCAACTTGTGGGCTTACATCTTGAAGCTTCTTGGGCTTTTGG 217
QY 177 GCACTGCTTGGCTATGCTGCTCCCAAGCTGAAACAAAGTTCTTATGCTGTCAGACA 236

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Dh 218 GCACACTGGTTCCTGCTGCTCCAGCTGGAAAAAGATTCTTAATGTCGGTCCAGCA 277
Qy 237 TTGTGACAGAGTGGTGGCTTCTCAAGGGGCTCTGGATGATGATGACACAGACAG 296
Db 278 TTGTGACAGAGTGGTGGCTTCTCAAGGGGCTCTGGATGATGATGACACAGACAG 337
Qy 297 GCATCACCAGTGTGACATCTATAGACCCCTTCTGGGCTGGCCGGTGAATCCAGGCTG 356
Db 338 GCATCACCAGTGTGACATCTATAGACCCCTTCTGGGCTGGCCGGTGAATCCAGGCTG 397
Qy 357 CCCAGGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 416
Db 398 CCCAGGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 457
Qy 417 TGGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 476
Db 458 TGGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 517
Qy 477 CAGGTGAGTCTTTTTCATCTTGAAGGCTCTGAGGATTCATCTGTTGCTGGAATC 536
Db 518 CAGGTGAGTCTTTTTCATCTTGAAGGCTCTGAGGATTCATCTGTTGCTGGAATC 577
Qy 537 TTGATGAGGATTCCTACGGGACCTTCTACACACACACACACACACACACACACACAC 596
Db 578 TTGATGAGGATTCCTACGGGACCTTCTACACACACACACACACACACACACACACAC 637
Qy 597 TTGAGAGGCTCTTACTTGGGACCTTATTTCTTCTGCTTCTGCTGATAGTGAATCA 656
Db 638 TTGAGAGGCTCTTACTTGGGACCTTATTTCTTCTGCTTCTGCTGATAGTGAATCA 697
Qy 657 TCCTCTGCTTCTGCTCATCCAGAAATGCTCCAACTACTAGATGCTTCAAG 716
Db 698 TCCTCTGCTTCTGCTCATCCAGAAATGCTCCAACTACTAGATGCTTCAAG 757
Qy 717 CCCAACTCTGCTCCAGAAAGCTCTCCAAAGGCTGATCAACCTCCAAAGTCAAGAGTG 776
Db 758 CCCAACTCTGCTCCAGAAAGCTCTCCAAAGGCTGATCAACCTCCAAAGTCAAGAGTG 817
Qy 777 AGTTCAATTCCTACAGGCTGACAGGATGATGATGATGATGATGATGATGATGATGATG 836
Db 818 AGTTCAATTCCTACAGGCTGACAGGATGATGATGATGATGATGATGATGATGATGATG 877
Qy 837 TGGCTGGGCTGTGAAAAAGTGAAGACACCCGAGGGCCACAGGTGAGGACACTAC 896
Db 878 TGGCTGGGCTGTGAAAAAGTGAAGACACCCGAGGGCCACAGGTGAGGACACTAC 937
Qy 897 CACTGATCGTGTGAGAAAGTGTGCTGAGAGGATGATGATGATGATGATGATGATGATG 956
Db 938 CACTGATCGTGTGAGAAAGTGTGCTGAGAGGATGATGATGATGATGATGATGATGATG 997
Qy 957 AAAGGCGAAGATGGGGCTAGTGAACATGACAGGTGGAATGCGAAGATGCTGCC 1016
Db 998 AAAGGCGAAGATGGGGCTAGTGAACATGACAGGTGGAATGCGAAGATGCTGCC 1057
Qy 1017 ATGCGACCTTTTCTGTTTCTCACTTGTGCTGCTCCCTGCTTAAGTCCCAACCTCA 1076
Db 1058 ATGCGACCTTTTCTGTTTCTCACTTGTGCTGCTCCCTGCTTAAGTCCCAACCTCA 1117
Qy 1077 ACTTGAACCCCATTCCTTAAGCAGAGA 1105
Db 1118 ACTTGAACCCCATTCCTTAAGCAGAGA 1146
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RESULT 4
US-09-134-000C-1944/C
; Sequence 1944, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
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; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1944
; LENGTH: 1485
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1944
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Query Match 0.7%; Score 20; DB 4; Length 1485;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1249 AGAAGCAGTGGCTTTGTGG 1268
Db 1149 AGAAGCAGTGGCTTTGTGG 1130
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RESULT 5

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US-09-976-594-1011/C
; Sequence 1011, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 1011
; LENGTH: 13930
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 331108.1
US-09-976-594-1011
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Query Match 0.7%; Score 20; DB 4; Length 13930;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2104 CATATCATGCCACGCTGC 2123
Db 11973 CATATCATGCCACGCTGC 11954
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RESULT 6

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US-09-220-132-20/C
; Sequence 20, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: Shvian, Andrew M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 13993
; TYPE: DNA
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ORGANISM: Homo sapiens
US-09-220-132-20

Query Match 0.7%; Score 20; DB 4; Length 13993;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2104 CATATCCATGCCACGGTGC 2123
DB 1203 CATATCCATGCCACGGTGC 12020

RESULT 7
US-09-108-006C-2/c
Sequence 2, Application US/09108006C
Patent No. 6524613
GENERAL INFORMATION:
APPLICANT: Steer, Clifford J.
Kren, Betsy T.
Bandopadhyay, Paramita
Roy-Chowdhury, Jayanta
TITLE OF INVENTION: Hepatocellular Chimeraplasty
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kimeragen, Inc.
STREET: 300 Pleasant Run
CITY: Newtown
STATE: PA
COUNTRY: USA
ZIP: 18940
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/108,006C
FILING DATE: 30-Jun-1992
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,288
FILING DATE: 30-APR-1997
APPLICATION NUMBER: 60/054,837
FILING DATE: 05-AUG-1997
APPLICATION NUMBER: 60/064,996
FILING DATE: 10-NOV-1997
APPLICATION NUMBER: 60/074,497
FILING DATE: 12-FEB-1998
APPLICATION NUMBER: PCT US 98/08834
FILING DATE: 30-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Fiedel, Thomas
REGISTRATION NUMBER: 29258
REFERENCE/DOCKET NUMBER: 7991-015-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-504-4444
TELEFAX: 215-504-4545
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 14070 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-108-006C-2

Query Match 0.7%; Score 20; DB 4; Length 14070;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2104 CATATCCATGCCACGGTGC 2123
|||||

DB 12117 CATATCCATGCCACGGTGC 12098

RESULT 8
US-08-916-421B-1
Sequence 1, Application US/08916421B
Patent No. 6503729
GENERAL INFORMATION:
APPLICANT: Built et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
Patent No. 6503729
FILE REFERENCE: jannaschii
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaschii
FEATURE:
NAME/KEY: misc_feature
LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98120)..(98120)
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LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature

LOCATION: (234187)..(234187)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (234220)..(234220)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (234814)..(234814)
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LOCATION: (309398)..(309398)
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LOCATION: (312837)..(312837)
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NAME/KEY: misc_feature
LOCATION: (312993)..(312993)
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NAME/KEY: misc_feature
LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (559167)..(559167)
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LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1084830)..(1084830)
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NAME/KEY: misc_feature
LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1119881)..(1119881)

OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1313224)..(1313224)
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NAME/KEY: misc_feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1349491)..(1349491)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1470091)..(1470091)
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US-08-916-421B-1

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1458 ACATTAAATAATAATAAT 1477
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US-09-692-570-1
Sequence 1, Application US/09692570
Patent No. 6797466
GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
Patent No. 6797466
TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275CI
CURRENT APPLICATION NUMBER: US/09/692,570
CURRENT FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
PRIOR APPLICATION NUMBER: US 08/916,421
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
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Search completed: October 30, 2004, 13:22:06
Job time : 298 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 29, 2004, 01:21:03 ; Search time 1793 Seconds
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Searched: 3413475 seqs, 256380928 residues

Word size : 20

Total number of hits satisfying chosen parameters: 816

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1472	53.7	1475	10 US-09-888-257A-1	Sequence 1, Appl
3	1472	53.7	1475	10 US-09-946-374-133	Sequence 133, App
4	1472	53.7	1475	13 US-10-006-867-79	Sequence 79, Appl
5	1472	53.7	1475	13 US-10-063-547-79	Sequence 79, Appl
6	1472	53.7	1475	13 US-10-063-551-79	Sequence 79, Appl
7	1472	53.7	1475	14 US-10-028-072-491	Sequence 491, App
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ALIGNMENTS

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Sequence 23, Application US/10301822
Publication No. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangt
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John B.
APPLICANT: Thibodeau, Stephen N.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MEM01-029P2RNM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
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Qy	2521	TCCCTCTCTCAACCCCTCCCTCCGCCCAACCTCAATGTAAATGCTTCTTGATGCTTAG	2580
Db	2633	TCCCTCTCTCAACCCCTCCCTCCGCCCAACCTCAATGTAAATGCTTCTTGATGCTTAG	2692
Qy	2581	CATTCACAATTTTGTATGTAATGTTATTTGTGTGTGTGTGTCCGATCTCACAGATATTT	2640
Db	2693	CATTCACAATTTTGTATGTAATGTTATTTGTGTGTGTGTGTCCGATCTCACAGATATTT	2752
Qy	2641	GTTAAACCTTTGGTGGGTGGGGGCCATATCTTAAGCTCTCTGTATCCCCAGACTACT	2700
Db	2753	GTTAAACCTTTGGTGGGTGGGGGCCATATCTTAAGCTCTCTGTATCCCCAGACTACT	2812
Qy	2701	GTTAAACCTTTGGTGGGTGGGGGCCATATCTTAAGCTCTCTGTATCCCCAGACTACT	2812
Db	2813	GTTAAACCTTTGGTGGGTGGGGGCCATATCTTAAGCTCTCTGTATCCCCAGACTACT	2829
RESULT 2			
US-09-888-257A-1			
Sequence 1, Application US/09888257A			
Publication No. US20030060612A1			
GENERAL INFORMATION:			
APPLICANT: Goddard, Audrey			
APPLICANT: Godowski, Paul J.			
APPLICANT: Gurney, Austin L.			
APPLICANT: Hillan, Kenneth J.			
APPLICANT: Polakis, Paul			
APPLICANT: Smith, Victoria			
APPLICANT: Wood, William I.			
APPLICANT: Wu, Thomas D.			
APPLICANT: Zhang, Zemin			
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND			
FILE OF INVENTION: TREATMENT OF TUMOR			
FILE REFERENCE: P5002R1			
CURRENT APPLICATION NUMBER: US/09/888,257A			
CURRENT FILING DATE: 2002-04-30			
PRIOR APPLICATION NUMBER: US 60/063,540			
PRIOR FILING DATE: 1997-10-28			
PRIOR APPLICATION NUMBER: US 60/089,653			
PRIOR FILING DATE: 1998-06-17			
PRIOR APPLICATION NUMBER: US 60/099,792			
PRIOR FILING DATE: 1998-09-10			
PRIOR APPLICATION NUMBER: US 60/103,678			
PRIOR FILING DATE: 1998-10-08			
PRIOR APPLICATION NUMBER: US 60/235,451			
PRIOR FILING DATE: 2000-09-26			

	Prior APPLICATION NUMBER:	PCT/US99/12252
	Prior FILING DATE:	1999-06-02
	Prior APPLICATION NUMBER:	PCT/US99/20111
	Prior FILING DATE:	1999-09-01
	Prior APPLICATION NUMBER:	PCT/US00/04342
	Prior FILING DATE:	2000-02-18
	Prior APPLICATION NUMBER:	PCT/US00/05841
	Prior FILING DATE:	2000-03-02
	Prior APPLICATION NUMBER:	PCT/US00/08439
	Prior FILING DATE:	2000-03-30
	Prior APPLICATION NUMBER:	PCT/US00/23328
	Prior FILING DATE:	2000-08-24
	Prior APPLICATION NUMBER:	PCT/US00/32678
	Prior FILING DATE:	2000-12-01
	Prior APPLICATION NUMBER:	PCT/US01/06520
	Prior FILING DATE:	2001-02-28
	Prior APPLICATION NUMBER:	PCT/US01/06666
	Prior FILING DATE:	2001-03-01
	NUMBER OF SEQ ID NOS:	10
	SEQ ID NO 1	
	LENGTH:	1475
	TYPE:	DNA
	ORGANISM:	Homo Sapien
	US-09-888-257A-1	
Query Match	53.7%; Score 1472; DB 10; Length 1475;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 1472; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
OY	1 AGAGTCACGCGTGGCAGAGAGACTCTGAATAAGAGGATTTAGAGGTTCAGAAGACAGAA	60
DB	4 AAGATCAAGCTTGAGAGAGACTCTGAATAAGAGGATTTAGAGGTTCAGAAGACAGAA	63
OY	61 GCTTCAGCGCTTAAGACAAGAGGAGCATCCCTGAAGACGCTTCTACTAGAGGTCTGCAT	120
DB	64 GCTTCAGCGCTTAAGACAAGAGGAGCATCCCTGAAGACGCTTCTACTAGAGGTCTGCAT	123
OY	121 GGCTCTCTTGGCTCCCACTTTGGGGTACATCCTTAGGCCCTTCTGGGGCTTTTGGGCAC	180
DB	124 GGCTCTCTTGGCTCCCACTTTGGGGTACATCCTTAGGCCCTTCTGGGGCTTTTGGGCAC	183
OY	181 ACTGTTGCCANTGCTGCTCCCCAGCTGGAAAACAAAGCTTATATGCGGTCAGCATTTGT	240
DB	184 ACTGTTGCCANTGCTGCTCCCCAGCTGGAAAACAAAGCTTATATGCGGTCAGCATTTGT	243
OY	241 GACAGCAGTTGGCTTCTCCAAGGGCTCTGGATGGATGTGCCACACACAGCACAGGCAT	300
DB	244 GACAGCAGTTGGCTTCTCCAAGGGCTCTGGATGGATGTGCCACACACAGCACAGGCAT	303
OY	301 CACCAGTGTACATCTATAGCACCCCTTCTGGGGCTGCCCCTGACATCCAGGCTGCCCA	360
DB	304 CACCAGTGTACATCTATAGCACCCCTTCTGGGGCTGCCCCTGACATCCAGGCTGCCCA	363
OY	361 GCCCATATGTGTACATCAGTGTGACATTCCTCTCCCTGGCCCTGCATTATCTCTGTGTGG	420
DB	364 GCCCATATGTGTACATCAGTGTGACATTCCTCTCCCTGGCCCTGCATTATCTCTGTGTGG	423
OY	421 CATGAGATGACAAGTCTTCTGCGCAGAAATCCGAGCCAAAAGACAGAGTGGCGGTAGCAG	480
DB	424 CATGAGATGACAAGTCTTCTGCGCAGAAATCCGAGCCAAAAGACAGAGTGGCGGTAGCAG	483
OY	481 TGAAGTCTTTTTCATCTTGAAGGCTCTGGGATTCATTCCTGTGTGCTGGAAATCTTCA	540
DB	484 TGAAGTCTTTTTCATCTTGAAGGCTCTGGGATTCATTCCTGTGTGCTGGAAATCTTCA	543
OY	541 TGGATATCTTAAGGACCTTCTACTACACACTGTGTGCTGACAGCAAGAAATTTGAAATTTG	600
DB	544 TGGATATCTTAAGGACCTTCTACTACACACTGTGTGCTGACAGCAAGAAATTTGAAATTTG	603
OY	601 AAGAGCTCTTACTTGGGCAATTAATTTCTCCCTGTCTTCCCTGATAGCTGAATCATCT	660
DB	604 AAGAGCTCTTACTTGGGCAATTAATTTCTCCCTGTCTTCCCTGATAGCTGAATCATCT	663

QY 661 CTGCTTTCTGCTCATCCAGAGAAATCGCTCCACTACTAGATGCTTACCAAGCCCA 720
DB 664 CTGCTTTCTGCTCATCCAGAGAAATCGCTCCACTACTAGATGCTTACCAAGCCCA 723
QY 721 ACCCTTGGCAAGAGGCTCTCCAGAGGCTGGTCACTCCCAAGTCAAGAGTGT 780
DB 724 ACCCTTGGCAAGAGGCTCTCCAGAGGCTGGTCACTCCCAAGTCAAGAGTGT 783
QY 781 CAATTCCTAGAGCTGACAGGGTATGTGTAGAGAACAGAGGGGCGACAGTGGGGGTGGC 840
DB 784 CAATTCCTAGAGCTGACAGGGTATGTGTAGAGAACAGAGGGGCGACAGTGGGGGTGGC 843
QY 841 TGGGTCTGTGAAAAACGTGACACGACCCCGAGGGGCAAGGTGAGGACACTACT 900
DB 844 TGGGTCTGTGAAAAACGTGACACGACCCCGAGGGGCAAGGTGAGGACACTACT 903
QY 901 GGATCGGTGAGAGGGTGTGAGGATGAGCTTGGCCCATTTGGAATTGAGCAAG 960
DB 904 GGATCGGTGAGAGGGTGTGAGGATGAGCTTGGCCCATTTGGAATTGAGCAAG 963
QY 961 GCAGAAATGGGGGCTAGTGTAAACAGATGACAGTGTGAATTGCCAAGAGTCTGCCATGC 1020
DB 964 GCAGAAATGGGGGCTAGTGTAAACAGATGACAGTGTGAATTGCCAAGAGTCTGCCATGC 1023
QY 1021 CAGCCTTTCTGTTTCTCTCACTTGTGCTGCTCCCTGCTTAACTGCTCCAACTT 1080
DB 1024 CAGCCTTTCTGTTTCTCTCACTTGTGCTGCTCCCTGCTTAACTGCTCCAACTT 1083
QY 1081 GAAACCCCATTCCTCTTAAGCAGAGACTCAAGAGATCCCTTGGCTGTTAACTGGG 1140
DB 1084 GAAACCCCATTCCTCTTAAGCAGAGACTCAAGAGATCCCTTGGCTGTTAACTGGG 1143
QY 1141 ACTGCATCCCAAAACCACTAATCAATCCCACTGACCTCTGTGATCAAAAGCC 1200
DB 1144 ACTGCATCCCAAAACCACTAATCAATCCCACTGACCTCTGTGATCAAAAGCC 1203
QY 1201 TCTCTGTGCTGAGTGTGGCTTAACTGCTGCTGAGGATGGGAGAGAGAGTGGC 1260
DB 1204 TCTCTGTGCTGAGTGTGGCTTAACTGCTGCTGAGGATGGGAGAGAGAGTGGC 1263
QY 1261 TTTTGTGGGAGTGTCTTAAGCTTCTCAAGTCTCCCTCAAGAAAGTGAATTGGCC 1320
DB 1264 TTTTGTGGGAGTGTCTTAAGCTTCTCAAGTCTCCCTCAAGAAAGTGAATTGGCC 1323
QY 1321 TGGAACTCCATCCCACTCTTGTATGACTCAACAGTGTCCAGACTAATTTGTGATGAA 1380
DB 1324 TGGAACTCCATCCCACTCTTGTATGACTCAACAGTGTCCAGACTAATTTGTGATGAA 1383
QY 1381 CTGAAATTAACCATCTTACGGTATCCAGGAGACAGAAAGCAGATGCGAGTGGAGGA 1440
DB 1384 CTGAAATTAACCATCTTACGGTATCCAGGAGACAGAAAGCAGATGCGAGTGGAGGA 1443
QY 1441 CAGGAGGAGCGCTGGGACATTTTAAAAATA 1472
DB 1444 CAGGAGGAGCGCTGGGACATTTTAAAAATA 1475

RESULT 3

US-09-946-374-133

Sequence 133, Application US/09946374

Publication No. US20030073129A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Bacon, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
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PRIOR FILING DATE: 1998-10-02
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PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/103314

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PRIOR FILING DATE: 1998-10-07
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PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103395
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PRIOR APPLICATION NUMBER: 60/105000
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PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105694
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105807

Query Match 53.7%; Score 1472; DB 10; Length 1475;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTACGCTGGCAGAGAGACTTGAATGAGGATTAGAGTGTTCAGAGCAAGA 60
DB 4 AGAAGTACGCTGGCAGAGAGACTTGAATGAGGATTAGAGTGTTCAGAGCAAGA 63
QY 61 GCTTCAGCTGAGAGCAAGGAGAGAGCTTGAAGAGCTTCTAGAGAGTCTGCAT 120
DB 64 GCTTCAGCTGAGAGCAAGGAGAGAGCTTGAAGAGCTTCTAGAGAGTCTGCAT 123
QY 121 GGCCTCTTGGGCTCCCACTTGTGGGCTAATCTAGGCTTCTGAGGCTTTGGGAC 180
DB 124 GGCCTCTTGGGCTCCCACTTGTGGGCTAATCTAGGCTTCTGAGGCTTTGGGAC 183
QY 181 ACTGTTGCAATGCTGTCTCCCAAGCTGAGAAACAAAGTTCTTAATGTGGTCCAGCATTT 240
DB 184 ACTGTTGCAATGCTGTCTCCCAAGCTGAGAAACAAAGTTCTTAATGTGGTCCAGCATTT 243
QY 241 GACAGAGTGGGCTTCTCCAAAGGAGCTTGGATGAAATGTCACACACAGCAGGAGAT 300
DB 244 GACAGAGTGGGCTTCTCCAAAGGAGCTTGGATGAAATGTCACACACAGCAGGAGAT 303
QY 301 CACCCAGTGTGACATCTATAGCAACCTTCTGAGGCTGCGCTGACATCCAGGCTGCGCA 360
DB 304 CACCCAGTGTGACATCTATAGCAACCTTCTGAGGCTGCGCGCTGACATCCAGGCTGCGCA 363
QY 361 GGCATATGTGTGACATCCAGTGCATCTCTCCCTGAGCTGATTAATCTGTGTGGG 420
DB 364 GGCATATGTGTGACATCCAGTGCATCTCTCCCTGAGCTGATTAATCTGTGTGGG 423

421 CATGAGTGCAGAGTCTTCTGCGAGGAAATCCGAGCCAAAGACAGAGTGGCGGTAGCAGG 480
 424 CATGAGTGCAGAGTCTTCTGCGAGGAAATCCGAGCCAAAGACAGAGTGGCGGTAGCAGG 483
 481 TGAAGCTTTTATCTTGGAGGCGCTCGGGAATTCATTCCTGTTGCTGGAATCTTCA 540
 484 TGAAGCTTTTATCTTGGAGGCGCTCGGGAATTCATTCCTGTTGCTGGAATCTTCA 543
 541 TGGGATCTCAGGGAATCTTACTACCACTGATGCTGAGAGCATGAAATTTGAGATTGG 600
 544 TGGGATCTCAGGGAATCTTACTACCACTGATGCTGAGAGCATGAAATTTGAGATTGG 603
 601 AGAGGCTCTTACTGAGGCAATATTTCTTCTGTTCTCCCTGATGAGTGAATCATCTT 660
 604 AGAGGCTCTTACTGAGGCAATATTTCTTCTGTTCTCCCTGATGAGTGAATCATCTT 663
 661 CTGCTTTTCTGCTCATCCGAGAAATGCTCCAACTACTAGATGCTTCAAGGCCA 720
 664 CTGCTTTTCTGCTCATCCGAGAAATGCTCCAACTACTAGATGCTTCAAGGCCA 723
 721 ACCTTTTCCAGAGAGTCTCTCCAGGCTGCTCAACTCCCAAGTCAAGATGAGTT 780
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 781 CAATTCCTACAGCTGACAGGCTATGTTGTAAGAACAGAGGCGCAGAGCTGGGGGCTGGC 840
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 844 TGGGCTGTGAAAGAGTGAAGAGCAGCAGGAGGCGCAGAGGCTGAGAGGCACTACCACT 903
 901 GATTCGTGAGAGGCTGCTGAGAGTGAAGTGAATTTGAGGCAATTTGAGGCAAG 960
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 1081 GAAAGCCCATTCCTTAAGCAGAGCTCAGAGATCCCTTTGCTGCTGCTGCTGCTGCTGCTGCT 1140
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 1201 TCTCTGAGTGAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
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 1261 TTTTGGGAGTGGCTTAACTTAAGCTTCAAGGCTTCCCTCAAGAACTGATTTGGCCC 1320
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 1381 CTGAAATTAAGCAATCTTACGATTCAGAGGAAAGAAAGAGATGCAAGATGGAGGA 1440
 1384 CTGAAATTAAGCAATCTTACGATTCAGAGGAAAGAAAGAGATGCAAGATGGAGGA 1443
 1441 CAGAGGAGCAGCTGGAGCATTTAAAAAATA 1472
 1444 CAGAGGAGCAGCTGGAGCATTTAAAAAATA 1475

RESULT 4
 US-10-006-867-79
 ; Sequence 79, Application US/10006867
 ; Publication No. US20020119130A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Geriltsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3230R1C1
 ; CURRENT APPLICATION NUMBER: US/10/006,867
 ; CURRENT FILING DATE: 2001-12-06
 ; PRIOR APPLICATION NUMBER: 60/063435
 ; PRIOR FILING DATE: 1997-10-29
 ; PRIOR APPLICATION NUMBER: 60/064215
 ; PRIOR FILING DATE: 1997-10-29
 ; PRIOR APPLICATION NUMBER: 60/082797
 ; PRIOR FILING DATE: 1998-04-22
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 64 GCTTCAAGCCCTGAAGAGAGAGAGAGCTTCTTAAGAGAGTGTCCAT 123
QY 121 GGCCTCTTGGCTTCAACTTGTGGCTTCACTTGAAGCTTGTGGGCTTTTGGGAC 180
DB 124 GGCCTCTTGGCTTCAACTTGTGGCTTCACTTGAAGCTTGTGGGCTTTTGGGAC 183

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DB 184 ACTGTTGCCATGCTGCTCCCAAGCTGAGAAACAAGTTCTTATGTGCGGTGCAGCATTTGT 243
QY 241 GACAGCAGTTGGCTTCTCCAAAGGCTCTGGATGGAAATGTGGCCACACAGCCACAGGCAT 300
DB 244 GACAGCAGTTGGCTTCTCCAAAGGCTCTGGATGGAAATGTGGCCACACAGCCACAGGCAT 303
QY 301 CACCCAGTGTGACATCTATAGCAACCTTCTGGAGCTCCGCGCTGACATCCAGGCTGCCA 360
DB 304 CACCCAGTGTGACATCTATAGCAACCTTCTGGAGCTCCGCGCTGACATCCAGGCTGCCA 363
QY 361 GGCCTATGATGGTGAATCTGACATCTGCAATCTCTCCCTGAGCTGATATCTCTGTGGG 420
DB 364 GGCCTATGATGGTGAATCTGACATCTGCAATCTCTCCCTGAGCTGATATCTCTGTGGG 423
QY 421 CATGAGATGCAACATCTTCTGCGCAGGAATCCCGAGCAAGAAAGAGATGGCGGTAGAGG 480
DB 424 CATGAGATGCAACATCTTCTGCGCAGGAATCCCGAGCAAGAAAGAGATGGCGGTAGAGG 483
QY 481 TGGAGTCTTTTTCATCTCTGGAGGCTCTCTGGAGATTCATCTCTGTGCTGGAATCTTCA 540
DB 484 TGGAGTCTTTTTCATCTCTGGAGGCTCTCTGGAGATTCATCTCTGTGCTGGAATCTTCA 543
QY 541 TGGGATCTTAAGGAGCTTCTAACAACAATGCTGCTGACAGCATGAAATTTGAGATTGG 600
DB 544 TGGGATCTTAAGGAGCTTCTAACAACAATGCTGCTGACAGCATGAAATTTGAGATTGG 603
QY 601 AGAGGCTCTTAACTTGGGCAATTAATTTCTCCCTGCTCTCCCTGATGCTGGAATCATCT 660
DB 604 AGAGGCTCTTAACTTGGGCAATTAATTTCTCCCTGCTCTCCCTGATGCTGGAATCATCT 663
QY 661 CTGCTTTCCTGCTCATCTCCAGAGAAATCGCTCCAACTACTACGATGCTCAACAGCCCA 720
DB 664 CTGCTTTCCTGCTCATCTCCAGAGAAATCGCTCCAACTACTACGATGCTCAACAGCCCA 723
QY 721 ACCTCTTCCCAAGAGAGCTCTCAAGGCTGCTGCAACCTTCCAAAGTCAAGAGTGTG 780
DB 724 ACCTCTTCCCAAGAGAGCTCTCAAGGCTGCTGCAACCTTCCAAAGTCAAGAGTGTG 783
QY 781 CAATTCCTACAGGCTGACAGGATATGTGTGAAGAACAGAGGCGCCAGAGCTGGGGGGTGGC 840
DB 784 CAATTCCTACAGGCTGACAGGATATGTGTGAAGAACAGAGGCGCCAGAGCTGGGGGGTGGC 843
QY 841 TGGGCTCTGTGAAAAACAGTGGACAGCAACCCGAGAGGCTCAAGTGTGAGGACATCAACT 900
DB 844 TGGGCTCTGTGAAAAACAGTGGACAGCAACCCGAGAGGCTCAAGTGTGAGGACATCAACT 903
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DB 904 GGATCTGTGCAAGAGTGTGCTGAGAGATGACTGCTTGGCCATTGATGAGCAAG 963
QY 961 GCAAGATGGGGGCTATGTGAACAGATGAGATGGAATGGCCAAAGATGCTGCCCATG 1020
DB 964 GCAAGATGGGGGCTATGTGAACAGATGAGATGGAATGGCCAAAGATGCTGCCCATG 1023
QY 1021 CAGGCTTCTGTTCCTCAACCTTGTGCTCCCTGCTGCTAAGTCCCAACCTCAACT 1080
DB 1024 CAGGCTTCTGTTCCTCAACCTTGTGCTCCCTGCTGCTAAGTCCCAACCTCAACT 1083
QY 1081 GAAACCCCATCTCTTAAGCAGAGACTGAGAGATCCCTTGGCTCTGATTAAGTGGG 1140
DB 1084 GAAACCCCATCTCTTAAGCAGAGACTGAGAGATCCCTTGGCTCTGATTAAGTGGG 1143
QY 1141 ACTTCATCCCAAAACCACTTAATGACATCCCACTGACAGCCCTGATGATCAAAAGCC 1200
DB 1144 ACTTCATCCCAAAACCACTTAATGACATCCCACTGACAGCCCTGATGATCAAAAGCC 1203
QY 1201 TCTCTCTGAGTGTGCTCTTATGCTCAATGCTGAGGAGATGGAGAAAGAGAGCTGGC 1260
DB 1204 TCTCTCTGAGTGTGCTCTTATGCTCAATGCTGAGGAGATGGAGAAAGAGAGCTGGC 1263
QY 1261 TTTTGTGGGCAATGCTCTAACTTAATCTTCAAGCTTCCCTCAAAAGAACTGATTTGGCC 1320
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QY 1381 CTGAAATTAACATCTCTAAGTATCCAGGAAACAGAAAGAGATGACAGATGGAGGA 1440
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QY 1441 CAGAAAGCAGCTGGAGCAATTAATAATA 1472
DB 1444 CAGAAAGCAGCTGGAGCAATTAATAATA 1475
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RESULT 5

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; Sequence 79, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,547
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
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; LENGTH: 1475
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; ORGANISM: Homo Sapien
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Query Match 53.7%; Score 1472; DB 13; Length 1475;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GCTTCAAGCTTGAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 64 GCTTCAAGCTTGAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
QY 121 GGCCTCTCTTGGCTTCAACTGTGTGGCTTCACTAGAGCTTGTGGGCTTTTGGGCA 180
DB 124 GGCCTCTCTTGGCTTCAACTGTGTGGCTTCACTAGAGCTTGTGGGCTTTTGGGCA 183
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QY 241 GACAGCAGTTGGCTTCTCCAAAGGCTCTGGATGGAATGTGCCACACAGACAGAGCAT 300
DB 244 GACAGCAGTTGGCTTCTCCAAAGGCTCTGGATGGAATGTGCCACACAGAGCAT 303
QY 301 CACCCAGTGTGACATCTATAGCAACCTTCTGGAGCTCCGCGCTGACATCCAGGCTGCCA 360
DB 304 CACCCAGTGTGACATCTATAGCAACCTTCTGGAGCTCCGCGCTGACATCCAGGCTGCCA 363
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QY 601 AGAGGCTCTTAACTTGGGCAATTAATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCTT 660
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DB 844 TGGGCTGTGAAAAACAGTGAAGCAAGCCGAGAGGCAAGGAGTGAAGGCACTACCACT 903
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DB 1444 CAGGAGGAG 1475

RESULT 7
US-10-028-072-491

Sequence 491, Application US/10028072

Publication No. US20030004311A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: Desrogers, Laura

APPLICANT: Desrogers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerltzen, Mary E.

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028, 072
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PRIOR FILING DATE: 1997-06-18
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;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07

Query Match 53.7%; Score 1472; DB 14; Length 1475;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4 AGAAGTCAGCCTGGCAGAGAGACTGGAATGAGGATTAGAGTTCAGAGAGAGA 63
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Db 64 GCTTCAGCCTGAAG 123
QY 121 GGCCTCTTGGGCTTCAACTTGTGGGCTACATCTTCAAGGCTTTGGGGCAC 180
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QY 181 ACTGGTTGCGATGCTGCTCCCGAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAG 240
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QY 241 GACAGCAGTTGGCTTCCAGAGGAGCTTGGATGAGATGTCACACAGCAGAGCAT 300
Db 244 GACAGCAGTTGGCTTCCAGAGGAGCTTGGATGAGATGTCACACAGCAGAGCAT 303
QY 301 CACCCAGTGTGATCTATATAGCAGCCTTGTGGGCTGCGCGTGAATTCAGAGCTTCCCA 360
Db 304 CACCCAGTGTGATCTATATAGCAGCCTTGTGGGCTGCGCGTGAATTCAGAGCTTCCCA 363

Db 544 TGGAGTCTTACGAGGACTTCTACTACCACTGGTGTCTGACAGCATGAATTTGAGATTGG 603
Qy 601 AGAGGCTCTTACTTGGGCAATTAATTTCTCCCTGTCCTCCCTGATCTGGAATCATCTT 660
Db 604 AGAGGCTCTTACTTGGGCAATTAATTTCTCCCTGTCCTCCCTGATCTGGAATCATCTT 663
Qy 661 CTGCTTTCTGCTCATCCGAGAAATGCTCCAACTACTAGCATCTCAAGCCCA 720
Db 664 CTGCTTTCTGCTCATCCGAGAAATGCTCCAACTACTAGCATCTCAAGCCCA 723
Qy 721 ACCTCTTCCCAAGAAGCTCTCCAAAGCTCTGTCCTCCAAAGTCAAGTGAAT 780
Db 724 ACCTCTTCCCAAGAAGCTCTCCAAAGCTCTGTCCTCCAAAGTCAAGTGAAT 783
Qy 781 CAATTTCTACAGCTGACAGGCTATGTGTAAAGAACAGAGGCGCAAGCTGGGGGGTGGC 840
Db 784 CAATTTCTACAGCTGACAGGCTATGTGTAAAGAACAGAGGCGCAAGCTGGGGGGTGGC 843
Qy 841 TGGGCTGTGAAAAAGTGAAGCAAGCCGAGGCGCAAGTGAAGGCACTACCACT 900
Db 844 TGGGCTGTGAAAAAGTGAAGCAAGCCGAGGCGCAAGTGAAGGCACTACCACT 903
Qy 901 GGATCGTGTGAGAGGCTGTCTGAGAGTGAATGACTTTGGCATTGATGAGCAAG 960
Db 904 GGATCGTGTGAGAGGCTGTCTGAGAGTGAATGACTTTGGCATTGATGAGCAAG 963
Qy 961 GCAGAAATGGGGGGCTAGTGTAAAGCATGCAAGCTTGAATTCGCAAGATGCTCCCATTC 1020
Db 964 GCAGAAATGGGGGGCTAGTGTAAAGCATGCAAGCTTGAATTCGCAAGATGCTCCCATTC 1023
Qy 1021 CAGGCTTTCTGTTTCTCACTTGTGTGCTCCCTGAGCTTGAATTCGCAAGATGCTCCCATTC 1080
Db 1024 CAGGCTTTCTGTTTCTCACTTGTGTGCTCCCTGAGCTTGAATTCGCAAGATGCTCCCATTC 1083
Qy 1081 GAAACCCCATTTCCCTTAAGCAGAGACTCAAGAGATCCCTTTGCTGTTTAACTGGG 1140
Db 1084 GAAACCCCATTTCCCTTAAGCAGAGACTCAAGAGATCCCTTTGCTGTTTAACTGGG 1143
Qy 1141 ACTCATATCCCAAAACCACTAATCAATCCCACTGACAGCTCTGTGATCAAAAGACC 1200
Db 1144 ACTCATATCCCAAAACCACTAATCAATCCCACTGACAGCTCTGTGATCAAAAGACC 1203
Qy 1201 TCTCTGAGGAGGTTGGCTCTTAGCTCATTTGCTGGGGATGGAGAGAGAGTGGC 1260
Db 1204 TCTCTGAGGAGGTTGGCTCTTAGCTCATTTGCTGGGGATGGAGAGAGAGTGGC 1263
Qy 1261 TTTTGTGGGCAATGCTCTTAACCTTCTCAAGCTTCCCTCAAAAGAACTGATTTGGCCC 1320
Db 1264 TTTTGTGGGCAATGCTCTTAACCTTCTCAAGCTTCCCTCAAAAGAACTGATTTGGCCC 1323
Qy 1321 TGGAACTCCATCCCACTCTTGTATGACTCAAGTGTCCAACTAATTTGTGATGAA 1380
Db 1324 TGGAACTCCATCCCACTCTTGTATGACTCAAGTGTCCAACTAATTTGTGATGAA 1383
Qy 1381 CTGAATTAATAACCATCTTAGGATTCAGGAGAACAGAAAGAGATGAGAGTGGAGGA 1440
Db 1384 CTGAATTAATAACCATCTTAGGATTCAGGAGAACAGAAAGAGATGAGAGTGGAGGA 1443
Qy 1441 CAGGAAGGCAAGCTGGAGCAATTTAAAAAATA 1472
Db 1444 CAGGAAGGCAAGCTGGAGCAATTTAAAAAATA 1475

RESULT 9

US-10-140-808-491
; Sequence 491, Application US/10140808
; Publication No. US20030017563A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang
APPLICANT: Geriltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C182
CURRENT APPLICATION NUMBER: US/10/140,808
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 491
LENGTH: 1475
TYPE: DNA
ORGANISM: Homo Sapien
US-10-140-808-491

Query Match 53.7%; Score 1472; DB 14; Length 1475;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 1472; Conservative 0; Indels 0; Gaps 0;

1 AGAAGTCAAGCTGTGAGAGAGACTCTGAAATGAGAGATTAGAGTGTTCAGAGCAAGA 60
4 AGAAGTCAAGCTGTGAGAGAGACTCTGAAATGAGAGATTAGAGTGTTCAGAGCAAGA 63
Qy 61 GCTTCAAGCTGAAAGCAAGGAGAGAGCTCTGAAAGAGCTTTCTACTAGAGAGTGGCAT 120
Db 64 GCTTCAAGCTGAAAGCAAGGAGAGAGCTCTGAAAGAGCTTTCTACTAGAGAGTGGCAT 123
Qy 121 GGCCTCTTGGGCTCCAACTTGGGCTTCACTCTTGAAGCTTCTGAGGCTTTTGGGAC 180
Db 124 GGCCTCTTGGGCTCCAACTTGGGCTTCACTCTTGAAGCTTCTGAGGCTTTTGGGAC 183
Qy 181 ACTGTTGCCATGTGTCTCCAGCTGGAAGAAAGAGTTCTTATGTGGTCCAGATGT 240
Db 184 ACTGTTGCCATGTGTCTCCAGCTGGAAGAAAGAGTTCTTATGTGGTCCAGATGT 243
Qy 241 GACAGAGTTGGCTTCTCCAGAGGCTCTGATGAAATGTCACACACAGCAGCAT 300
Db 244 GACAGAGTTGGCTTCTCCAGAGGCTCTGATGAAATGTCACACACAGCAGCAT 303
Qy 301 CACCAATGTGACATCTTATGACACCTTCTGGGCTGCGCGCTGACATCCAGGCTGCCA 360
Db 304 CACCAATGTGACATCTTATGACACCTTCTGGGCTGCGCGCTGACATCCAGGCTGCCA 363
Qy 361 GGCATGATGTGACATCCAGTCAATCTCTCTGCTGGCTGTGATTAATCTGTGTGG 420
Db 364 GGCATGATGTGACATCCAGTCAATCTCTCTGCTGGCTGTGATTAATCTGTGTGG 423
Qy 421 CATGATGACACAGCTTCTGCGAGAGATCCAGACCAAGACAGAGTGGCGTGAAG 480
Db 424 CATGATGACACAGCTTCTGCGAGAGATCCAGACCAAGACAGAGTGGCGTGAAG 483
Qy 481 TGGAGCTTTTCACTCTGAGGCTCTGGGATTCATTCCTGTTGCTGGAATCTTCA 540
Db 484 TGGAGCTTTTCACTCTGAGGCTCTGGGATTCATTCCTGTTGCTGGAATCTTCA 543
Qy 541 TGGAGTCTACAGGAGCTTCTACTACCACTGTGTCTGACAGCATGAATTTGAGATTGG 600
Db 544 TGGAGTCTACAGGAGCTTCTACTACCACTGTGTCTGACAGCATGAATTTGAGATTGG 603
Qy 601 AGAGGCTCTTACTTGGGCAATTAATTTTCTCTGTTCTCCCTGATAGCTGGAATCATCT 660
Db 604 AGAGGCTCTTACTTGGGCAATTAATTTTCTCTGTTCTCCCTGATAGCTGGAATCATCT 663

QY 661 CTGCTTTCTGCTCATCCAGAGAAATCGCTCCAACTACTAGATGCTTACCAAGCCCA 720
DB 664 CTGCTTTCTGCTCATCCAGAGAAATCGCTCCAACTACTAGATGCTTACCAAGCCCA 723
QY 721 ACCCTTGGCCACAGAGAGCTTCCAGAGCTTCCAGAGCTTCCAGAGCTTCCAGAGCTT 780
DB 724 ACCCTTGGCCACAGAGAGCTTCCAGAGCTTCCAGAGCTTCCAGAGCTTCCAGAGCTT 783
QY 781 CAATTCTTACAGCTGACAGGGATATGTGTGAGAGAACAGAGGGGCGAGAGCTGAGGGGTGGC 840
DB 784 CAATTCTTACAGCTGACAGGGATATGTGTGAGAGAACAGAGGGGCGAGAGCTGAGGGGTGGC 843
QY 841 TGGGCTGTGAGAAAAAGTGGACAGCAAGCCGAGGGGCGAGAGCTGAGGGGCACTACCACT 900
DB 844 TGGGCTGTGAGAAAAAGTGGACAGCAAGCCGAGGGGCGAGAGCTGAGGGGCACTACCACT 903
QY 901 GGAATCGTGCAGAGAGGCTGCTGAGAGATAGACTGATTTGGCCATTGAGTGAAGCAAG 960
DB 904 GGAATCGTGCAGAGAGGCTGCTGAGAGATAGACTGATTTGGCCATTGAGTGAAGCAAG 963
QY 961 GCAGAAATGGGGGCTAGTGTAAAGAGATGAGAGTGAATGCAAGAGTCTGCGCATGC 1020
DB 964 GCAGAAATGGGGGCTAGTGTAAAGAGATGAGAGTGAATGCAAGAGTCTGCGCATGC 1023
QY 1021 CAGCTTTCTGTTTCTCACTTGTGCTGCTCCCTGCTTAAATGCTCCCAAGCTTCACTT 1080
DB 1024 CAGCTTTCTGTTTCTCACTTGTGCTGCTCCCTGCTTAAATGCTCCCAAGCTTCACTT 1083
QY 1081 GAAACCCCATTTCTTAAAGCAGAGATCAGAGAGATCCCTTGGCTGAGTTTACCTGGG 1140
DB 1084 GAAACCCCATTTCTTAAAGCAGAGATCAGAGAGATCCCTTGGCTGAGTTTACCTGGG 1143
QY 1141 ACTTCATCTCCCAAAAGCAGATATCAATCCCACTGAGTGAAGCTTGTGATCAAGAGCC 1200
DB 1144 ACTTCATCTCCCAAAAGCAGATATCAATCCCACTGAGTGAAGCTTGTGATCAAGAGCC 1203
QY 1201 TCTCTGCTGAGTGGCTCTTAACTTCTGAGTCTGAGGAGTGGAGAGAGAGAGTGGC 1260
DB 1204 TCTCTGCTGAGTGGCTCTTAACTTCTGAGTCTGAGGAGTGGAGAGAGAGAGTGGC 1263
QY 1261 TTTTGTGGGAGTGGCTTAACTTCTGAGTCTTCCCTCAAGAGAGAGAGTGGGCC 1320
DB 1264 TTTTGTGGGAGTGGCTTAACTTCTGAGTCTTCCCTCAAGAGAGAGAGTGGGCC 1323
QY 1321 TGGAACTCCATCCCACTTGTATGATCTCAAGTGTCCAGACTAATTTGTGATGAA 1380
DB 1324 TGGAACTCCATCCCACTTGTATGATCTCAAGTGTCCAGACTAATTTGTGATGAA 1383
QY 1381 CTGAATTAACATCTTACGGTATCAAGGAGACAGAAAGAGATGAGATGGAGGA 1440
DB 1384 CTGAATTAACATCTTACGGTATCAAGGAGACAGAAAGAGATGAGATGGAGGA 1443
QY 1441 CAGGAGGCGAGCTGGGACATTTTAAAAATA 1472
DB 1444 CAGGAGGCGAGCTGGGACATTTTAAAAATA 1475

RESULT 10

US-10-063-569-79
; Sequence 79, Application US/10063569
; Publication No. US20030018168A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Pivaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,569
CURRENT FILING DATE: 2002-05-02
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 79
LENGTH: 1475
TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-569-79

Query Match 53.7%; Score 1472; DB 14; Length 1475;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAGGCTGGCAGAGAGACTTGAATATGAGGAGATTAGAGTTCAGAGAGCAGA 60
DB 4 AGAAGTCAGGCTGGCAGAGAGACTTGAATATGAGGAGATTAGAGTTCAGAGAGCAGA 63
QY 61 GCTTACAGCTGAAAGACAGAGAGAGTCCCTGAAAGCGCTTCTACTGAGAGTCTGCCAT 120
DB 64 GCTTACAGCTGAAAGACAGAGAGAGTCCCTGAAAGCGCTTCTACTGAGAGTCTGCCAT 123
QY 121 GGCCTCTTGGGCTCCAACTTGTGGGCTACATCTTACGCTTCTGAGGCTTTTGGGCA 180
DB 124 GGCCTCTTGGGCTCCAACTTGTGGGCTACATCTTACGCTTCTGAGGCTTTTGGGCA 183
QY 181 ACTGTTGACATGCTCTCCCGAGCTGAGAAACAAATTTCTATGTCGGTGCAGACTTGT 240
DB 184 ACTGTTGACATGCTCTCCCGAGCTGAGAAACAAATTTCTATGTCGGTGCAGACTTGT 243
QY 241 GACAGAGTGGCTTTCAGAGGGGCTGTGATGAAATGTGCCACACAGACAGAGCAT 300
DB 244 GACAGAGTGGCTTTCAGAGGGGCTGTGATGAAATGTGCCACACAGACAGAGCAT 303
QY 301 CACCCAGTGTGACATCTATAGACACCTTCTGGGCTGCGCCGCTGACATCAGGCTGCCA 360
DB 304 CACCCAGTGTGACATCTATAGACACCTTCTGGGCTGCGCCGCTGACATCAGGCTGCCA 363
QY 361 GGCAGATATGATGACATCAGATGACATCTCTCCCTGAGCTGATATCTCTGTGGTGG 420
DB 364 GGCAGATATGATGACATCAGATGACATCTCTCCCTGAGCTGATATCTCTGTGGTGG 423
QY 421 CATGAGATGACAGTCTTTCAGAGGAATCCGAGCCAAAGACAGATGAGGCTGACAG 480
DB 424 CATGAGATGACAGTCTTTCAGAGGAATCCGAGCCAAAGACAGATGAGGCTGACAG 483
QY 481 TGAAGTCTTTTCAATCTTGAAGGCTCTGAGATTCATCTCTGTTGCTGGAATCTTGA 540
DB 484 TGAAGTCTTTTCAATCTTGAAGGCTCTGAGATTCATCTCTGTTGCTGGAATCTTGA 543
QY 541 TGGGATCTTACGAGGACTTCTCACTCACTGAGTGTCTGACAGATGAAATTTGAGATTGG 600
DB 544 TGGGATCTTACGAGGACTTCTCACTCACTGAGTGTCTGACAGATGAAATTTGAGATTGG 603
QY 601 AGAGGCTCTTACTTGGGCAATATTTCTTCCCTGTTCTCCCTGATATGCTGAATCTCT 660
DB 604 AGAGGCTCTTACTTGGGCAATATTTCTTCCCTGTTCTCCCTGATATGCTGAATCTCT 663
QY 661 CTGCTTTTCTGCTCATCCAGAGAAATGGCTCCAACTTACGAATGCTTACCAAGCCCA 720
DB 664 CTGCTTTTCTGCTCATCCAGAGAAATGGCTCCAACTTACGAATGCTTACCAAGCCCA 723
QY 721 ACCCTTGGCCACAGAGAGCTTCCAGAGCTTCCAGAGCTTCCAGAGCTTCCAGAGCTT 780
DB 724 ACCCTTGGCCACAGAGAGCTTCCAGAGCTTCCAGAGCTTCCAGAGCTTCCAGAGCTT 783
QY 781 CAATTCTTACAGCTGACAGGGATATGTGTGAGAGAACAGAGGGGCGAGAGTCTGAGGGTGGC 840
DB 784 CAATTCTTACAGCTGACAGGGATATGTGTGAGAGAACAGAGGGGCGAGAGTCTGAGGGTGGC 843
QY 841 TGGGCTGTGAGAAAAAGTGGACAGCAAGCCGAGGGGCGAGAGCTGAGGGGCACTACCACT 900

QY 1081 GAAACCCATTCCTTAAGCAGAGACTCAGAGATCCCTTGGCTTGTTACTGGG 1140
 DB 1084 GAAACCCATTCCTTAAGCAGAGACTCAGAGATCCCTTGGCTTGTTACTGGG 1143
 QY 1141 ACTCCATCCCAAAACCACTAATCAATCCCACTGAACCCCTGTGTATCAAGAACC 1200
 DB 1144 ACTCCATCCCAAAACCACTAATCAATCCCACTGAACCCCTGTGTATCAAGAACC 1203
 QY 1201 TCTCTGAGTGAAGTGGCTCTTAAGCTCATTTGCTGGAGATGGAGAGAGAGTGGC 1260
 DB 1204 TCTCTGAGTGAAGTGGCTCTTAAGCTCATTTGCTGGAGATGGAGAGAGTGGC 1263
 QY 1261 TTTTGTGGGATGCTCTTAACCTTAAGCTCTCAAGCTTCCCTCAAGAACTGAATGGCCC 1320
 DB 1264 TTTTGTGGGATGCTCTTAACCTTAAGCTCTCAAGCTTCCCTCAAGAACTGAATGGCCC 1323
 QY 1321 TGAACCTCATCCACTCTTTTATATGATCCACAGTCCAGCTAATTTGGCATGAA 1380
 DB 1324 TGAACCTCATCCACTCTTTTATATGATCCACAGTCCAGCTAATTTGGCATGAA 1383
 QY 1381 CTGAATATAAACCTCTTACGCTATCCAGGAAACAGAAACAGAGATGAGATGGAGGA 1440
 DB 1384 CTGAATATAAACCTCTTACGCTATCCAGGAAACAGAAACAGAGATGAGATGGAGGA 1443
 QY 1441 CAGGAAGGCGCTGGGACATTTAAAAATA 1472
 DB 1444 CAGGAAGGCGCTGGGACATTTAAAAATA 1475

RESULT 12
 US-10-063-515-79
 ; Sequence 79, Application US/10063515
 ; Publication No. US20030018173A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ealon, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerltsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Metanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3230R1C1
 ; CURRENT APPLICATION NUMBER: US/10/063,515
 ; CURRENT FILING DATE: 2002-05-01
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 79
 ; LENGTH: 1475
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-10-063-515-79

Query Match 53.7%; Score 1472; DB 14; Length 1475;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTAGCTGGCAGAGAGACTCTGAATAGAGGATTAGAGTGTTCAGAGCAAGA 60
 DB 4 AGAAGTAGCTGGCAGAGAGACTCTGAATAGAGGATTAGAGTGTTCAGAGCAAGA 63
 QY 61 GCTTCAGCTGAAGACAAAGGAGAGAGTCCCTGAAGAGCTTCTAAGAGGTCTGGCAT 120
 DB 64 GCTTCAGCTGAAGACAAAGGAGAGAGTCCCTGAAGAGCTTCTAAGAGGTCTGGCAT 123
 QY 121 GGGCTCTCTTGGCTCTCAACTTGTGGCTATCATCTTGAAGGCTTCTGGGGCTTTTGGGAC 180
 DB 124 GGGCTCTCTTGGCTCTCAACTTGTGGCTATCATCTTGAAGGCTTCTGGGGCTTTTGGGAC 183
 QY 181 ACTGTGGCATGTGCTCTCCCGAGCTGAAAAAAAGATTCTTAATGTGGTCCAGCATTTGT 240

DB 184 ACTGTGGCATGTGCTCTCCCGAGCTGAAAAAAAGATTCTTAATGTGGTCCAGCATTTGT 243
 QY 241 GACAGAGTGTGGCTTCTCAAGAGGCTCTGATATGATATGCAACACAGACAGAGCAT 300
 DB 244 GACAGAGTGTGGCTTCTCAAGAGGCTCTGATATGATATGCAACACAGACAGAGCAT 303
 QY 301 CACCAAGTGAATATATAGCAACCTTGTGGGCTCTGGCCGCTGATCATCAGGCTGCCA 360
 DB 304 CACCAAGTGAATATATAGCAACCTTGTGGGCTCTGGCCGCTGATCATCAGGCTGCCA 363
 QY 361 GGGCATGATGATGATATCAAGATGCAATCTCCCTGGGCTGATATATCTGTGGTGGG 420
 DB 364 GGGCATGATGATGATATCAAGATGCAATCTCCCTGGGCTGATATATCTGTGGTGGG 423
 QY 421 CATGATATCAAGTCTTCTGCAAGAAATCCGAGCAAAAGACAGATGGGCTGACAG 480
 DB 424 CATGATATCAAGTCTTCTGCAAGAAATCCGAGCAAAAGACAGATGGGCTGACAG 483
 QY 481 TGAAGTCTTTTCAATCTTGAAGGCTCTGGGATCATTTCTGTCTGATATTTCA 540
 DB 484 TGAAGTCTTTTCAATCTTGAAGGCTCTGGGATCATTTCTGTCTGATATTTCA 543
 QY 541 TGGGATCTAAGGGAATTTCACTCAACAGTGGGCTGACAGATGAAATTTGAGATTGG 600
 DB 544 TGGGATCTAAGGGAATTTCACTCAACAGTGGGCTGACAGATGAAATTTGAGATTGG 603
 QY 601 AGAGGCTCTTACTTGGGATTAATTTCTTCCCTGTCTCTGATATGATGATATCTCT 660
 DB 604 AGAGGCTCTTACTTGGGATTAATTTCTTCCCTGTCTCTGATATGATGATATCTCT 663
 QY 661 CTGCTTTTCTGCTATCTCCAGAGAAATGCTTCAACTATACATGCTTACCAAGCCA 720
 DB 664 CTGCTTTTCTGCTATCTCCAGAGAAATGCTTCAACTATACATGCTTACCAAGCCA 723
 QY 721 ACCTCTTGCAAGAGGCTCTCAAGGCTGGTCAACCTCCAAAGTCAAGATGAGTT 780
 DB 724 ACCTCTTGCAAGAGGCTCTCAAGGCTGGTCAACCTCCAAAGTCAAGATGAGTT 783
 QY 781 CAATTCCTACAGCTGACAGGATATGTGAAGAACAGAGGCTGAGGCTGGGCTGGC 840
 DB 784 CAATTCCTACAGCTGACAGGATATGTGAAGAACAGAGGCTGAGGCTGGGCTGGC 843
 QY 841 TGGGCTGTGAAGAAACAGTGAACAGACCCCGAGGCTCAAGGTGAGGACACTTACACT 900
 DB 844 TGGGCTGTGAAGAAACAGTGAACAGACCCCGAGGCTCAAGGTGAGGACACTTACACT 903
 QY 901 GATTCGTGCAAGAGTGTGCTGAGATGATGATGCTTGGCATTTGATGAGCAAG 960
 DB 904 GATTCGTGCAAGAGTGTGCTGAGATGATGATGCTTGGCATTTGATGAGCAAG 963
 QY 961 GCAGAAATGGGGCTATGATTAACAGCATCAGATGTAATTTGCCAAGATGCTGGCATGC 1020
 DB 964 GCAGAAATGGGGCTATGATTAACAGCATCAGATGTAATTTGCCAAGATGCTGGCATGC 1023
 QY 1021 CAGCTTTCTGTTTCTCACTTGTCTGCTCCCTGCTCAAGTCCCAACCTCAACTT 1080
 DB 1024 CAGCTTTCTGTTTCTCACTTGTCTGCTCCCTGCTCAAGTCCCAACCTCAACTT 1083
 QY 1081 GAAACCCATTCCTTAAGCAGAGACTCAGAGGATCCCTTGGCCCTGATTTTAACTGGG 1140
 DB 1084 GAAACCCATTCCTTAAGCAGAGACTCAGAGGATCCCTTGGCCCTGATTTTAACTGGG 1143
 QY 1141 ACTCCATCCCAAAACCACTAATCAATCCCACTGAACCCCTGTGTATCAAGAACC 1200
 DB 1144 ACTCCATCCCAAAACCACTAATCAATCCCACTGAACCCCTGTGTATCAAGAACC 1203
 QY 1201 TCTCTGAGTGAAGTGGCTCTTAAGCTCATTTGCTGGAGATGGAGAGAGACAGTGGC 1260
 DB 1204 TCTCTGAGTGAAGTGGCTCTTAAGCTCATTTGCTGGAGATGGAGAGAGACAGTGGC 1263
 QY 1261 TTTTGTGGGATGCTCTTAACCTTAAGCTCTCAAGCTTCCCTCAAGAACTGAATGGGCC 1320

Db 1264 TTTTGGGCACTTGTCTAACCCTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCC 1323
 Qy 1321 TGAACCTCCATCCCACTCTTGTATGATCCAGAGTCCAGACTAATTTGTGCAATA 1380
 Db 1324 TGAACCTCCATCCCACTCTTGTATGATCCAGAGTCCAGACTAATTTGTGCAATA 1383
 Qy 1381 CTGAATTAACCACTCTTGTATGATCCAGAGTCCAGAGTCCAGACTAATTTGTGCAATA 1440
 Db 1384 CTGAATTAACCACTCTTGTATGATCCAGAGTCCAGAGTCCAGACTAATTTGTGCAATA 1443
 Qy 1441 CAGGAAGGCAAGCTTGGGCAATTTAAATAAATA 1472
 Db 1444 CAGGAAGGCAAGCTTGGGCAATTTAAATAAATA 1475

RESULT 13

US-10-063-512-79
 ; Sequence 79, Application US/10063512
 ; Publication No. US20030018183A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3230R1C1
 ; CURRENT APPLICATION NUMBER: US/10/063.512
 ; PRIORITY FILING DATE: 2002-05-01
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 79
 ; LENGTH: 1475
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-10-063-512-79

Query Match 53.7%; Score 1472; DB 14; Length 1475;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAAGTCAGCTTGGCAGAGAGACTCTGAATGAGGATTTAGAGTGTTCAGAGCAAGA 60
 Db 4 AGAAGTCAGCTTGGCAGAGAGACTCTGAATGAGGATTTAGAGTGTTCAGAGCAAGA 63
 Qy 61 GCTTCAGCTTGAAGCAAGGAGAGAGCTCCAGAGAGCTTCTAAGAGTGTTCAGAGCAAGA 120
 Db 64 GCTTCAGCTTGAAGCAAGGAGAGAGCTCCAGAGAGCTTCTAAGAGTGTTCAGAGCAAGA 123
 Qy 121 GGCCTCTCTTGGCTTCCAACTTGTGAGCTACATCTTGAAGCTTGTGAGGCTTTTGGGAC 180
 Db 124 GGCCTCTCTTGGCTTCCAACTTGTGAGCTACATCTTGAAGCTTGTGAGGCTTTTGGGAC 183
 Qy 181 ACTGTTGCTTGGCTTCCAACTTGTGAGCTACATCTTGAAGCTTGTGAGGCTTTTGGGAC 240
 Db 184 ACTGTTGCTTGGCTTCCAACTTGTGAGCTACATCTTGAAGCTTGTGAGGCTTTTGGGAC 243
 Qy 241 GAGCAGAGTGGCTTCTCCAAAGGCTCTGAGTGAATGTGACCAAGCAGAGGAT 300
 Db 244 GAGCAGAGTGGCTTCTCCAAAGGCTCTGAGTGAATGTGACCAAGCAGAGGAT 303
 Qy 301 CACCAAGTGTGACATCTTAAGCAAGCTTGTGAGCTTGTGAGGCTTGTGAGGCTTGTGAGG 360
 Db 304 CACCAAGTGTGACATCTTAAGCAAGCTTGTGAGCTTGTGAGGCTTGTGAGGCTTGTGAGG 363
 Qy 361 GGCATGATGTGACATCTTAAGCAAGCTTGTGAGCTTGTGAGGCTTGTGAGGCTTGTGAGG 420
 Db 364 GGCATGATGTGACATCTTAAGCAAGCTTGTGAGCTTGTGAGGCTTGTGAGGCTTGTGAGG 423

Qy 421 CATGAGATGACAGACTCTTGTGAGAGATCCGAGCCAAAGACAGAGTGGCGGTAGCAGG 480
 Db 424 CATGAGATGACAGACTCTTGTGAGAGATCCGAGCCAAAGACAGAGTGGCGGTAGCAGG 483
 Qy 481 TGAAGTCTTTTCACTCTTGAAGGCTTCTGAGATTTATCTTGTGCTTGTGCAATCTTCA 540
 Db 484 TGAAGTCTTTTCACTCTTGAAGGCTTCTGAGATTTATCTTGTGCTTGTGCAATCTTCA 543
 Qy 541 TGGATCTCTACGGGACTTCTACTACAGCACTGTGCTGAGAGATTTGAGATTGG 600
 Db 544 TGGATCTCTACGGGACTTCTACTACAGCACTGTGCTGAGAGATTTGAGATTGG 603
 Qy 601 AGAGGCTCTTACTTGTGAGCAATTTCTTCTGCTTCTGCTGATGAGTGAATCATCT 660
 Db 604 AGAGGCTCTTACTTGTGAGCAATTTCTTCTGCTTCTGCTGATGAGTGAATCATCT 663
 Qy 661 CTGCTTTTCTGCTCATCTCCAGAGAAATGCTCTCAACTTACAGATGCTTCAAGCCCA 720
 Db 664 CTGCTTTTCTGCTCATCTCCAGAGAAATGCTCTCAACTTACAGATGCTTCAAGCCCA 723
 Qy 721 ACCCTTGGCAAGAGGCTCTCCAGAGGCTGCTGCAAGCTTCCCAAGTCAAGAGTGT 780
 Db 724 ACCCTTGGCAAGAGGCTCTCCAGAGGCTGCTGCAAGCTTCCCAAGTCAAGAGTGT 783
 Qy 781 CAATTCTTACAGCTTGAAGGATGATGTAAGAACAGAGGCTGAGGCTGAGGCTGAGG 840
 Db 784 CAATTCTTACAGCTTGAAGGATGATGTAAGAACAGAGGCTGAGGCTGAGGCTGAGG 843
 Qy 841 TGGCTCTGTAAGAAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
 Db 844 TGGCTCTGTAAGAAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 903
 Qy 901 GGAATGCTGTAAG 960
 Db 904 GGAATGCTGTAAG 963
 Qy 961 GCAAGAAATGGGAGCTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
 Db 964 GCAAGAAATGGGAGCTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1023
 Qy 1021 CAGCTTGTGTTTCTCTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
 Db 1024 CAGCTTGTGTTTCTCTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083
 Qy 1081 GAAACCCATTTCTTGAAG 1140
 Db 1084 GAAACCCATTTCTTGAAG 1143
 Qy 1141 ACTCATCTCCCAAG 1200
 Db 1144 ACTCATCTCCCAAG 1203
 Qy 1201 TCTCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1260
 Db 1204 TCTCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1263
 Qy 1261 TTTTGTGAGCAATGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCA 1320
 Db 1264 TTTTGTGAGCAATGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCA 1323
 Qy 1321 TGGAACTCTCATCCCACTTCTTGTATGATCCAGAGTCCAGAGTCAAGTCAATTTGTGAG 1380
 Db 1324 TGGAACTCTCATCCCACTTCTTGTATGATCCAGAGTCCAGAGTCAAGTCAATTTGTGAG 1383
 Qy 1381 CTGAATTAACCACTCTTGAAGGATGATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
 Db 1384 CTGAATTAACCACTCTTGAAGGATGATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1443
 Qy 1441 CAGGAAGGCAAGCTTGGGCAATTTAAATAAATA 1472
 Db 1444 CAGGAAGGCAAGCTTGGGCAATTTAAATAAATA 1475

RESULT 14
US-10-121-049-491
; Sequence 491, Application US/10121049
; Publication No. US2003002239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; PRIORITY FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 491
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-121-049-491

Query Match 53.7%; Score 1472; DB 14; Length 1475;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTACGCTGGCAGAGACTCTGAATAGAGGATGAGGTTCAGAGGAGAGA 60
DB 4 AGAAGTACGCTGGCAGAGAGACTCTGAATAGAGGATGAGGTTCAGAGGAGAGA 63
QY 61 GCTTCAAGCTGAGAGAGAGGAGAGTCCCTGAGAGAGCTTCTACTGAGAGTCTGCCAT 120
DB 64 GCTTCAAGCTGAGAGAGAGGAGAGTCCCTGAGAGAGCTTCTACTGAGAGTCTGCCAT 123
QY 121 GGCCTCTCTTGGCCTCCAACTTGTGGGCTACATCTAAGGCTTCTGGGGCTTTTGGGCAC 180
DB 124 GGCCTCTCTTGGCCTCCAACTTGTGGGCTACATCTAAGGCTTCTGGGGCTTTTGGGCAC 183
QY 181 ACTGTTGGCCATGCTGTCTCCCACTGAGAAACAAAGTTCTTAATGCTGGTCCAGCATTTGT 240
DB 184 ACTGTTGGCCATGCTGTCTCCCACTGAGAAACAAAGTTCTTAATGCTGGTCCAGCATTTGT 243
QY 241 GACAGCAGTTGGCTTCTTCCAGAGGCTCTGGATGGAATGTCACACAGACAGACAGGAT 300
DB 244 GACAGCAGTTGGCTTCTTCCAGAGGCTCTGGATGGAATGTCACACAGACAGGAT 303
QY 301 CACCAAGTGTGACATCTAATAGCACTTCTGGGCTGCGCTGACATCCAGGCTGGCCA 360
DB 304 CACCAAGTGTGACATCTAATAGCACTTCTGGGCTGCGCTGACATCCAGGCTGGCCA 363
QY 361 GGCCTATATGTCATCTGTCAGTCAGTCATCTCTCTGCTGGCTGCTATTTCTGTGGTGGG 420
DB 364 GGCCTATATGTCATCTGTCAGTCAGTCATCTCTCTGCTGGCTGCTATTTCTGTGGTGGG 423
QY 421 CATGAGATGACAGTCTTCTGTCAGAGAAATCCCGAGCAAGAGAGAGAGGAGGAGG 480
DB 424 CATGAGATGACAGTCTTCTGTCAGAGAAATCCCGAGCAAGAGAGAGAGGAGGAGG 483
QY 481 TGAAGTCTTTTTCATCTCTGGAGGCTCTCGGATTCATTCCTGTTGCTGGAATCTTCA 540

DB 484 TGAAGTCTTTTTCATCTCTGGAGGCTCTCGGATTCATTCCTGTTGCTGGAATCTTCA 543
QY 541 TGGGATCTACAGGAGCTTCTACTACCACTGTGTGCTGACAGATGAATTTGAGATTGG 600
DB 544 TGGGATCTACAGGAGCTTCTACTACCACTGTGTGCTGACAGATGAATTTGAGATTGG 603
QY 601 AGAGGCTCTTTTACTTGGGCAATTAATTTCTCCCTGTCTCCCTGATATGCTGGAATCTCT 660
DB 604 AGAGGCTCTTTTACTTGGGCAATTAATTTCTCCCTGTCTCCCTGATATGCTGGAATCTCT 663
QY 661 CTGCTTTCTGCTGCTACCTCCAGAGAAATGCTCCAACTACTAGATGCTTACCAAGCCCA 720
DB 664 CTGCTTTCTGCTGCTACCTCCAGAGAAATGCTCCAACTACTAGATGCTTACCAAGCCCA 723
QY 721 ACCTTGTGCCACAGAGAGCTCTCCAGAGGCTGTGTCAACTCCCAAGTCAAGATGAGTT 780
DB 724 ACCTTGTGCCACAGAGAGCTCTCCAGAGGCTGTGTCAACTCCCAAGTCAAGATGAGTT 783
QY 781 CAATTCCTACAGCTTGAACAGGATATGTGTGAAGAACCAAGGAGCAGAGCTGGGGGTGGC 840
DB 784 CAATTCCTACAGCTTGAACAGGATATGTGTGAAGAACCAAGGAGCAGAGCTGGGGGTGGC 843
QY 841 TGGGTCTGTGAAGAAAGATGAGACAGCAACCCGAGGGCCACAGGTGAGGACACTACACT 900
DB 844 TGGGTCTGTGAAGAAAGATGAGACAGCAACCCGAGGGCCACAGGTGAGGACACTACACT 903
QY 901 GGAATGTCAGAGAGTGTGTGCTGAGAGATGACTGACTTTTGGCCATTGATGAGCAAG 960
DB 904 GGAATGTCAGAGAGTGTGTGCTGAGAGATGACTGACTTTTGGCCATTGATGAGCAAG 963
QY 961 GCAAGAAATGGGGGCTATGTGTAACAGCATGAGGTGAATTTGCCAGAGATCTGCCATGC 1020
DB 964 GCAAGAAATGGGGGCTATGTGTAACAGCATGAGGTGAATTTGCCAGAGATCTGCCATGC 1023
QY 1021 CAGCCTTCTGTTTCTCTCACTGCTGCTGCTCCCTGAGGCTTCCCAAGTCCCAAGCTCACTT 1080
DB 1024 CAGCCTTCTGTTTCTCTCACTGCTGCTGCTCCCTGAGGCTTCCCAAGTCCCAAGCTCACTT 1083
QY 1081 GAAACCCCAATCCCTTAAAGCAGAGACTCAGAGAGATCCCTTGGCTTCTGATTAACCTGAG 1140
DB 1084 GAAACCCCAATCCCTTAAAGCAGAGACTCAGAGAGATCCCTTGGCTTCTGATTAACCTGAG 1143
QY 1141 ACTTCATCCCAAGCCCAATCAATCACTCACTCACTGACTGACTGCTGTGATCAAGACCC 1200
DB 1144 ACTTCATCCCAAGCCCAATCAATCACTCACTCACTGACTGACTGCTGTGATCAAGACCC 1203
QY 1201 TCTCTCTGCTGAGTGTGTGCTCTTACTCAATGCTGTGGGATGAGGAGAGAGAGTGGC 1260
DB 1204 TCTCTCTGCTGAGTGTGTGCTCTTACTCAATGCTGTGGGATGAGGAGAGAGAGTGGC 1263
QY 1261 TTTTGTGGGCAATGCTCTAAGCTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCC 1320
DB 1264 TTTTGTGGGCAATGCTCTAAGCTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCC 1323
QY 1321 TGAACCTCCATCCCACTCTTGTATGACTCCACAGTGTCCAGACTAATTTGTGATGA 1380
DB 1324 TGAACCTCCATCCCACTCTTGTATGACTCCACAGTGTCCAGACTAATTTGTGATGA 1383
QY 1381 CTGAATTAAGAACTCTTACGATATCCAGGAAACAGAAAGCAGATGCGAGATGGAGGA 1440
DB 1384 CTGAATTAAGAACTCTTACGATATCCAGGAAACAGAAAGCAGATGCGAGATGGAGGA 1443
QY 1441 CAGGAAGGAGGCTGGGACATTTAAATAATA 1472
DB 1444 CAGGAAGGAGGCTGGGACATTTAAATAATA 1475

RESULT 15
US-10-123-904-491
; Sequence 491, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
 APPLICANT: Beresini, Maureen
 APPLICANT: DeForge, Laura
 APPLICANT: Desnoyers, Luc
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Geriltsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Matanabe, Colin K
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 TITLE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P330R1C54
 CURRENT APPLICATION NUMBER: US/10/123,904
 CURRENT FILING DATE: 2002-04-16
 Prior Application removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 550
 SEQ ID NO 491
 LENGTH: 1475
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-123-904-491

Query Match 53.7%; Score 1472; DB 14; Length 1475;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGAAGTCAGCTGGCAGAGAGACTCTGAATGAGGATTAAGAGTGTTCAGAGCAAGA 60
 4 AGAAGTCAGCTGGCAGAGAGACTCTGAATGAGGATTAAGAGTGTTCAGAGCAAGA 63
 61 GCTTCAGCTGGCAG 120
 64 GCTTCAGCTGGCAG 123
 121 GGCCTCTCTGGCCTCCAGCTTGGGCTAATCTTGAAGCTTCTGGGCTTCTTGGGAC 180
 124 GGCCTCTCTGGCCTCCAGCTTGGGCTAATCTTGAAGCTTCTGGGCTTCTTGGGAC 183
 181 ACTGTTGTCATGCTGCTCCAGCTGAGAAACAAAGTTTATATGTCGATGTCAGATTTG 240
 184 ACTGTTGTCATGCTGCTCCAGCTGAGAAACAAAGTTTATATGTCGATGTCAGATTTG 243
 241 GACAGAGTGGCTTCTCCAGAGGCTCTGATGGAATGTCACACACAGACAGAGCAT 300
 244 GACAGAGTGGCTTCTCCAGAGGCTCTGATGGAATGTCACACACAGAGCAT 303
 301 CACCAAGTGAACATCTATAGCACTTCTGGGCTGCGCTGACATCCAGGCTGCGCA 360
 304 CACCAAGTGAACATCTATAGCACTTCTGGGCTGCGCTGACATCCAGGCTGCGCA 363
 361 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 364 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 423
 421 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
 424 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 483
 481 TGAGATCTTTTCACTCTGAGAGGCTCTGAGATTCATTCCTGTCCTGAAATCTTCA 540
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 541 TGAGATCTTTTCACTCTGAGAGGCTCTGAGATTCATTCCTGTCCTGAAATCTTCA 600
 544 TGAGATCTTTTCACTCTGAGAGGCTCTGAGATTCATTCCTGTCCTGAAATCTTCA 603

601 AGAGGCTCTTTAATTGGGCAATTAATTTCTTCCCTGTTCTCCCTGATGAGTGAATCACT 660
 604 AGAGGCTCTTTAATTGGGCAATTAATTTCTTCCCTGTTCTCCCTGATGAGTGAATCACT 663
 661 CTGCTTTTCTGCTCATCCAGAGAAATGCTCAACTAATGATGCTTCAAGGCCA 720
 664 CTGCTTTTCTGCTCATCCAGAGAAATGCTCAACTAATGATGCTTCAAGGCCA 723
 721 ACCTTTCGCAAGAGAGCTTCCAGAGGCTGCTCAACTCCCAAGTCAAGGATGAT 780
 724 ACCTTTCGCAAGAGAGCTTCCAGAGGCTGCTCAACTCCCAAGTCAAGGATGAT 783
 781 CAATTCCTACAGCTGACAGGATGATGATGATGATGATGATGATGATGATGATGAT 840
 784 CAATTCCTACAGCTGACAGGATGATGATGATGATGATGATGATGATGATGATGAT 843
 841 TGAGTCTGTGAAACAGTGAACAGACACCCCGAGGCCACAGGTGAGGACACTCACT 900
 844 TGAGTCTGTGAAACAGTGAACAGACACCCCGAGGCCACAGGTGAGGACACTCACT 903
 901 GATTCGTGCAAGAGAGTGTGCTGAGATGATGATGATGATGATGATGATGATGATG 960
 904 GATTCGTGCAAGAGAGTGTGCTGAGATGATGATGATGATGATGATGATGATGATG 963
 961 GCAAAATGAGGAGCTAGTGAACAGATGATGATGATGATGATGATGATGATGATGATG 1020
 964 GCAAAATGAGGAGCTAGTGAACAGATGATGATGATGATGATGATGATGATGATGATG 1023
 1021 CAGCTTTTCTGTTTCTCACTGCTGCTCCCTGCTCCCTGATGATGATGATGATGAT 1080
 1024 CAGCTTTTCTGTTTCTCACTGCTGCTCCCTGCTCCCTGATGATGATGATGATGAT 1083
 1081 GAAACCCCATTCCTTTAAGCAGAGACTCAGAGATTCCTTTGCTGCTGTTTACTG 1140
 1084 GAAACCCCATTCCTTTAAGCAGAGACTCAGAGATTCCTTTGCTGCTGTTTACTG 1143
 1141 ACTCAATCCCAACCAACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1200
 1144 ACTCAATCCCAACCAACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1203
 1201 TCTCTGCTGAGTGGCTTCTTGAATGATGATGATGATGATGATGATGATGATGATG 1260
 1204 TCTCTGCTGAGTGGCTTCTTGAATGATGATGATGATGATGATGATGATGATGATG 1263
 1261 TTTTGTGGGATGCTCTTAACTTCTTCAAGCTTCCCTCCAAAGAACTGATTTGGCCC 1320
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 1321 TGAACCTCCATCCCACTCTGTTATGATGATGATGATGATGATGATGATGATGATG 1380
 1324 TGAACCTCCATCCCACTCTGTTATGATGATGATGATGATGATGATGATGATGATG 1383
 1381 CTGAATTAATAACCATCTACGATATCAGGAAACAGAAAGCAGATGATGATGATG 1440
 1384 CTGAATTAATAACCATCTACGATATCAGGAAACAGAAAGCAGATGATGATGATG 1443
 1441 CAGGAAGCAGCTGGGACATTTAAAAATA 1472
 1444 CAGGAAGCAGCTGGGACATTTAAAAATA 1475

Search completed: October 30, 2004, 18:00:41
 Job time : 1798 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: October 28, 2004, 11:47:04 ; Search time 12495 Seconds
(without alignments)
7996.618 Million cell updates/sec

Title: US-09-787-677a-7

Sequence: 1 agaatgcagcctgcgcagaga.....ggtgatcaataatcctgac 2742

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 18219865908 residues

Word size : 20

Total number of hits satisfying chosen parameters: 936

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : EST.*

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_hic.*
- 4: gb_est3.*
- 5: gb_est4.*
- 6: gb_est5.*
- 7: gb_est6.*
- 8: gb_gsa1.*
- 9: gb_gsa2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	693	25.3	693	9 AY400251	AY400251 Homo sapi
2	690	25.2	832	4 BG386074	BG386074 602455248
3	643	23.5	680	2 BE304667	BE304667 601105783
4	588	21.4	693	9 AY400252	AY400252 Pan trogl
5	582	21.2	589	5 BU071883	BU071883 im5d11.y
6	572	20.9	662	4 BU0791379	BU0791379 K-EST0071
7	555	20.2	555	5 BU073403	BU073403 im5d11.x
8	537	19.6	728	4 BG325755	BG325755 602424466
9	500	18.2	810	4 BG427780	BG427780 602497154
10	493	18.0	494	4 BG385562	BG385562 602453858
11	491	17.9	945	2 BE513091	BE513091 601171545
12	474	17.3	788	6 CB999779	CB999779 AGENCOURT
13	468	17.1	485	5 BU073420	BU073420 im5f11.x
14	459	16.7	459	1 AA552647	AA552647 nk14b01.8
15	457	16.7	459	6 CA389170	CA389170 c806d06.y
16	457	16.7	464	5 BX096908	BX096908 BX096908
17	440	16.0	978	4 BG164062	BG164062 602341087
18	433	15.8	546	2 BF819923	BF819923 MRI-RT002
19	424	15.5	477	4 BF819108	BF819108 K-EST0070
20	420	15.3	420	1 AI343787	AI343787 qp12b03.x
21	420	15.3	557	4 BG399901	BG399901 602441435
22	420	15.3	623	2 AW837724	AW837724 CML-LT004
23	408	14.9	1025	2 BE249990	BE249990 600943168
24	407	14.8	407	1 AI285131	AI285131 gk57a09.x

C 25	403	14.7	448	1 AA973123	AA973123 OP45F04.8
C 26	394	14.4	511	1 AM006504	AM006504 w05e05.x
C 27	373	13.6	374	2 AW351531	AW351531 IL2-CT003
C 28	350	12.8	652	7 CR628947	CR628947 DKFZp469L
C 29	349	12.7	650	7 CR546700	CR546700 DKFZp470L
C 30	348	12.7	424	2 AM361715	AM361715 PM0-CT026
C 31	334	12.2	446	2 BE048787	BE048787 hr53e12.x
C 32	330	12.0	420	2 AM015998	AM015998 UI-H-B10P
C 33	323	11.8	341	4 BG985977	BG985977 CML-DT004
C 34	321	11.7	368	1 AI685788	AI685788 lu20f12.x
C 35	321	11.7	630	2 AM837727	AM837727 CML-LT004
C 36	313	11.4	391	2 AM083920	AM083920 xc25h04.x
C 37	307	11.2	420	5 BQ322242	BQ322242 RC4-CT084
C 38	302	11.0	302	1 AI469683	AI469683 cm2a03.x
C 39	301	11.0	301	1 AI244378	AI244378 qj76d10.x
C 40	300	10.9	300	1 AI659323	AI659323 lu29b10.x
C 41	300	10.9	300	1 AI685439	AI685439 t88c07.x
C 42	297	10.8	297	4 BM852012	BM852012 K-EST0133
C 43	294	10.7	336	1 AI949846	AI949846 wg14e11.x
C 44	290	10.6	1043	4 BG164241	BG164241 602341250
C 45	288	10.5	361	2 AW938611	AW938611 PM1-DT006

ALIGNMENTS

RESULT 1
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DEFINITION Homo sapiens C12D2 gene, VIRUAL TRANSCRIPT, partial sequence,
ACCESION AY400251
VERSION AY400251.1 GI:39756240
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shteynberg,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Inferred nonneutral evolution from human-chimp-mouse orthologous
Gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shteynberg,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment
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1. 693
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/gene="C12D2"
/locus_tag="HC0495"
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Query Match 25.3%; Score 693; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 ATGGCCCTCTCTGGCCCTCCAACTTGAGGGCTACATCCATAGGCTCTTGGGGCTTTTGGGC 60
QY 179 ACATGGTGGCCATGCTGTCTCCCAAGCTGGAAAAAGATTCTTATGTGGTCCAGCAT 238
Db 61 ACATGGTGGCCATGCTGTCTCCCAAGCTGGAAAAAGATTCTTATGTGGTCCAGCAT 120
QY 239 GTGACAGAGAGTGGCTTCTCCAAAGGGCTCTGTGATGGAATGTGCACACACAGCAGGC 238
Db 121 GTGACAGAGAGTGGCTTCTCCAAAGGGCTCTGTGATGGAATGTGCACACACAGCAGGC 180
QY 299 ATACACCAAGTGTACATCTTATAGCAACCTTCTGGGCTGCGCCGTGACATCCAGGCTGCC 358
Db 181 ATACACCAAGTGTACATCTTATAGCAACCTTCTGGGCTGCGCCGTGACATCCAGGCTGCC 240
QY 359 CAGGACCATGATGATGATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 418
Db 241 CAGGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 419 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 478
Db 301 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 479 GGTGAGATCTTTTATCTTCTTGAAGGCTCTGTGGATTCATCTCTGTGGCTGGAATCTT 538
Db 361 GGTGAGATCTTTTATCTTCTTGAAGGCTCTGTGGATTCATCTCTGTGGCTGGAATCTT 420
QY 539 CATGGATCTCTTACCTTCTTGAAGGCTCTGTGGATTCATCTCTGTGGCTGGAATCTT 598
Db 421 CATGGATCTCTTACCTTCTTGAAGGCTCTGTGGATTCATCTCTGTGGCTGGAATCTT 480
QY 599 GGAAGGCTCTTATCTTGAAGGCTCTGTGGATTCATCTCTGTGGCTGGAATCTT 658
Db 481 GGAAGGCTCTTATCTTGAAGGCTCTGTGGATTCATCTCTGTGGCTGGAATCTT 540
QY 659 CTCTGCTTTTCT 718
Db 541 CTCTGCTTTTCT 600
QY 719 CAACCTCTTCT 778
Db 601 CAACCTCTTCT 660
QY 779 TTCAATCTCTACAGCTCTGACAGGCTATGTGA 811
Db 661 TTCAATCTCTACAGCTCTGACAGGCTATGTGA 693

RESULT 2
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LOCUS 602455248F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4583675 5',
DEFINITION mRNA sequence.
ACCESSION BG386074
VERSION BG386074.1 GI:13279520
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 822)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
http://image.llnl.gov
Plate: L1CM1307 row: p column: 12

FEATURES
source High quality sequence stop: 746.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4583675"
/issue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 15"
/note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCAAGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN
Query Match 25.2%; Score 690; DB 4; Length 822;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGAAGTCAAGCTTGGCAGAGAGACTGTGAATAGGAGATTAGAGTCTTCAAGAGCAAGA 60
Db 9 AGAAGTCAAGCTTGGCAGAGAGACTGTGAATAGGAGATTAGAGTCTTCAAGAGCAAGA 68
QY 61 GCTTCAAGCTTGAAG 120
Db 69 GCTTCAAGCTTGAAG 128
QY 121 GGCCTCTCTTGGGCTCCAACTTGTGGGCTACATCTTGAAGGCTTCTTGGGCTTTTGGGCAC 180
Db 129 GGCCTCTCTTGGGCTCCAACTTGTGGGCTACATCTTGAAGGCTTCTTGGGCTTTTGGGCAC 188
QY 181 ACTGTTGCCAGTCT 240
Db 189 ACTGTTGCCAGTCT 248
QY 241 GAGAGAGAGTGGCTTCCAAAGGAGGCTCTGAGTGAATGTGCACACAGCAGAGCAT 300
Db 249 GAGAGAGAGTGGCTTCCAAAGGAGGCTCTGAGTGAATGTGCACACAGCAGAGCAT 308
QY 301 CACCCAGTGAATATATAGCAACCTTCTGGGCTGCGCGGTGATCATCAGGCTGCCCA 360
Db 309 CACCCAGTGAATATATAGCAACCTTCTGGGCTGCGCGGTGATCATCAGGCTGCCCA 368
QY 361 GGCATGATGTGATCATCAGTGAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Db 369 GGCATGATGTGATCATCAGTGAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 428
QY 421 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Db 429 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 488
QY 481 TGGAGTCTTTTATCTTCTGAGAGGCTCTGAGGATTCATCTCTGCTGAGATCTTCA 540
Db 489 TGGAGTCTTTTATCTTCTGAGAGGCTCTGAGGATTCATCTCTGCTGAGATCTTCA 548
QY 541 TGGAGTCTTACAGGAGCTTCTACTACCACTGTGCTGACAGCATGAATAATTGAGATTGG 600
Db 549 TGGAGTCTTACAGGAGCTTCTACTACCACTGTGCTGACAGCATGAATAATTGAGATTGG 608
QY 601 AGAGGCTCTTATCTTGGGATTAATTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
Db 609 AGAGGCTCTTATCTTGGGATTAATTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 668
QY 661 CTGCTTTCTGCTCATCCAGAGAAATG 690
Db 669 CTGCTTTCTGCTCATCCAGAGAAATG 698

RESULT 3
BE304667
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
JOURNAL
COMMENT
FEATURES
source

BE304667 680 bp mRNA linear EST 13-JUL-2000
601105783F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988309 5',
mRNA sequence.
BE304667
BE304667.1 GI:9176036
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 680)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgsaps-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: LNCMT7 row: f column: 22
High quality sequence start: 27
High quality sequence stop: 680.
Location/Qualifiers
1. 680
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2988309"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH MGC 15"
/note="Organ: colon; Vector: pOT81; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN

Query Match 23.5%; Score 643; DB 2; Length 680;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 643; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 GTCGGTCCAGCATTGTGACAGCAGTTGCTTCCAAAGGCTCTGTGATGGAATGTC 283
DB 38 GTCGGTCCAGCATTGTGACAGCAGTTGCTTCCAAAGGCTCTGTGATGGAATGTC 97
QY 284 ACAACAGCAGCAGGATCACCAGTGTGACATCTATAGCACCCTTGGGGCTGCGCGCT 343
DB 98 ACAACAGCAGCAGGATCACCAGTGTGACATCTATAGCACCCTTGGGGCTGCGCGCT 157
QY 344 GACATTCAGAGGCTGCGCGCGCATGATGTGACATTCAGTGAATCTCTCCCTGAGCTGC 403
DB 158 GACATTCAGAGGCTGCGCGCGCATGATGTGACATTCAGTGAATCTCTCCCTGAGCTGC 217
QY 404 ATTATCTCTGTGGGGCATGATGACAGTCTTTCGCCGGAATCCCGAGCCAAAGAC 463
DB 218 ATTATCTCTGTGGGGCATGATGACAGTCTTTCGCCGGAATCCCGAGCCAAAGAC 277
QY 464 AGATGCGCGTGAAGAGGAGTCTTTTTCATCCCTGGAGGCTCCCGGATTCATTCCT 523
DB 278 AGATGCGCGTGAAGAGGAGTCTTTTTCATCCCTGGAGGCTCCCGGATTCATTCCT 337
QY 524 GTTCCCTGGAATCTTTCATGAGGATCTTACGGGATCTTACTACCACTGTGCTGACAGC 583
DB 338 GTTCCCTGGAATCTTTCATGAGGATCTTACGGGATCTTACTACCACTGTGCTGACAGC 397

QY 584 ATGAATTTGAGATTGAGAGGCTCTTTTACTTGGGATTATTTCTCCCTGTTCCCTG 643
DB 398 ATGAATTTGAGATTGAGAGGCTCTTTTACTTGGGATTATTTCTCCCTGTTCCCTG 457
QY 644 ATAGCTGAATCATCTCTGCTTTTCTGCTCATCCCAAGAAATGCTCCAACTACTAC 703
DB 458 ATAGCTGAATCATCTCTGCTTTTCTGCTCATCCCAAGAAATGCTCCAACTACTAC 517
QY 704 GATGCTTACCAAGCCCAAGCTCTTGGCACAAGAGGCTTCCAAAGGCTGATCACTCC 763
DB 518 GATGCTTACCAAGCCCAAGCTCTTGGCACAAGAGGCTTCCAAAGGCTGATCACTCC 577
QY 764 AAGTCAAGAGTGAATTCCTTCAAGCTGACAGGATATGTGAAGAACAGAGGCT 823
DB 578 AAGTCAAGAGTGAATTCCTTCAAGCTGACAGGATATGTGAAGAACAGAGGCT 637
QY 824 CAGAGCTGGGGGCTGCTGCTGCTGTGTAAGAAACAGTGCACAGC 866
DB 638 CAGAGCTGGGGGCTGCTGCTGCTGTGTAAGAAACAGTGCACAGC 680

RESULT 4
AY400252
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
COMMENT
JOURNAL
FEATURES
source
gene
ORIGIN

AY400252 693 bp DNA linear GSS 15-DEC-2003
Pan troglodytes CLDN2 gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
AY400252
AY400252.1 GI:39756241
GSS.
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
1 (bases 1 to 693)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 693)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
Location/Qualifiers
1. 693
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
1. >693
/gene="CLDN2"
/locus_tag="HGM0495"

ORIGIN

Query Match 21.4%; Score 588; DB 9; Length 693;
Best Local Similarity 100.0%; Pred. No. 2; 5e-295; Indels 0; Gaps 0;
Matches 588; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 GTCGGTCCAGCATTGTGACAGCAGTTGCTTCCAAAGGCTCTGTGATGGAATGTC 283
DB 106 GTCGGTCCAGCATTGTGACAGCAGTTGCTTCCAAAGGCTCTGTGATGGAATGTC 165
QY 284 ACAACAGCAGCAGGATCACCAGTGTGACATCTATAGCACCCTTGGGGCTGCGCGCT 343

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 662)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongseung@mail.krrib.re.kr
 Plate: 14 row: C column: 06
 High quality sequence stop: 662.
FEATURES
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 1..662
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S21SNV520-14-C06"
 /sex="F"
 /tissue_type="Stomach"
 /cell_type="floating aggregates"
 /cell_line="SNU-520"
 /lab_host="Top10"
 /clone_1fb="S21SNV520"
 /note="Organ: Stomach; Vector: pTZ19BP1; Site 1: EcoRI;
 Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10" by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN

Query Match 20.9%; Score 572; DB 4; Length 662;
 Best Local Similarity 100.0%; Pred. No. 5.9e-287;

Matches 572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1685 TAGGGACCTGACCTGCTTCTTCTTAACCAAGGCTATAGACATGTT 1744
 1 TAGGGACCTGACCTGCTTCTTCTTAACCAAGGCTATAGACATGTT 60
Qy 1745 TCCTTAGGAACAGTAAACAGATTTTCTAGGATGCTTGTGGGGATGACAGTGT 1804
 61 TCCTTAGGAACAGTAAACAGATTTTCTAGGATGCTTGTGGGGATGACAGTGT 120
Db 1805 GGGAGCTGTGGGATCTGAGGAAGACACCATCTTCTTACCGTCTTAAGAACCGAGGTGG 1864
 121 GGGAGCTGTGGGATCTGAGGAAGACACCATCTTCTTACCGTCTTAAGAACCGAGGTGG 180
Qy 1865 ATGTGTGTGTGGCTCCAGTGGGTGTCTTACTCTGACAGTGAAGGAGCCCTTAGAA 1924
 181 ATGTGTGTGTGGCTCCAGTGGGTGTCTTACTCTGACAGTGAAGGAGCCCTTAGAA 240
Qy 1925 ACTCTTAGGGGTATAGAAATCAGCTCAATATGATCAGGCCCTCCAGGCTCCACC 1984
 241 ACTCTTAGGGGTATAGAAATCAGCTCAATATGATCAGGCCCTCCAGGCTCCACC 300

Qy 1985 ACAGACACTACAGACCTCTTGAAAGACCAAGCAGGCCCTTCAGATTCGCC 2044
Db 301 ACAGACACTACAGACCTCTTGAAAGACCAAGCAGGCCCTTCAGATTCGCC 360
Qy 2045 CACTGTCCATCGGAAGATGCTCCAGAGTGGCTTGAAGGATCTTAAGGGCTCCAGCATGGC 2104
Db 361 CACTGTCCATCGGAAGATGCTCCAGAGTGGCTTGAAGGATCTTAAGGGCTCCAGCATGGC 420
Qy 2105 ATATCCATGCCAGGAGTGTGTCTTCATGATCTGAATGATGCTGCTGCTGGGA 2164
Db 421 ATATCCATGCCAGGAGTGTGTCTTCATGATCTGAATGATGCTGCTGCTGGGA 480
Qy 2165 TTGCAGCTGAGTGGAGTGGAGTGAAGATGTTCCAGGAAGACAGTTCACCTTAAGGTCC 2224
Db 481 TTGCAGCTGAGTGGAGTGGAGTGAAGATGTTCCAGGAAGACAGTTCACCTTAAGGTCC 540
Qy 2225 GAAATGTTCCCTTTTACCTCTGAGTGGAGTGG 2256
Db 541 GAAATGTTCCCTTTTACCTCTGAGTGGAGTGG 572

RESULT 7

BU073403/c 555 bp mRNA linear EST 27-AUG-2002
 LOCUS Im35d11.x1 Human insulinoma Homo sapiens cDNA clone IMAGE:6036933
 DEFINITION 3', mRNA sequence.

ACCESSION BU073403 GI:22514592
 VERSION BU073403
 KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 555)
 Melton,D., Brown,D., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
 Lemishka,I., Seacore,M., Brestelli,J., Gradwohl,G., Clifton,S.,
 Hillier,L., Merra,M., Pape,D., Wylie,T., Martin,J., Bilstain,A.,
 Schmitt,A., Theising,B., Ritzer,E., Ronko,I., Bennett,J.,
 Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarisvilli,R.,
 Williams,T., Jackson,Y. and Bowers,Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557

TITLE JOURNAL
COMMENT Email: dmelton@hobn.harvard.edu
 Library was constructed by Dr. J. Ferrer in vivo mass-excised to
 pluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
 University Genome Sequencing Center for information on obtaining a
 clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
 Seq primer: -400P from Gibco
 High quality sequence stop: 436.

FEATURES

source

1..555
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6036933"
 /tissue_type="Insulinoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: pancreas; Vector: pluescript SK-; Site 1:
 XhoI; Site 2: EcoRI; Constructed with lambda ZapII system
 (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
 pluescript SK- by Dr. H. Inoue following the Washington
 University protocol
 (http://genome.wustl.edu/est/lambda_protocol.shtml).
 Please contact Hiroshi Inoue, MD/PhD for further
 information on this library (Metabolism Division, Permutt

ORIGIN Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library."

Query Match 20.2%; Score 555; DB 5; Length 555;

Best Local Similarity 100.0%; Pred. No. 4.6e-278; Mismatches 0; Indels 0; Gaps 0;

Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 908 GTGAGAGGTCGTGAGTACGATCTTGGCCATTGGATGGAGCAAGGCAAAA 967

DB 555 GTGAGAGGTCGTGAGTACGATCTTGGCCATTGGATGGAGCAAGGCAAAA 496

QY 968 TGGGGGCTAGTGTACAGCATGAGTGTGAATGTCAGAGTGTCCGACAGCTT 1027

DB 495 TGGGGGCTAGTGTACAGCATGAGTGTGAATGTCAGAGTGTCCGACAGCTT 436

QY 1028 TGTGTTTCTCAGCTTGTGCTCCCTGCTTAAAGTCCCAACCTGAACTGAAACC 1087

DB 435 TGTGTTTCTCAGCTTGTGCTCCCTGCTTAAAGTCCCAACCTGAACTGAAACC 376

QY 1088 CATTCCTTAAGCAGGAGTCAAGAGATCCCTTGGCTGTTTACCTGGGACTGCTAT 1147

DB 375 CATTCCTTAAGCAGGAGTCAAGAGATCCCTTGGCTGTTTACCTGGGACTGCTAT 316

QY 1148 CCCCAGAACCATATATCATATCCCATGACTGACCTCTGTGTATCAAGAACCTCTCTCT 1207

DB 315 CCCCAGAACCATATATCATATCCCATGACTGACCTCTGTGTATCAAGAACCTCTCTCT 256

QY 1208 GCGTGAAGTGTGCTTAACTGCTTAACTGCTGAGGATGGAGAGAGAGAGAGAGAGAG 1267

DB 255 GCGTGAAGTGTGCTTAACTGCTTAACTGCTGAGGATGGAGAGAGAGAGAGAGAGAG 196

QY 1268 GGCATTGCTCTAAGCTTCTCAAGCTTCCCTCAAGAACTGATTTGGCCCTGAAACC 1327

DB 195 GGCATTGCTCTAAGCTTCTCAAGCTTCCCTCAAGAACTGATTTGGCCCTGAAACC 136

QY 1328 TCCATCCCACTCTTGTATGATCTCAAGTGTCCAGATTAATTTGTCATGAATGAAAT 1387

DB 135 TCCATCCCACTCTTGTATGATCTCAAGTGTCCAGATTAATTTGTCATGAATGAAAT 76

QY 1388 AAAACCATCTAAGGATCCAGGAGAGAGAGAGAGAGAGATGGAGAGAGAGAG 1447

DB 75 AAAACCATCTAAGGATCCAGGAGAGAGAGAGAGAGATGGAGAGAGAGAG 16

QY 1448 GCAGCTGGAGACATT 1462

DB 15 GCAGCTGGAGACATT 1

RESULT 8

BG325755 728 bp mRNA linear EST 27-FEB-2001

LOCUS 60244446F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4562273 5',

DEFINITION mRNA sequence.

ACCESSION BG325755

VERSION BG325755.1 GI:13132179

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

CHORDATA; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 728)

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: gsabbs-remail.nih.gov

Tissue Procurement: DCTD/DRP

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLCM1274 row: d column: 18
High quality sequence stop: 708.
Location/Qualifiers

FEATURES

Source

1..728

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4562273"

/issue_type="renal cell adenocarcinoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_14"

/note="Organ: Kidney; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGG(G) Site-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using Zap-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 19.6%; Score 537; DB 4; Length 728;

Best Local Similarity 100.0%; Pred. No. 1.2e-268;

Matches 537; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 TTTGGGACACTGGTGGCCATGCTGCTCCAGCTGGAAGAAAGTTATGTCGGTGC 231

DB 82 TTTGGGACACTGGTGGCCATGCTGCTCCAGCTGGAAGAAAGTTATGTCGGTGC 141

QY 232 CAGCATTTGACAGCAGTGTGCTTTCAGAGGCTCTGGATGAATGTGCCACACAG 291

DB 142 CAGCATTTGACAGCAGTGTGCTTTCAGAGGCTCTGGATGAATGTGCCACACAG 201

QY 292 CAGAGGATCAACCATGTGACATCTATAGCAACCTTCTGGGCTCCGCTGACATCCA 351

DB 202 CAGAGGATCAACCATGTGACATCTATAGCAACCTTCTGGGCTCCGCTGACATCCA 261

QY 352 GCGTGCAGAGCCATGATGGTGAATCCAGTGAATCTCTCCCTGGCTGATTAATCTC 411

DB 262 GCGTGCAGAGCCATGATGGTGAATCCAGTGAATCTCTCCCTGGCTGATTAATCTC 321

QY 412 TGTGTGGGATGATGACAGTCTTTCAGAGATCCAGAAATCCAGAAAGACAGATGCC 471

DB 322 TGTGTGGGATGATGACAGTCTTTCAGAGATCCAGAAATCCAGAAAGACAGATGCC 381

QY 472 GGTAGCAGGTGAGTCTTTTCACTCTTGAAGGCTCTGGGATTAATCTCTGTCCTG 531

DB 382 GGTAGCAGGTGAGTCTTTTCACTCTTGAAGGCTCTGGGATTAATCTCTGTCCTG 441

QY 532 GAATCTTCATGGAGTCTTACAGGAGCTTCTACTACACAGCTGAGCTGACAGATGAAT 591

DB 442 GAATCTTCATGGAGTCTTACAGGAGCTTCTACTACACAGCTGAGCTGACAGATGAAT 501

QY 592 TGAAGATTGAGAGAGCTCTTACTTGGGCAATTAATTTCTCTCTGTTCTCTGATAGCTG 651

DB 502 TGAAGATTGAGAGAGCTCTTACTTGGGCAATTAATTTCTCTCTGTTCTCTGATAGCTG 561

QY 652 AATCATCTCTGCTTTCTCTGCTCATCCAGAGAAATGCTCCAACTACTAGATGTC 708

DB 562 AATCATCTCTGCTTTCTCTGCTCATCCAGAGAAATGCTCCAACTACTAGATGTC 618

RESULT 9

BG427780 810 bp mRNA linear EST 14-MAR-2001

LOCUS 602497154F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4610844 5',

DEFINITION mRNA sequence.

ACCESSION BG427780

VERSION BG427780.1 GI:13334286

KEYWORDS EST.

SOURCE Homo sapiens (human)

DB 242 CTTCTGGGCGCTGCGCTGCATCCAGGCTGCGCCCATGATGTCATCCAGTCA 301
QY 386 ATTCCTCCCTGGAGCTGATTCCTGCTGCTGAGGAGTATGATGACAGCTTCTGCGAG 445
DB 302 ATTCCTCCCTGGAGCTGATTCCTGCTGCTGAGGAGTATGATGACAGCTTCTGCGAG 361
QY 446 GAATCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGAGTCTTTTTCATCTTGAAGGC 505
DB 362 GAATCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGAGTCTTTTTCATCTTGAAGGC 421
QY 506 CTCTCTGGAGTTCATCTCTGCTGCTGAGATCTTCATGAGATCTTACGAGGACTTCTACTCA 565
DB 422 CTCTCTGGAGTTCATCTCTGCTGCTGAGATCTTCATGAGATCTTACGAGGACTTCTACTCA 481
QY 566 CCACTGTGCTGCTG 578
DB 482 CCACTGTGCTGCTG 494

RESULT 11
BE513091 945 bp mRNA linear EST 07-AUG-2000
LOCUS 60171545F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3545171 5',
DEFINITION mRNA sequence.

ACCESSION BE513091
VERSION BE513091.1 GI:9720302
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 945)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@rs-rcmail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: LNCM241 row: 1 column: 12
High quality sequence start: 36
High quality sequence stop: 782.
Location/Qualifiers

FEATURES

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source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 15"
/note="Organ: colon; Vector: pOT7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCAAGAG(G). Size selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN

Query Match 17.9%; Score 491; DB 2; Length 945;
Best Local Similarity 100.0%; Pred. No. 1.5e-244;
Matches 491; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGAAGTCAGGCTGGCAGAGAGCTCTGAATGAGGATTTGAGGTGTTCAAGAGCAAGA 60
DB 69 AGAAGTCAGGCTGGCAGAGAGAGCTCTGAATGAGGATTTGAGGTGTTCAAGAGCAAGA 128

QY 61 GCTTCAGCCTGAAGACAGAGAGAGCTCCCTGAGACGCTTTACTGAGAGTCTGCCAT 120
DB 129 GCTTCAGCCTGAAGACAGAGAGAGAGCTCCCTGAGACGCTTTACTGAGAGTCTGCCAT 188
QY 121 GGCCTCTCTTGGCTCCCACTTGTGGGCTACATCCAGGCTTTGGGGGCGAC 180
DB 189 GGCCTCTCTTGGCTCCCACTTGTGGGCTACATCCAGGCTTTGGGGGCGAC 248
QY 181 ACTGTTGACATGCTGCTCCCGAGCTGAGAAAACAATTCTATGTCGTGCCAGATTGT 240
DB 249 ACTGTTGACATGCTGCTCCCGAGCTGAGAAAACAATTCTATGTCGTGCCAGATTGT 308
QY 241 GACAGAGTTGGCTTCTCCAGAGGCTCTGATGATGTGCCACACAGCAGAGCAT 300
DB 309 GACAGAGTTGGCTTCTCCAGAGGCTCTGATGATGTGCCACACAGCAGAGCAT 368
QY 301 CACCCAGTGTGACATCTATAGCACCCCTTGGGCTCCCGGCTGACATCAGGCTGCCCA 360
DB 369 CACCCAGTGTGACATCTATAGCACCCCTTGGGCTCCCGGCTGACATCAGGCTGCCCA 428
QY 361 GGCATGATGATGACATCCAGTGCATCTCTCCCTGAGCTGATTCCTGCTGAGG 420
DB 429 GGCATGATGATGACATCCAGTGCATCTCTCCCTGAGCTGATTCCTGCTGAGG 488
QY 421 CATGATGATGACATCTCTCCAGGATCCGAGCCAAAGACAGAGTGGCGTACAG 480
DB 489 CATGATGATGACATCTCTCCAGGATCCGAGCCAAAGACAGAGTGGCGTACAG 548
QY 481 TGGAGTCTTTT 491
DB 549 TGGAGTCTTTT 559

RESULT 12

CB999779 758 bp mRNA linear EST 01-MAY-2003
LOCUS AGENCOURT_13642925 NIH_MGC_186 Homo sapiens cDNA clone
DEFINITION IMAGE:30322852 5', mRNA sequence.

ACCESSION CB999779
VERSION CB999779.1 GI:30294299
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 758)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@rs-rcmail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

CDNA Library Preparation: CLOUTIERE Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: NDCM124 row: 1 column: 05
High quality sequence stop: 592.
Location/Qualifiers

FEATURES

1. 758
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="30322852"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 186"
/note="Organ: Pooled-Skin; Vector: pDNR-LIB; Site 1: SfiI
(ggccatctggcc); Site 2: SfiI (ggccgcccggcc); Library is
oligo-dT primed and directionally cloned. cDNA was
prepared from a pooled samples of tissues from skin,

meninges, duramater, pia mater and choroid plexus. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGGCGGCGGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.47 kb (range 0.50-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC Library"

ORIGIN

Query Match 17.3%; Score 474; DB 6; Length 758;
 Best Local Similarity 100.0%; Pred. No. 1.1e-235;
 Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAGCTTGGCAGAGGAGCTCTGAATGAGGATTGAGGTTCAGAGCAGA 60
 DB 213 AGAAGTCAGCTTGGCAGAGGAGCTCTGAATGAGGATTGAGGTTCAGAGCAGA 272
 QY 61 GCTTCAGCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
 DB 273 GCTTCAGCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 332
 QY 121 GGCCTCTCTGGCTCCCACTTGTGGCTAATCTTGAAGGCTTCTGGGCTTTTGGG 180
 DB 333 GGCCTCTCTGGCTCCCACTTGTGGCTAATCTTGAAGGCTTCTGGGCTTTTGGG 392
 QY 181 ACTGTTGTCATGCTGCTCCGAGCTGGAAGGAGGAGGAGGAGGAGGAGGAGGAG 240
 DB 393 ACTGTTGTCATGCTGCTCCGAGCTGGAAGGAGGAGGAGGAGGAGGAGGAGGAG 452
 QY 241 GAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
 DB 453 GAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 512
 QY 301 CACCGAGTGAATCTATAGCAACCTTCTGGGCTCCGCTGAGATCCAGGCTGCCA 360
 DB 513 CACCGAGTGAATCTATAGCAACCTTCTGGGCTCCGCTGAGATCCAGGCTGCCA 572
 QY 361 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 DB 573 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 632
 QY 421 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 474
 DB 633 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 686

RESULT 13
 BU073420/c 485 bp mRNA linear EST 27-AUG-2002
 LOCUS BU073420 485 bp mRNA linear EST 27-AUG-2002
 DEFINITION 3', mRNA sequence.
 ACCESSION BU073420
 VERSION BU073420.1 GI:22514609
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 485)

REFERENCE
 AUTHORS Melton, D., Brown, J., Keny, G., Permutt, A., Lee, C., Kaestner, K.,
 Lemishka, I., Scaer, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistein, A.,
 Schmitt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J.,
 Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, W., R.,
 Williams, T., Jackson, Y., and Bowers, Y.
 TITLE Endocrine Pancreas Consortium
 JOURNAL Unpublished (2000)
 COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@mol.biol.harvard.edu
 Library was constructed by Dr. J. Ferrer in vivo mass-excised to
 pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
 University Genome Sequencing Center For information on obtaining a
 clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
 Seq primer: -40UP from Gibco
 High quality sequence stop: 427.

FEATURES

source
 1. .485
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6037029"
 /tissue_type="Insulinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="Human Insulinoma"
 /note="Organ: pancreas; Vector: pBluescript SK-; Site 1:
 XhoI; Site 2: EcoRI; Constructed with lambda ZapR system
 (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
 pBluescript SK- by Dr. H. Inoue following the Washington
 University protocol
 (http://genome.wustl.edu/est/lambda_protocol.shtml).
 Please contact Hiroshi Inoue, MD/PhD for further
 information on this library (Metabolism Division, Permutt
 Laboratory, Washington University School of Medicine, Box
 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
 is a Washington University Pancreas EST project library."

ORIGIN

Query Match 17.1%; Score 468; DB 5; Length 485;
 Best Local Similarity 100.0%; Pred. No. 1.5e-232;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1003 CAAGATGCTGCGCATGCAAGCCTTCTGTTTCTCACTTCTGCTGCTGCTGCTGCTGCT 1062
 DB 485 CAAGATGCTGCGCATGCAAGCCTTCTGTTTCTCACTTCTGCTGCTGCTGCTGCTGCT 426
 QY 1063 GTCCCAACCTCACTTGAACCCCAATTCCTTAAGCAGAGCTCAGAGATCCCTTTG 1122
 DB 425 GTCCCAACCTCACTTGAACCCCAATTCCTTAAGCAGAGCTCAGAGATCCCTTTG 366
 QY 1123 CCTCTGTTTACCTGGAGATCCATGCCCAACCACTATACATCCCACTGAGACC 1182
 DB 365 CCTCTGTTTACCTGGAGATCCATGCCCAACCACTATACATCCCACTGAGACC 306
 QY 1183 CTCTGATCAAGAACCTCTCTCTGAGTGAAGTGGCTCTTGAAGTCAATGCTGGAGATG 1242
 DB 305 CTCTGATCAAGAACCTCTCTCTGAGTGAAGTGGCTCTTGAAGTCAATGCTGGAGATG 246
 QY 1243 GAAAGGAAAGAGAGTGGCTTTTGTGGCATGTCTTAACCTTCTGAAGTTCCTCC 1302
 DB 245 GAAAGGAAAGAGAGTGGCTTTTGTGGCATGTCTTAACCTTCTGAAGTTCCTCC 186
 QY 1303 AAAGAAATGATTTGGCTTGGAACTTCATCCCACTTTTATGACTCCAGAGTCCCA 1362
 DB 185 AAAGAAATGATTTGGCTTGGAACTTCATCCCACTTTTATGACTCCAGAGTCCCA 126
 QY 1363 GACTAATTTGTGATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 1422
 DB 125 GACTAATTTGTGATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 66
 QY 1423 GATGTCAGATGAG 1470
 DB 65 GATGTCAGATGAG 18

RESULT 14
 AA552647/c 459 bp mRNA linear EST 05-SEP-1997
 LOCUS AA552647

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DEFINITION  nkl1401.s1 NCI_CGAP_Co2 Homo sapiens cDNA clone IMAGE:1013449 3',
mRNA sequence.
ACCESSION  AA552647
VERSION    AA552647.1 GI:2322901
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 459)
            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgaps-remail.nih.gov
            Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            CDNA Library Preparation: Stratagene, Inc., David B. Krizman,
            Ph.D.
            CDNA Library Arraying: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/ILMIL ac:
            www-bio.11nl.gov/bdrip/image/image.html
            Insert Length: 1604 Std Error: 0.00
            Seq primer: -40ml3 fwd. RT from Amersham
            High quality sequence stop: 439.
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                /clone="IMAGE:1013449"
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                /lab_host="SOLR (kanamycin resistant)"
                /clone_1lb="NCI_CGAP Co2"
                /note="Organ: colon; Vector: Bluescript SK-; Site: 1;
                EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
                Oligo dt. Bulk colon villous adenoma. 5' adaptor sequence:
                5' GAATTCGGCAGAG 3' 3' adaptor sequence: 5'
                CTCGAGTTTTTTTTTTTTTTT 3' Average insert size: 1.1 kb."
ORIGIN
Query Match      16.7%; Score 459; DB 1; Length 459;
Best Local Similarity 100.0%; Pred. No. 7.6e-228;
Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1007 GATGCTGCGCATGCGACGCTTTTCTGTTCTCTCACTTGTCTGCCCTGCTCCCTTAAGTCC 1066
DB 459 GATGCTGCGCATGCGACGCTTTTCTGTTCTCTCACTTGTCTGCCCTGCTCCCTTAAGTCC 400
QY 1067 CGAACCTCAACTTGAACCCCATTCCTTAAGCAGAGACTCAGAGATCCCTTGGCCT 1126
DB 399 CGAACCTCAACTTGAACCCCATTCCTTAAGCAGAGACTCAGAGATCCCTTGGCCT 340
QY 1127 CTGCTTACTCGGAGACTCCATCCCAACCACTAATCAATCCCACTGACCTCT 1186
DB 339 CTGCTTACTCGGAGACTCCATCCCAACCACTAATCAATCCCACTGACCTCT 280
QY 1187 GTGATCAAGAACCTCTCTCTGCTGAGTGGTGGCTTACTGCTGCTGAGGAGTGGAA 1246
DB 279 GTGATCAAGAACCTCTCTCTGCTGAGTGGTGGCTTACTGCTGCTGAGGAGTGGAA 220
QY 1247 GGAAGACGACTGCTTTTGGGAGATGCTTAACCTTTCACACTTCCCTCCAAAG 1306
DB 219 GGAAGACGACTGCTTTTGGGAGATGCTTAACCTTTCACACTTCCCTCCAAAG 160
QY 1307 AAATGATTTGGCCCTGGAGACCTCATCCCACTCTTGTATGATCCAGAGTCCAGACT 1366
DB 159 AAATGATTTGGCCCTGGAGACCTCATCCCACTCTTGTATGATCCAGAGTCCAGACT 100
QY 1367 AATTGTGATGAATGAAATAAACCATCTCAAGTATCCAGGAAACAGAAAGCAGAT 1426

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DB 99 AATTGTGATGAATGAAATAAACCATCTCTGAGTATCCAGGAAACAGAAAGCAGAT 40
QY 1427 GCAGATGGAGAGACAGAAAGCAGGCTGGAGCACTTAA 1465
DB 39 GCAGATGGAGAGACAGAAAGCAGGCTGGAGCACTTAA 1

RESULT 15
LOCUS    CA389170
DEFINITION  CA389170 459 bp mRNA linear EST 06-NOV-2002
            cs0606.y1 Human Retinal pigment epithelium/choroid cDNA
            (un-normalized, unamplified): cs Homo sapiens cDNA clone cs0606
            5', mRNA sequence.
ACCESSION  CA389170
VERSION    CA389170.1 GI:24719072
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 459)
            Wistow, G., Bernstein, S.L., Wyatt, M.K., Farria, R.N., Behal, A.,
            Touchman, J.W., Bouffard, G., Smith, D., and Peterson, K.
            Expressed sequence tag analysis of human RPE/choroid for the
            NIDBank Project: Over 6000 non-redundant transcripts, novel genes
            and splice variants
            MOL. Vis. 8 (4), 205-220 (2002)
JOURNAL    MEDLINE
PUBMED     22103460
            12107410
COMMENT    Contact: Wistow G
            Section on Molecular Structure and Function
            National Eye Institute
            6/331, NIH, Bethesda, MD 20892-2740, USA
            Tel: 301 402 3452
            Fax: 301 496 0078
            Email: graeme@helix.nih.gov
            Plate: 06 row: d column: 06
            Seq primer: M13RPI reverse primer (ABI).
            Location/Qualifiers
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                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="cs0606"
                /tissue_type="RPE/choroid"
                /dev_stage="Adult"
                /lab_host="EMDH10B"
                /clone_1lb="Human Retinal pigment epithelium/choroid cDNA
                (un-normalized, unamplified): cs"
                /note="Organ: Eye; Vector: pCMVSPORT6; Two different donor
                eyes (75-80 years old) yielded approximately 600 mg of
                dissected RPE/choroid tissue. This in turn yielded 340 ug
                of total RNA and 7 ug of mRNA. A directionally cloned cDNA
                library in the pCMVSPORT6 vector was constructed at Life
                Technologies (Rockville, MD; now part of Invitrogen Corp),
                essentially following the protocols of the Superscript
                Plasmid System (Invitrogen Corp).
                <http://www.invitrogen.com/>. The library code
                designation was cs. For this library, cDNA inserts were
                cloned into the NotI/MluI sites of the vector. EST
                analysis was performed on the unamplified library at the
                NIH Intramural Sequencing Center (NISC). "
ORIGIN
Query Match      16.7%; Score 457; DB 6; Length 459;
Best Local Similarity 100.0%; Pred. No. 8.4e-227;
Matches 457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAGGCTGGCAGAGACTCTGAATGAGGAGATTAGAGGTTCAGAGCAGAG 60
DB 3 AGAAGTCAGGCTGGCAGAGACTCTGAATGAGGAGATTAGAGGTTCAGAGCAGAG 62

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QY	61	GCTTAGCCTGAAGCAAGGGAGCAGTCCCTGTAAGCGTTCTACTGAGAGGCTGCAT	120
Dp	63	GCTTAGCCTGAAGCAGAGGAGCACTCCCTGAAGCGTTCTACTGAGAGGCTGCAT	122
QY	121	GGCCTCTCTTGGCCTCCACATTTGTGGGCTACATCTTAGGCCTTCTGAGGCTTTTGGGCAC	180
Dp	123	GGCCTCTCTTGGCCTCCACATTTGTGGGCTACATCTTAGGCCTTCTGAGGCTTTTGGGCAC	182
QY	181	ACTGTTTGCCATGCTGCTGCCCAAGCTGGAAAACAAATTCTTATGTGCGTGCACAGCATTTGT	240
Dp	183	ACTGTTTGCCATGCTGCTGCCCAAGCTGGAAAACAAATTCTTATGTGCGTGCACAGCATTTGT	242
QY	241	GACAGCAGTTGGCTTCTCCAAAGGCGCTCTGAGATGAAATGAGCCACACAGACACAGGCAT	300
Dp	243	GACAGCAGTTGGCTTCTCCAAAGGCGCTCTGAGATGAAATGAGCCACACAGACACAGGCAT	302
QY	301	CACCCAGTGTGACATCTATAGCAACCCCTTCTGGGCGTCCCGGTGACATCCAGGCTGCCA	360
Dp	303	CACCCAGTGTGACATCTATAGCAACCCCTTCTGGGCGTCCCGGTGACATCCAGGCTGCCA	362
QY	361	GGCCATGATGTGACATCCAGTGCATCTCTCTCCCTGGCTGATATCTCTGTGTGGG	420
Dp	363	GGCCATGATGTGACATCCAGTGCATCTCTCTCCCTGGCTGATATCTCTGTGTGGG	422
QY	421	CATGAGATGACAGTCTTCTGCGAAGATCCCGAGCC	457
Dp	423	CATGAGATGACAGTCTTCTGCGAAGATCCCGAGCC	459

Search completed: October 29, 2004, 04:49:20
Job time : 12499 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 27, 2004, 06:55:26 ; Search time 155 Seconds

(without alignments)
532.308 Million cell updates/sec

Title: US-09-787-677A-3

Perfect score: 1174
Sequence: 1 MASIQLVIGLVIGLGLD.....PGQPKVSEFNGSYLGYV 230Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1174	100.0	230	2 AAY36181	AAY36181 Human sec
2	1174	100.0	230	3 AAY84609	AAY84609 A human m
3	1174	100.0	230	3 AAY99378	AAY99378 Human PRO
4	1174	100.0	230	4 AAB66127	AAB66127 Protein o
5	1174	100.0	230	4 AAE04207	AAE04207 Human gen
6	1174	100.0	230	4 AAU12417	AAU12417 Human PRO
7	1174	100.0	230	4 AAU09178	AAU09178 Human PRO
8	1174	100.0	230	4 AAB87565	AAB87565 Human PRO
9	1174	100.0	230	5 AAB88342	AAB88342 Human mem
10	1174	100.0	230	5 ABP67991	ABP67991 Human col
11	1174	100.0	230	5 ABG95890	ABG95890 Human sec
12	1174	100.0	230	5 ABB84912	ABB84912 Human PRO
13	1174	100.0	230	5 AAU76534	AAU76534 Tumor-as
14	1174	100.0	230	5 ABG64507	ABG64507 Human alb
15	1174	100.0	230	5 ABB04707	ABB04707 Human SP8
16	1174	100.0	230	5 ABB95518	ABB95518 Human ang
17	1174	100.0	230	6 ABO17861	ABO17861 Novel hum
18	1174	100.0	230	6 ABU81115	ABU81115 Human PRO
19	1174	100.0	230	6 ABU90915	ABU90915 Novel hum
20	1174	100.0	230	6 ABO33974	ABO33974 Human sec
21	1174	100.0	230	6 ABU71991	ABU71991 Novel hum
22	1174	100.0	230	6 ABU66815	ABU66815 Human PRO
23	1174	100.0	230	6 ABU71545	ABU71545 Human sec
24	1174	100.0	230	6 ABR47946	ABR47946 Human sec
25	1174	100.0	230	6 ABU59896	ABU59896 Novel sec

26	1174	100.0	230	6 ABU72326	ABU72326 Human PRO
27	1174	100.0	230	6 ABU90999	ABU90999 Human PRO
28	1174	100.0	230	6 ABO27320	ABO27320 Human sec
29	1174	100.0	230	6 ABO25086	ABO25086 Human sec
30	1174	100.0	230	6 ABR00178	ABR00178 Human gen
31	1174	100.0	230	6 ABU92515	ABU92515 Human sec
32	1174	100.0	230	6 ABU81185	ABU81185 Human sec
33	1174	100.0	230	6 ABO53299	ABO53299 Novel hum
34	1174	100.0	230	6 ABU67091	ABU67091 Human sec
35	1174	100.0	230	6 ABU98302	ABU98302 Novel hum
36	1174	100.0	230	6 ABU89307	ABU89307 Novel hum
37	1174	100.0	230	6 ABU82514	ABU82514 Novel hum
38	1174	100.0	230	6 ABU96478	ABU96478 Human PRO
39	1174	100.0	230	6 ABU72148	ABU72148 Human PRO
40	1174	100.0	230	6 ADA46011	ADA46011 Novel hum
41	1174	100.0	230	6 ADA76442	ADA76442 Human PRO
42	1174	100.0	230	6 ADB17137	ADB17137 Human tra
43	1174	100.0	230	6 ADA19092	ADA19092 Human PRO
44	1174	100.0	230	6 ADA61715	ADA61715 Homo bapl
45	1174	100.0	230	6 ADB19500	ADB19500 Novel hum

ALIGNMENTS

RESULT 1		ALIGNMENTS	
AAV36181	ID	AAV36181 standard; protein; 230 AA.	
XX	AC	AAV36181;	
XX	DT	23-SEP-1999 (first entry)	
XX	XX	Human secreted protein #53.	
XX	KW	Secreted protein; human; cytosolic; thrombotic; osteopathic; forensic;	
XX	XX	diagnostic; gene therapy; chromosome mapping; secretion vector.	
XX	OS	Homo sapiens.	
XX	XX		
XX	PN	W09925825-A2.	
XX	PD	27-MAY-1999.	
XX	PF	13-NOV-1998; 98NO-IB001862.	
XX	XX		
XX	PR	13-NOV-1997; 97US-0066677P.	
XX	PR	17-DEC-1997; 97US-0069957P.	
XX	PR	09-FEB-1998; 98US-0074121P.	
XX	PR	13-APR-1998; 98US-0081563P.	
XX	PR	10-AUG-1998; 98US-0096116P.	
XX	PR	04-SEP-1998; 98US-0099273P.	
XX	PA	(GENST) GENSET.	
XX	PI	Bougueleret L, Duclert A, Dumas Milne Edwards J;	
XX	XX	WPI, 1999-347472/29.	
XX	DR	N-PSDB; AAX97865.	
XX	PT	Extended cDNAs encoding secreted proteins.	
XX	PS	Claim 7; Page 289; 307pp; English.	
XX	XX	AAV36129-Y36222 represent novel human secreted proteins encoded by the	
XX	CC	extended cDNA sequences represented in AAV97813-X97906. The proteins of	
XX	CC	the invention have cytosolic, thrombotic and osteopathic activity. The	
XX	CC	extended cDNAs can be used to express secreted proteins or parts of them	
XX	CC	or to obtain antibodies capable of binding to the secreted proteins. They	
XX	CC	may also be used in diagnostic, forensic, gene therapy and chromosome	
XX	CC	mapping procedures. Uses also include design of expression vectors and	
XX	CC	secretion vectors	

SQ Sequence 230 AA;

Query Match 100.0%; Score 1174; DB 2; Length 230;
 Best Local Similarity 100.0%; Pred. No. 1.1e-116;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYIIGLGLGLTLVAMLLPSWKTSYVGASIVTVAVGSKGLMECAHSTG 60
 DB 1 MASLGQLVGYIIGLGLGLTLVAMLLPSWKTSYVGASIVTVAVGSKGLMECAHSTG 60
 QY 61 ITQCDIYSTLLGLPADIOAQAAMWVTSSAISLACIIISVGMKCTVFCQESRAKDRVAVA 120
 DB 61 ITQCDIYSTLLGLPADIOAQAAMWVTSSAISLACIIISVGMKCTVFCQESRAKDRVAVA 120
 QY 121 GGVPFLLGLGLGFIPVAMNHLGILRDFYSPPLVDSMKFEIGALYGIISLPSLIAGII 180
 DB 121 GGVPFLLGLGLGFIPVAMNHLGILRDFYSPPLVDSMKFEIGALYGIISLPSLIAGII 180
 QY 181 LCFSCSSQRRNSNYDAYQAQPLATRSSPRPGPPKVKSEFNSYSLTGYV 230
 DB 181 LCFSCSSQRRNSNYDAYQAQPLATRSSPRPGPPKVKSEFNSYSLTGYV 230

RESULT 2
 AAY84609
 ID AAY84609 standard; protein; 230 AA.
 AC AAY84609;
 XX
 DT 25-JUL-2000 (first entry)
 DE A human membrane associated organizational protein (HUNCT).
 XX
 KM Human; membrane associated organizational protein; HUNCT;
 KM cell proliferative disorder; cancer; autoimmune disorder;
 KM inflammatory disorder; neurological disorder; developmental disorder;
 KM vesicle trafficking; reproductive disorder; gastrointestinal disorder;
 KM renal disorder; atherosclerosis; leukaemia; rheumatoid arthritis;
 KM Alzheimer's disease; anxiety; diabetes; ovulatory defect; renal failure;
 KM irritable bowel syndrome; allergy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 29
 FT Modified-site /note= "potential phosphorylation site"
 FT Modified-site 62
 FT Modified-site /note= "potential phosphorylation site"
 FT Domain 117..138
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 FT Domain 164..182
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 PN MO200018915-A2.
 XX
 PD 06-APR-2000.
 XX
 PF 23-SEP-1999; 99MO-US022082.
 XX
 PR 25-SEP-1998; 98US-0155215P.
 PR 13-OCT-1998; 98US-0155251P.
 PR 04-MAY-1999; 99US-0172228P.
 XX

PA (INCY-) INCYTE PHARM INC.
 XX
 PI Yue H, Lai P, Corley NC, Guegler KJ, Baughn MR, Lu AD, Tang YT;
 XX WPI: 2000-293154/25.
 XX DR N-PSDB; AAA12585.
 XX
 PT Human membrane associated organizational protein and nucleic acid
 PT sequences useful in the diagnosis, treatment and prevention of cell
 PT proliferative associated disorders e.g. cancer, rheumatoid arthritis and
 PT Alzheimer's disease.
 XX
 PS Claim 1; Page 76-77; 84pp; English.
 XX
 CC The present sequence represents a membrane associated organizational
 CC protein (HUNCT). HUNCT is used for the diagnosis, treatment and
 CC prevention of cell proliferative disorders including cancer and
 CC autoimmune/inflammatory, neurological, developmental, vesicle
 CC trafficking, reproductive, gastrointestinal and renal disorders. These
 CC disorders may include atherosclerosis, leukaemia, allergies, rheumatoid
 CC arthritis, Alzheimer's disease, anxiety, diabetes, ovulatory defects,
 CC renal failure and irritable bowel syndrome. A vector expressing HUNCT,
 CC and an agonist of HUNCT can be used to treat or prevent a disorder
 CC associated with decreased expression or activity of HUNCT. An antagonist
 CC of HUNCT or a vector expressing the complement of a polynucleotide
 CC encoding HUNCT can be used to treat or prevent a disorder associated with
 CC increased expression or activity of HUNCT. Antibodies which bind HUNCT
 CC can be used for diagnosis of disorders associated with HUNCT expression
 CC or to monitor patients being treated with HUNCT. Agonists, antagonists or
 CC inhibitors of HUNCT. Assays are preferably carried out on body fluids
 CC from a patient using radioimmunoassay, enzyme linked immunosorbent assays
 CC or fluorescent activated cell sorting assays. Polynucleotides encoding
 CC HUNCT are also used in hybridisation assays to determine absence,
 CC presence, or excess expression of HUNCT and to monitor regulation of HUNCT
 CC levels during disease therapy
 XX
 SQ Sequence 230 AA;

Query Match 100.0%; Score 1174; DB 3; Length 230;
 Best Local Similarity 100.0%; Pred. No. 1.1e-116;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYIIGLGLGLTLVAMLLPSWKTSYVGASIVTVAVGSKGLMECAHSTG 60
 DB 1 MASLGQLVGYIIGLGLGLTLVAMLLPSWKTSYVGASIVTVAVGSKGLMECAHSTG 60
 QY 61 ITQCDIYSTLLGLPADIOAQAAMWVTSSAISLACIIISVGMKCTVFCQESRAKDRVAVA 120
 DB 61 ITQCDIYSTLLGLPADIOAQAAMWVTSSAISLACIIISVGMKCTVFCQESRAKDRVAVA 120
 QY 121 GGVPFLLGLGLGFIPVAMNHLGILRDFYSPPLVDSMKFEIGALYGIISLPSLIAGII 180
 DB 121 GGVPFLLGLGLGFIPVAMNHLGILRDFYSPPLVDSMKFEIGALYGIISLPSLIAGII 180
 QY 181 LCFSCSSQRRNSNYDAYQAQPLATRSSPRPGPPKVKSEFNSYSLTGYV 230
 DB 181 LCFSCSSQRRNSNYDAYQAQPLATRSSPRPGPPKVKSEFNSYSLTGYV 230

RESULT 3
 AAY9378
 ID AAY9378 standard; protein; 230 AA.
 AC AAY9378;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Human PRO1356 (UNQ705) amino acid sequence SEQ ID NO:134.
 XX
 KM Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
 KM transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
 XX
 OS Homo sapiens.

XX WO200012708-A2.
XX
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US020111.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 03-SEP-1998; 98US-0099536P.
PR 03-SEP-1998; 98US-0099596P.
PR 03-SEP-1998; 98US-0099598P.
PR 03-SEP-1998; 98US-0099602P.
PR 03-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099782P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 15-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 17-SEP-1998; 98US-0100948P.
PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101476P.
PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101479P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101915P.
PR 24-SEP-1998; 98US-0101916P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102307P.
PR 29-SEP-1998; 98US-0102310P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102484P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-0103314P.

PR 07-OCT-1998; 98US-0103315P.
PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103395P.
PR 07-OCT-1998; 98US-0103396P.
PR 07-OCT-1998; 98US-0103401P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105000P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 21-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 22-OCT-1998; 98US-0105693P.
PR 26-OCT-1998; 98US-0105944P.
PR 26-OCT-1998; 98US-0105870P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106062P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.

(GETH) GENENTECH INC.
PA Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WT;
PI
XX
XX WPI: 2000-237871/20.
DR N-PSDB; AAA37060.
XX
XX
XX New mammalian DNA sequences encoding transmembrane, receptor or secreted
PT PRO polypeptides, useful for screening of potential peptide or small
XX molecule inhibitors of the relevant receptor/ligand interactions.
XX
PS Claim 12; Fig 78; 773pp; English.
XX
XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC receptor or secreted PRO polypeptides given in AA99340 to AA99462. The
CC transmembrane and receptor PRO proteins can be used for screening of

CC potential peptide or small molecule inhibitors of the relevant
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences
 CC encoding them have various industrial applications, including uses as
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
 CC primers and hybridization probes used in the isolation of the PRO
 CC polypeptides from the present invention

XX Sequence 230 AA;

Query Match 100.0%; Score 1174; DB 3; Length 230;
 Best Local Similarity 100.0%; Pred. No. 1.1e-116;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGLQVGYIIGLGLGLTLVAMLLPSWKTSSYVGASIVTVAVGFSKGLMECAHSTG 60
 DB 1 MASLGLQVGYIIGLGLGLTLVAMLLPSWKTSSYVGASIVTVAVGFSKGLMECAHSTG 60
 QY 61 ITQCDIYSTLLGLPADIOAQAAMMTSSAISLACIISVGMKCTVFCQESRAKRVAVA 120
 DB 61 ITQCDIYSTLLGLPADIOAQAAMMTSSAISLACIISVGMKCTVFCQESRAKRVAVA 120
 QY 121 GGVFFILGILGLFIPVAMNLHGILRDFYSPVLPDSMKFEIGALYIGIISLPSLIAGII 180
 DB 121 GGVFFILGILGLFIPVAMNLHGILRDFYSPVLPDSMKFEIGALYIGIISLPSLIAGII 180
 QY 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPPRQPPKVKSEFNSYSLTGYV 230
 DB 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPPRQPPKVKSEFNSYSLTGYV 230

RESULT 4
 AAB66127
 ID AAB66127 standard; protein; 230 AA.

AC AAB66127;

DT 02-APR-2001 (first entry)

XX Protein of the invention #39.

XX Secreted; transmembrane; gene therapy.

XX Unidentified.

PN WO200078961-A1.

PD 28-DEC-2000.

PF 18-FEB-2000; 2000MO-US004342.

XX 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99MO-US020111.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99MO-US028313.
 PR 02-DEC-1999; 99MO-US028551.
 PR 16-DEC-1999; 99MO-US030095.
 PR 05-JAN-2000; 2000MO-US000219.
 PR 06-JAN-2000; 2000MO-US000376.

XX (GETH) GENENTECH INC.

XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ,
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Thomas D, Watanabe CK,
 PI Williams PM, Wood WI;

XX WPI; 2001-071395/08.

PT Secreted and transmembrane proteins and nucleic acids designated PRO,
 PT useful as hybridization probes, in chromosome and gene mapping and gene
 PT therapy.

XX Claim 1; Fig 78; 787pp; English.

XX The present invention relates to secreted and transmembrane proteins.
 CC These proteins and the DNA encoding them may be used as hybridization
 CC probes, in chromosome and gene mapping and in the generation of anti-
 CC sense RNA and DNA. They may also be used used to generate either
 CC transgenic animals or knockout animals which are in turn useful for
 CC development and screening of therapeutically useful reagents. The nucleic
 CC acids may also be used in gene therapy

XX Sequence 230 AA;

Query Match 100.0%; Score 1174; DB 4; Length 230;
 Best Local Similarity 100.0%; Pred. No. 1.1e-116;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGLQVGYIIGLGLGLTLVAMLLPSWKTSSYVGASIVTVAVGFSKGLMECAHSTG 60
 DB 1 MASLGLQVGYIIGLGLGLTLVAMLLPSWKTSSYVGASIVTVAVGFSKGLMECAHSTG 60
 QY 61 ITQCDIYSTLLGLPADIOAQAAMMTSSAISLACIISVGMKCTVFCQESRAKRVAVA 120
 DB 61 ITQCDIYSTLLGLPADIOAQAAMMTSSAISLACIISVGMKCTVFCQESRAKRVAVA 120
 QY 121 GGVFFILGILGLFIPVAMNLHGILRDFYSPVLPDSMKFEIGALYIGIISLPSLIAGII 180
 DB 121 GGVFFILGILGLFIPVAMNLHGILRDFYSPVLPDSMKFEIGALYIGIISLPSLIAGII 180
 QY 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPPRQPPKVKSEFNSYSLTGYV 230
 DB 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPPRQPPKVKSEFNSYSLTGYV 230

RESULT 5
 AAE04207
 ID AAE04207 standard; protein; 230 AA.

AC AAE04207;

DT 09-AUG-2001 (first entry)

DE Human gene 10 encoded secreted protein HRP1H83, SEQ ID NO:62.

XX Human; secreted protein; proliferative disorder; cancer; tumour;
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 KW cardiovascular disorder; angiogenic disorder; kidney disorder;
 KW gastrointestinal disorder; pregnancy-related disorder; gene therapy;
 KW endocrine disorder; infection; wound healing; vlnerary; cell culture;
 KW chemotaxis; food additive; binding partner identification.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..24
 FT /label= signal_peptide
 FT Protein 25..230
 FT /note= "Mature secreted protein"

PN WO200136432-A2.

PD 25-MAY-2001.

PF 15-NOV-2000; 2000MO-US031162.

PR 19-NOV-1999; 99US-0166415P.
 PR 30-JUN-2000; 2000US-0215136P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Komatsoulis GA, Baker KP, Young PE;
 XX WPI, 2001-343793/36.
 DR N-PSDB; AAD08497.
 XX
 PT Isolated nucleic acid molecule encoding a human secreted protein is used
 PT in preventing, treating or ameliorating a medical condition.
 XX
 PS Claim 11; Page 439; 509pp; English.
 XX
 CC AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted
 CC protein genes, and AAE04199-AAE04239 represent the proteins they encode.
 CC AAE04240-AAE04297 represent human secreted protein fragments or variants.
 CC The secreted proteins and their genes are useful for preventing, treating
 CC or ameliorating medical conditions, e.g., by protein or gene therapy.
 CC Pathological conditions can be diagnosed by determining the amount of the
 CC new protein in a sample or by determining the presence of mutations in
 CC the new genes. Specific uses are described for each of the 18 genes,
 CC based on the tissues in which they are most highly expressed, and include
 CC developing products for the diagnosis or treatment of proliferative
 CC disorders, cancer, tumors, foetal and developmental abnormalities,
 CC hematopoietic disorders, diseases of the immune system, AIDS, autoimmune
 CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
 CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
 CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
 CC angiogenic disorders, kidney disorders, gastrointestinal disorders,
 CC pregnancy-related disorders, endocrine disorders, and infections. The
 CC proteins can also be used to aid wound healing and epithelial cell
 CC proliferation, to prevent skin ageing due to sunburn, to maintain organs
 CC before transplantation, for supporting cell culture of primary tissues,
 CC to regenerate tissues, to identify their cognate ligands or binding
 CC partners, and in chemotaxis, and can be used as a food additive or
 CC preservative to modify storage properties. Antibodies specific for a
 CC protein of the invention can be used in alleviating symptoms associated
 CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
 CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The
 CC present sequence represents a human secreted protein of the invention
 XX
 SQ Sequence 230 AA;
 Query Match 100.0%; Score 1174; DB 4; Length 230;
 Best Local Similarity 100.0%; Pred. No. 1, 1e-116;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MASIGQLVGVYIGLGLGLTLVAMLLPSWKTSSYVAGSIYVAVGFSKGLMECATSTG 60
 DB 1 MASIGQLVGVYIGLGLGLTLVAMLLPSWKTSSYVAGSIYVAVGFSKGLMECATSTG 60
 QY 61 ITQCDIYITLGLPADIQAAQAMWVTSSAISLACIISVGMRTVCQESRADRYAVA 120
 DB 61 ITQCDIYITLGLPADIQAAQAMWVTSSAISLACIISVGMRTVCQESRADRYAVA 120
 QY 121 GGVEFFIGLGLGFIVAMNHLGLRDYSPVLPDSMKPEIGCALYLGITSLFSLIAGII 180
 DB 121 GGVEFFIGLGLGFIVAMNHLGLRDYSPVLPDSMKPEIGCALYLGITSLFSLIAGII 180
 QY 181 LCFSSCSQNRNSNYDAYQAQPLATRSSPRGQPKYKSEFNSYSLNGYV 230
 DB 181 LCFSSCSQNRNSNYDAYQAQPLATRSSPRGQPKYKSEFNSYSLNGYV 230
 RESULT 6
 AAU12417
 ID AAU12417 standard; protein; 230 AA.
 AC AAU12417;
 XX
 XX 24-OCT-2001 (first entry)
 XX Human PRO1356 polypeptide sequence.
 DE
 XX

KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
 KW prostate; cervical; tumor necrosis factor-alpha; TNF-alpha; cartilage;
 KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
 KW A-peptide; factor VIIa; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200140466-A2.
 XX
 PD 07-JUN-2001.
 XX
 XX 01-DEC-2000; 2000MO-US032678.
 PF
 XX 01-DEC-1999; 99MO-US028301.
 PR 01-DEC-1999; 99MO-US028634.
 PR 02-DEC-1999; 99MO-US028551.
 PR 02-DEC-1999; 99MO-US028564.
 PR 02-DEC-1999; 99MO-US028565.
 PR 09-DEC-1999; 99US-0170262P.
 PR 16-DEC-1999; 99MO-US030095.
 PR 20-DEC-1999; 99MO-US030911.
 PR 20-DEC-1999; 99MO-US030999.
 PR 30-DEC-1999; 99MO-US031243.
 PR 30-DEC-1999; 99MO-US031274.
 PR 05-JAN-2000; 2000MO-US000219.
 PR 06-JAN-2000; 2000MO-US000277.
 PR 11-FEB-2000; 2000MO-US003565.
 PR 18-FEB-2000; 2000MO-US004341.
 PR 18-FEB-2000; 2000MO-US004342.
 PR 22-FEB-2000; 2000MO-US004414.
 PR 24-FEB-2000; 2000MO-US004914.
 PR 24-FEB-2000; 2000MO-US005004.
 PR 01-MAR-2000; 2000MO-US005601.
 PR 02-MAR-2000; 2000MO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 10-MAR-2000; 2000MO-US006319.
 PR 15-MAR-2000; 2000MO-US006884.
 PR 20-MAR-2000; 2000MO-US007377.
 PR 21-MAR-2000; 2000MO-US007532.
 PR 30-MAR-2000; 2000MO-US008439.
 PR 17-MAY-2000; 2000MO-US013705.
 PR 22-MAY-2000; 2000MO-US014042.
 PR 30-MAY-2000; 2000MO-US014941.
 PR 02-JUN-2000; 2000MO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000MO-US020710.
 PR 11-AUG-2000; 2000MO-US022031.
 PR 23-AUG-2000; 2000MO-US023522.
 PR 24-AUG-2000; 2000MO-US023328.
 PR 08-NOV-2000; 2000MO-US030952.
 PR 10-NOV-2000; 2000MO-US030873.
 PA (GENTH) GENENTECH INC.
 XX
 XX Baker KP, Beresini W, Deforge L, Desnoyers L, Filvaroff E, Gao W,
 PI Gerritsen ME, Goddard A, Godowski P, Gurney AL, Sherwood S,
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI, 2001-408281/43.
 DR N-PSDB; AAS21489.
 XX
 XX Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
 PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
 PT breast, prostate, cervical.
 XX
 PS Claim 12; Fig 492; 813pp; English.
 XX
 CC AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
 CC polypeptides. The PRO polypeptides are useful to detect other PRO
 CC polypeptides, to link bioactive molecules to cells expressing PRO
 CC polypeptides, to modulate biological activities of cells expressing PRO

CC polypeptides, and to detect the presence of mammalian lung, colon, CC breast, prostate, rectal, cervical or liver tumours by comparing PRO CC polypeptide expression in a cell sample to that in a control sample. Some CC of the 275 sequences are also useful to stimulate the release of tumour CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the CC proliferation of inner ear utricular supporting cells or of T- CC lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO CC polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO CC polypeptides can be used to generate probes, antisense RNA/DNA, CC transgenic or knock out animals and can be used in gene therapy

XX Sequence 230 AA;

Query Match 100.0%; Score 1174; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.1e-116;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYIIGLGLGLTLVAMLPWKTSYVGSIVTAVGSKGLMECATHTSG 60
DB 1 MASLGQLVGYIIGLGLGLTLVAMLPWKTSYVGSIVTAVGSKGLMECATHTSG 60
QY 61 ITCCDIYSTLLGPADIQAAQAMVNTSSAISLACIISVGMCTVCOESRAKDRVAVA 120
DB 61 ITCCDIYSTLLGPADIQAAQAMVNTSSAISLACIISVGMCTVCOESRAKDRVAVA 120
QY 121 GGVFFILGLLGFIPVAMNLHGLRDFSPVDPMSKEFGEALYGIISLSFLNGIT 180
DB 121 GGVFFILGLLGFIPVAMNLHGLRDFSPVDPMSKEFGEALYGIISLSFLNGIT 180
QY 181 LCRSSCGRRNSRYDYQAQPLATRSSPRPGQPKRSFNSYSLTGYV 230
DB 181 LCRSSCGRRNSRYDYQAQPLATRSSPRPGQPKRSFNSYSLTGYV 230

RESULT 7

AAU09178
ID AAU09178 standard; protein; 230 AA.

AC AAU09178;

XX 16-JAN-2002 (first entry)

XX Human PRO1356 polypeptide.

XX Human; PRO1356; clone DNA64886-1601; immune-related disorder;
XX inflammatory disorder; infectious disorder; immunodeficiency disorder;
XX autoimmune disorder; renal disease; demyelinating disease; skin disease;
XX neoplasia; transplantation associated disease; immunosuppressive;
XX anti-inflammatory; antiaesthetic; antidiabetic.

OS Homo sapiens.

XX Location/Qualifiers

FT Key 1..24

FT Peptide /label= Signal_peptide

FT Modified-site 17..23

FT /note= "N-myristoylation site"

FT Modified-site 20..26

FT /note= "N-myristoylation site"

FT Protein 25..230

FT /label= Mature_PRO1356_polypeptide

FT Region 46..60

FT /note= "Also found in PMP-22, EMP and MP20 family

FT proteins"

FT Modified-site 60..66

FT /note= "N-myristoylation site"

FT Domain 82..102

FT /label= Transmembrane_domain
FT Modified-site 101..107
FT /note= "N-myristoylation site"
FT Domain 117..140
FT /label= Transmembrane_domain
FT Modified-site 128..134
FT /note= "N-myristoylation site"
FT Domain 153..182
FT /label= Transmembrane_domain
FT Modified-site 167..173
FT /note= "N-myristoylation site"
FT Modified-site 178..184
FT /note= "N-myristoylation site"
FT Modified-site 190..194
FT /note= "N-glycosylation site"
FT Modified-site 216..225
FT /note= "Tyrosine kinase phosphorylation site"

XX WO200166740-A2.

XX 13-SEP-2001.

XX 01-MAR-2001; 2001WO-US006666.

XX 03-MAR-2000; 2000US-0187202P.

XX 21-MAR-2000; 2000US-0191015P.

XX 30-MAY-2000; 2000WO-US014941.

XX 05-JUN-2000; 2000US-0209832P.

XX 24-AUG-2000; 2000WO-US023328.

XX 01-DEC-2000; 2000WO-US032678.

XX (GETH) GENENTECH INC.

XX Baton DU, Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;

XX Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WPI, 2001-625876/72.

XX N-PSDB; AAS15360.

XX Claim 10; Fig 2; 122pp; English.

XX The present invention relates to the isolation of 9 novel human PRO

XX polypeptides and the cDNA sequences (AAS15360-AAS15368) encoding them.

XX The novel PRO polypeptides include PRO1356, PRO1268, PRO1884, PRO1444,

XX PRO151, PRO4322, PRO9964, PRO10008 and PRO13598. The cDNA sequences

XX encoding these PRO polypeptides have been designated as clones DNA64886-

XX 1601, DNA64903-1553, DNA84318-2520, DNA87997, DNA89273, DNA92223-2567,

XX DNA96973, DNA101921 and DNA145887 respectively. Compositions (e.g.

XX vaccines) containing PRO polypeptides and methods of using these

XX compositions are useful in the treatment and diagnosis of immune-related

XX disorders. Such disorders include immune-mediated inflammatory disorders

XX (e.g. osteoarthritis), non-immune-mediated inflammatory disorders (e.g.

XX diabetes mellitus), infectious disorders (e.g. granulomatous hepatitis),

XX immunodeficiency disorders (e.g. AIDS), autoimmune disorders (e.g.

XX rheumatoid arthritis), immune-related renal diseases (e.g. cirrhosis),

XX demyelinating diseases of the peripheral or central nervous system (e.g.

XX Guillain-Barre syndrome), immune-mediated skin diseases (e.g. contact

XX dermatitis), neoplasias and transplantation associated diseases. The

XX polynucleotide sequences of the invention may be used in gene therapy.

XX AAU09178-AAU09186 represent the novel human PRO polypeptides of the

XX invention

XX Sequence 230 AA;

Query Match 100.0%; Score 1174; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.1e-116;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYIIGLGLGLTLVAMLPWKTSYVGSIVTAVGSKGLMECATHTSG 60

```
Db      |||
1 MASLGQLVGYIILGLGLTLVAMLLPSWKTSYVGASIVTVAGFSKGLMECATHTSG 60
Qy      61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIISVVGKCTVFCQESRAKDRVAVA 120
Db      61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIISVVGKCTVFCQESRAKDRVAVA 120
Qy      121 GGVFFILGILGLPIPAVMNLHGILRDYSPFLVPDSMKFEIAGEALYIGIISLPSLIAGII 180
Db      121 GGVFFILGILGLPIPAVMNLHGILRDYSPFLVPDSMKFEIAGEALYIGIISLPSLIAGII 180
Qy      181 LCFSCSSQRRNSNYDAYOAOPLATRSSPRPGQPPVKSEFNSYSLTGYV 230
Db      181 LCFSCSSQRRNSNYDAYOAOPLATRSSPRPGQPPVKSEFNSYSLTGYV 230

RESULT 8
AAB87565
ID      AAB87565 standard; protein; 230 AA.
AC      AAB87565;
DT      15-MAY-2001 (first entry)
DE      Human PRO1356.
XX      Human; PRO protein; mapping.
XX      Homo sapiens.
XX      MO200116318-A2.
XX      08-MAR-2001.
XX      24-AUG-2000; 2000WO-US023328.
XX      01-SEP-1999; 99MO-US020111.
XX      15-SEP-1999; 99MO-US021090.
XX      07-DEC-1999; 99US-0169495P.
XX      09-DEC-1999; 99US-0170262P.
XX      11-JAN-2000; 2000US-0175481P.
XX      18-FEB-2000; 2000WO-US004341.
XX      18-FEB-2000; 2000WO-US004342.
XX      22-FEB-2000; 2000WO-US004414.
XX      01-MAR-2000; 2000WO-US005601.
XX      03-MAR-2000; 2000US-0187202P.
XX      21-MAR-2000; 2000US-0191007P.
XX      30-MAR-2000; 2000WO-US008439.
XX      25-APR-2000; 2000US-0199397P.
XX      22-MAY-2000; 2000WO-US014042.
XX      05-JUN-2000; 2000US-0209832P.
XX      (GETH ) GENENTECH INC.
XX      Baton DL, Flvaroff B, Gerritsen ME, Goddard A, Godowski PJ,
PI      Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI,
XX      WPI; 2001-183260/18.
XX      N-PSDB; AAF92097.
XX      Bighey four nucleic acids encoding PRO polypeptides, useful in molecular
PT      biology, including use as hybridization probes, and in chromosome and
PT      gene mapping.
XX      Claim 12; Fig 80; 278pp; English.
XX      The present sequence is a human PRO polypeptide (secreted and
XX      transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
XX      anti-PRO antibodies are useful for preparation of a medicament useful in
XX      the treatment of a condition which is responsive to the PRO protein,
XX      CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
XX      employed as molecular weight markers for protein electrophoresis. The PRO
XX      coding sequence has applications in molecular biology, including use as
```

```
CC      hybridisation probes, and in chromosome and gene mapping
XX      Sequence 230 AA:
Qy      Query Match 100.0%; Score 1174; DB 4; Length 230;
Db      Best Local Similarity 100.0%; Pred. No. 1.1e-116;
Db      Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 MASLGQLVGYIILGLGLTLVAMLLPSWKTSYVGASIVTVAGFSKGLMECATHTSG 60
Db      1 MASLGQLVGYIILGLGLTLVAMLLPSWKTSYVGASIVTVAGFSKGLMECATHTSG 60
Qy      61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIISVVGKCTVFCQESRAKDRVAVA 120
Db      61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIISVVGKCTVFCQESRAKDRVAVA 120
Qy      121 GGVFFILGILGLPIPAVMNLHGILRDYSPFLVPDSMKFEIAGEALYIGIISLPSLIAGII 180
Db      121 GGVFFILGILGLPIPAVMNLHGILRDYSPFLVPDSMKFEIAGEALYIGIISLPSLIAGII 180
Qy      181 LCFSCSSQRRNSNYDAYOAOPLATRSSPRPGQPPVKSEFNSYSLTGYV 230
Db      181 LCFSCSSQRRNSNYDAYOAOPLATRSSPRPGQPPVKSEFNSYSLTGYV 230

RESULT 9
AAB88342
ID      AAB88342 standard; protein; 230 AA.
AC      AAB88342;
DT      23-MAY-2001 (first entry)
DE      Human membrane or secretory protein clone PSEC0059.
XX      Human; secretory protein; membrane protein; vaccine; gene therapy;
XX      rheumatoid arthritis; diabetes.
XX      Homo sapiens.
XX      EP1067182-A2.
XX      10-JAN-2001.
XX      07-JUL-2000; 2000EP-00114090.
XX      08-JUL-1999; 99JP-00194179.
XX      11-JAN-2000; 2000JP-00118775.
XX      02-MAY-2000; 2000JP-00183766.
XX      (HELI-) HELIX RES INST.
XX      Oca T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K,
PI      WPI; 2001-093989/11.
XX      N-PSDB; AAF93769.
XX      Nucleic acids encoding secretory protein/membrane proteins, useful in
PT      gene therapy or as candidate target molecules in drug development.
XX      Claim 1; SEQ ID NO 52; 609pp + Sequence listing; English.
XX      This invention relates to nucleic acid sequences AAF93744 - AAF93916
XX      which encode human secretory or membrane proteins represented by AAB88317
XX      CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
XX      CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
XX      CC invention. The invention also includes methods for the production of
XX      CC antibodies directed against the proteins, and cDNA sequences, which can
XX      CC be used in vaccines. The polynucleotide sequences can be used in gene
XX      CC therapy. The polynucleotide sequences and the proteins they encode may be
XX      CC used in the prevention, treatment and diagnosis of diseases associated
XX      CC with inappropriate secretory protein/membrane protein expression. The
XX      CC nucleic acids and complementary sequences may also be used as DNA probes
```

CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
CC and quantitate the presence of similar nucleic acid sequences in samples.
CC They may also be used to study the expression and function of secretory
CC proteins/membrane polypeptides and their role in metabolism. The
CC polypeptides may be used as antigens in the production of antibodies
CC against them and in assays to identify modulators (agonists and
CC antagonists) of expression and activity. The antibodies and antagonists
CC may also be used as therapeutic agents to down regulate expression and
CC activity. The antibodies may also be used as diagnostic agents for
CC detecting the presence of the polypeptides in samples (e.g. by enzyme
CC linked immunosorbent assay (ELISA). Examples of diseases which may be
CC treated include rheumatoid arthritis and diabetes

XX Sequence 230 AA;

Query Match 100.0%; Score 1174; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.1e-116;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASIGQLVGYITGLGLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60
DB 1 MASIGQLVGYITGLGLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60
QY 61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKRVAVA 120
DB 61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKRVAVA 120
QY 121 GGVFILGLGLGFIPTVAMNHLGILRDPYSPVPDSMKFEIGELALYGIISLPSLIGI 180
DB 121 GGVFILGLGLGFIPTVAMNHLGILRDPYSPVPDSMKFEIGELALYGIISLPSLIGI 180
QY 181 LCFSSCSQRRNSNYDAYOAOPLATRSSPRPGPPKVKSEFNSYSLTGYV 230
DB 181 LCFSSCSQRRNSNYDAYOAOPLATRSSPRPGPPKVKSEFNSYSLTGYV 230

RESULT 10
ABPe7991

ID ABPe7991 standard; protein; 230 AA.

XX AC ABPe7991;

DT 13-DEC-2002 (first entry)

DE Human colon cancer related polypeptide SEQ ID NO 2590.

KM Human; colon; cancer; cytostatic; tumour; gene therapy; vaccine.

OS Homo sapiens.

PN WO200258534-A2.

PD 01-AUG-2002.

PF 16-NOV-2001; 2001WO-US043704.

PR 20-NOV-2000; 2000US-0252222P.

PR 06-FEB-2001; 2001US-0267011P.

PR 28-MAR-2001; 2001US-0279670P.

PR 10-JUL-2001; 2001US-0304037P.

XX (CORI-) CORIXA CORP.

XX Stolk JA, Xu J, Chenault RA, Meagher MJ, Secrist H, King GE;

XX WPI; 2002-608400/65.

XX N-PSDB; ABV89278.

XX New isolated tumor colon-polynucleotide and polypeptide, useful for the
XX diagnosis, prevention and/or treatment of cancer, in particular colon
XX cancer.

PS Claim 2; SEQ ID NO 2590; 266pp + Sequence Listing; English.

XX The invention relates to a human colon tumour expressed polynucleotide
CC (i) encoding a polypeptide (II, ABPe7991-ABPe7996) comprising: (i) any of
CC 2600 fully defined nucleotide sequences (ABV8669-ABV89289); (ii)
CC complements of (i); (iii) at least 20 contiguous residues of (i); (iv)
CC sequences that hybridize to (i), under moderately stringent conditions;
CC (v) sequences having at least 75% or 90% identity to (i); or (vi)
CC degenerate variants of (i). The compositions and methods of the present
CC invention are useful for the diagnosis, prevention and/or treatment of
CC cancer, particularly colon cancer. (ii) can be used in gene therapy and
CC (i) and (ii) are useful in pharmaceutical compositions such as vaccines.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 230 AA;

Query Match 100.0%; Score 1174; DB 5; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.1e-116;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASIGQLVGYITGLGLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60
DB 1 MASIGQLVGYITGLGLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60
QY 61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKRVAVA 120
DB 61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKRVAVA 120
QY 121 GGVFILGLGLGFIPTVAMNHLGILRDPYSPVPDSMKFEIGELALYGIISLPSLIGI 180
DB 121 GGVFILGLGLGFIPTVAMNHLGILRDPYSPVPDSMKFEIGELALYGIISLPSLIGI 180
QY 181 LCFSSCSQRRNSNYDAYOAOPLATRSSPRPGPPKVKSEFNSYSLTGYV 230
DB 181 LCFSSCSQRRNSNYDAYOAOPLATRSSPRPGPPKVKSEFNSYSLTGYV 230

RESULT 11
ABG95890

ID ABG95890 standard; protein; 230 AA.

XX AC ABG95890;

DT 10-DEC-2002 (first entry)

DE Human secreted/transmembrane protein PRO1356.

KM Human; secreted protein; transmembrane protein; antirheumatic;
KM antiarthritic; osteopathic; sports-related joint problem;
KM articular cartilage defect; osteoarthritis; rheumatoid arthritis.

OS Homo sapiens.

PN US2002119130-A1.

PD 29-AUG-2002.

PF 06-DEC-2001; 2001US-0006867.

PR 28-OCT-1997; 97US-0063435P.

PR 29-OCT-1997; 97US-0064215P.

PR 22-APR-1998; 98US-0082797P.

PR 29-APR-1998; 98US-0083495P.

PR 15-MAY-1998; 98US-0085599P.

PR 02-JUN-1998; 98US-0087599P.

PR 04-JUN-1998; 98US-0088021P.

PR 04-JUN-1998; 98US-0088029P.

PR 04-JUN-1998; 98US-0088030P.

PR 10-JUN-1998; 98US-0088734P.

PR 10-JUN-1998; 98US-0088740P.

PR 10-JUN-1998; 98US-0088811P.

PR 10-JUN-1998; 98US-0088824P.

ID ABB84912 standard; protein; 230 AA.
XX
AC ABB84912;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO1356 protein sequence SEQ ID NO:192.
XX
KM Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;
KM vlnnary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KM gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KM angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KM age-related macular degeneration; arterial restenosis; angina;
KM rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KM lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KM wound healing; chromosome mapping; gene mapping.
XX
OS Homo sapiens.
XX
PN MO20020690-A2.
XX
PD 03-JAN-2002.
XX
PE 20-JUN-2001; 2001MO-US019692.
XX
PR 23-JUN-2000; 2000US-0213637P.
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220662P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000MO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000MO-US023522.
PR 24-AUG-2000; 2000MO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000MO-US030952.
PR 10-NOV-2000; 2000MO-US030873.
PR 01-DEC-2000; 2000MO-US032578.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000MO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001MO-US006520.
PR 01-MAR-2001; 2001MO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 30-MAY-2001; 2001MO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001MO-US017443.
PR 01-JUN-2001; 2001MO-US017800.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen MB, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WT, Ye W;
XX
XX MPI; 2002-090516/12.
XX
XX N-PSDB; ABL88167.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX
XX PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX
XX PT infection), endothelial or angiogenic disorders in a mammal.

XX
PS Claim 11; Fig 192; 565pp; English.
XX
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABL885003. The PRO proteins and polynucleotides have cardiant, cyostatic,
CC antiangiogenic, hypotensive, vlnnary and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarction, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The PRO polynucleotides have applications in molecular biology,
CC including use as hybridisation probes, and in chromosome and gene
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC exemplification of the present invention
XX
SQ Sequence 230 AA;
XX
Query Match 100.0%; Score 1174; DB 5; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.1e-116;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASLGQLVGYIIGLLGLGLVYAMLPEPKTSSYVGAISIVAVGSKGLMECAHSTG 60
DB 1 MASLGQLVGYIIGLLGLGLVYAMLPEPKTSSYVGAISIVAVGSKGLMECAHSTG 60
QY 61 ITQCDIYSTLLGLPADIOAAMMTSSAISLACTISVVGKCTVFCQESBAKRVAVA 120
DB 61 ITQCDIYSTLLGLPADIOAAMMTSSAISLACTISVVGKCTVFCQESBAKRVAVA 120
QY 121 GGVFFILGGLGPIVAMNHLGLRDYSPVYDSKFEIGALYGIISLPSLIAGII 180
DB 121 GGVFFILGGLGPIVAMNHLGLRDYSPVYDSKFEIGALYGIISLPSLIAGII 180
QY 181 LCFSCSSQRRNSRYNDAYOAPLATSSPPQPPVKSEFNSYSITGV 230
DB 181 LCFSCSSQRRNSRYNDAYOAPLATSSPPQPPVKSEFNSYSITGV 230
XX
RESULT 13
AAU76534 standard; protein; 230 AA.
XX
AC AAU76534;
XX
DT 05-JUN-2002 (first entry)
XX
DE Tumour-associated antigenic target protein, TAT134.
XX
XX TAT134; Tumour-associated Antigenic Target; tumour; breast cancer;
XX colorectal cancer; lung cancer; ovarian cancer;
XX central nervous system cancer; liver cancer; bladder cancer; melanoma;
XX pancreatic cancer; leukaemia; gene therapy.
XX
XX Homo sapiens.
XX
OS
XX
FH Key Location/Qualifiers
FT Peptide 1..24
FT Region /note= "Signal sequence"
FT Modified-site 4..181
FT /note= "PMP-32/EMP/MP20/Claudin family (not defined)"
FT Modified-site 17..22
FT /note= "N-myristoylation site"
FT Modified-site 20..25
FT /note= "N-myristoylation site"
FT Protein 25..230
FT /note= "Mature TAT134"
FT Modified-site 60..65
FT /note= "N-myristoylation site"
FT Domain 82..102
FT /note= "Transmembrane domain"

FT Modified-site 101..106
FT /note="N-myristoylation site"
FT Domain 120..140
FT /note="Transmembrane domain"
FT Modified-site 128..133
FT /note="N-myristoylation site"
FT Domain 160..180
FT /note="Transmembrane domain"
FT Modified-site 167..172
FT /note="N-myristoylation site"
FT Modified-site 178..183
FT /note="N-myristoylation site"
FT Modified-site 190..193
FT /note="Asn is N-glycosylated"
FT Modified-site 215..224
FT /note="Tyrosine kinase phosphorylation site"
XX WO200216429-A2.
XX
XX 28-FEB-2002.
XX
XX 22-JUN-2001; 2001WO-US020118.
XX
XX 24-AUG-2000; 2000WO-US023328.
XX 26-SEP-2000; 2000US-0235451P.
XX 01-DEC-2000; 2000WO-US032678.
XX 28-FEB-2001; 2001WO-US006520.
XX 01-MAR-2001; 2001WO-US006666.
XX
XX (GETH) GENENTECH INC.
XX
XX Goddard A, Godowski FJ, Gurney AL, Hillan KJ, Polakis P, Smith V,
XX Wood WI, Wu TD, Zhang Z;
XX WPI; 2002-280917/32.
XX N-PSDB; ABK11089.
XX
XX Novel isolated tumor-associated antigenic target polypeptides which are
XX useful as targets for cancer therapy and diagnosis in mammals.
XX
XX Claim 12; Fig 6; 121pp; English.
XX
XX The invention relates to an isolated tumour-associated antigenic target
XX polypeptide (TAP) (I), specifically TAP134-TAP138 polypeptides, and the
XX polynucleotides (II) encoding them. (II) is useful for diagnosing the
XX presence of a tumour in a mammal, where the level of expression of (II)
XX is indicative of the presence of tumour in the mammal from which the test
XX sample was obtained. Antibody to (I) is useful for killing a cancer cell
XX (e.g. breast cancer cell, a colorectal cancer cell, a lung cancer cell,
XX an ovarian cancer cell, a central nervous system (CNS) cancer cell, a
XX liver cancer cell, a bladder cancer cell, a pancreatic cancer cell, a
XX melanoma cell or a leukemia cell) that expresses (I). Oligonucleotides
XX hybridizing to (II) are useful as diagnostic probes, antisense
XX oligonucleotide probes or for encoding fragments of full length TAP
XX polypeptide. (II) is also useful in chromosome and gene mapping and in
XX the generation of antisense RNA and DNA probes, for constructing
XX hybridisation probes for mapping the gene encoding TAP and for genetic
XX analysis of individuals with genetic disorders. (II) is also useful for
XX generating either transgenic animals or knockout animals, and in gene
XX therapy. The TAP polypeptides and nucleic acids may also be used for
XX tissue typing and the TAP polypeptides are useful for screening compounds
XX that mimic the TAP polypeptide (agonist) or prevent the effect of TAP
XX polypeptide (antagonist). The antibody is useful for staging TAP
XX polypeptide-expressing cancers, purifying or immunoprecipitating TAP
XX polypeptide from cells, for detection and quantitation of TAP polypeptide
XX in vitro, e.g., in an enzyme linked immunosorbent assay (ELISA) or
XX western blot. The antibodies are also useful for treating a TAP-
XX expressing cancer or alleviating one or more symptoms of cancer in a
XX mammal. The present sequence represents the amino acid sequence of TAP134
XX
XX Sequence 230 AA;
XX
XX Query Match 100.0%; Score 1174; DB 5; Length 230;

Best Local Similarity 100.0%; Pred. No. 1.1e-116;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASLGQLVGYIIGLLGLTAVAMLLPSWKTSYVGASIVFAVGSKGLAMECATHTSTG 60
DB 1 MASLGQLVGYIIGLLGLTAVAMLLPSWKTSYVGASIVFAVGSKGLAMECATHTSTG 60
QY 61 ITQCDIYSTLLGLPADIOAAQAMWVTSASISLACTIISVGMKCTVFCQESRAKDRVAVA 120
DB 61 ITQCDIYSTLLGLPADIOAAQAMWVTSASISLACTIISVGMKCTVFCQESRAKDRVAVA 120
QY 121 GGVPFLIGLGLGPIPVAMNHLGIRDPFSPLVDSNKFPEIGELLYIGIISLSFLAGIT 180
DB 121 GGVPFLIGLGLGPIPVAMNHLGIRDPFSPLVDSNKFPEIGELLYIGIISLSFLAGIT 180
QY 181 LCFSCSSQRNRSNYDAYOQAPLATRSSPPGQPPVKYSFNSYSLTGYY 230
DB 181 LCFSCSSQRNRSNYDAYOQAPLATRSSPPGQPPVKYSFNSYSLTGYY 230
RESULT 14
ABG64507 standard; protein; 230 AA.
XX
XX ABG64507;
XX
XX 27-AUG-2002 (first entry)
XX
XX Human albumin fusion protein #1182.
XX
XX Albumin fusion protein; therapeutic protein X; human albumin; HA;
XX human serum albumin; HSA; cancer; reproductive disorder;
XX digestive disorder; immune disorder; endocrine disorder;
XX hematopoietic disorder; neural disorder; connective disorder;
XX cytostatic; antiinfectility; antiinflammatory; anticler;
XX immunomodulator; anti-HIV; antidiabetic; haemostatic; nocotropic;
XX neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
XX osteopathic; antiarthritic.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200177137-A1.
XX
XX 18-OCT-2001.
XX
XX 12-APR-2001; 2001WO-US011988.
XX
XX 12-APR-2000; 2000US-0229358P.
XX 25-APR-2000; 2000US-0199384P.
XX 21-DEC-2000; 2000US-0256931P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Haseltine WA;
XX WPI; 2002-010886/01.
XX
XX New fusion protein for treating disease e.g. diabetes comprises an
XX albumin fused to a therapeutic protein.
XX
XX Claim 1; Page 1277-1278; 2102pp; English.
XX
XX The present invention relates to albumin fusion proteins comprising a
XX therapeutic protein X and human albumin (HA, also known as human serum
XX albumin, HSA). The proteins are useful for treating a disease or disorder
XX that may be modulated by therapeutic protein X. The albumin extends the
XX shelf-life of protein X, and may increase its biological in vitro/in vivo
XX activity. The protein is useful for treating and diagnosing disorders
XX such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's
XX disease, ulcerative colitis), immune disorders (e.g. acquired
XX immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),
XX hematopoietic disorders, neural disorders (e.g. Alzheimer's,

CC Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,
CC schistosomiasis, and connective tissue disorders (e.g. osteoporosis, arthritis).
CC ABG63326-ABG65518 represent albumin fusion proteins of the invention
XX
SQ Sequence 230 AA:

Query Match 100.0%; Score 1174; DB 5; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.1e-116;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYILGLGLTLVAMLLPSMKTSSYVGASIVTAVGFSKGLMECAHSTG 60
DB 1 MASLGQLVGYILGLGLTLVAMLLPSMKTSSYVGASIVTAVGFSKGLMECAHSTG 60
QY 61 ITQCDIYSTLLGLPADIQAAQAMMTSSAISLACIIISVGMCTVFCQESRAKRVAVA 120
DB 61 ITQCDIYSTLLGLPADIQAAQAMMTSSAISLACIIISVGMCTVFCQESRAKRVAVA 120
QY 121 GGVFFILGLGLGFIPIVAMNHLGILRDFSPPLVDSMKFEIGBALYIGIISLPSLIAGII 180
DB 121 GGVFFILGLGLGFIPIVAMNHLGILRDFSPPLVDSMKFEIGBALYIGIISLPSLIAGII 180
QY 181 LCFSSCSQRNRSNYYDAYQAOPLATRSSPRPGQPKVKSSEFNSYSLTGYV 230
DB 181 LCFSSCSQRNRSNYYDAYQAOPLATRSSPRPGQPKVKSSEFNSYSLTGYV 230

RESULT 15

ABB04707
ID ABB04707 standard; protein; 230 AA.
XX
AC ABB04707;
XX
DT 11-MAR-2002 (first entry)
XX
DE Human SP82 protein SEQ ID NO:2.
XX
KW Human; SP82; cancer suppression.
XX
OS Homo sapiens.
XX
FN CN1313315-A.
XX
PD 19-SEP-2001.
XX
PF 13-MAR-2000; 2000CN-00111989.
XX
PR 13-MAR-2000; 2000CN-00111989.
XX
PA (SHAN-) SHANGHAI INST ONCOLOGY.
XX
PI Gu J, Yang S;
XX
DR WPI, 2002-042193/06.
XX
DR N-PSDB; ABA0424.
XX
PT New human protein able to suppress growth of cancer cells and its
XX encoding polynucleotide sequence.
XX
PS Claim 1; Page 12 (Disclosure); 42pp; Chinese.
XX
CC The present sequence represents human SP82 protein, which has cancer-
XX suppressing activity. The present invention also describes a method for
XX the preparation of the protein by recombination, and the application of
XX the protein in treating diseases such as cancer
SQ Sequence 230 AA:

Query Match 100.0%; Score 1174; DB 5; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.1e-116;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYILGLGLTLVAMLLPSMKTSSYVGASIVTAVGFSKGLMECAHSTG 60

DB 1 MASLGQLVGYILGLGLTLVAMLLPSMKTSSYVGASIVTAVGFSKGLMECAHSTG 60
QY 61 ITQCDIYSTLLGLPADIQAAQAMMTSSAISLACIIISVGMCTVFCQESRAKRVAVA 120
DB 61 ITQCDIYSTLLGLPADIQAAQAMMTSSAISLACIIISVGMCTVFCQESRAKRVAVA 120
QY 121 GGVFFILGLGLGFIPIVAMNHLGILRDFSPPLVDSMKFEIGBALYIGIISLPSLIAGII 180
DB 121 GGVFFILGLGLGFIPIVAMNHLGILRDFSPPLVDSMKFEIGBALYIGIISLPSLIAGII 180
QY 181 LCFSSCSQRNRSNYYDAYQAOPLATRSSPRPGQPKVKSSEFNSYSLTGYV 230
DB 181 LCFSSCSQRNRSNYYDAYQAOPLATRSSPRPGQPKVKSSEFNSYSLTGYV 230

Search completed: October 27, 2004, 07:17:45
Job time : 159 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model

Run on: October 27, 2004, 07:11:26 ; Search time 40 Seconds
(without alignments)
381.329 Million cell updates/sec

Title: US-09-787-677a-3

Perfect score: 1174

Sequence: 1 MASLGLVGYITGLGLG.....PGQPKVSEFNSYSTGYV 230

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued_Patente_AA:*
2: /cgn2_6/prodata/1/iaa/5A COMB .pep:*
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6: /cgn2_6/prodata/1/iaa/backfile1 .pep:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1174	100.0	230	US-09-663-600A-186	Sequence 186, App
2	1174	100.0	230	US-10-140-002-492	Sequence 492, App
3	1162	99.0	230	US-09-663-600A-92	Sequence 92, App
4	450	38.3	220	US-09-603-552-13	Sequence 13, App
5	427.5	36.4	225	US-09-673-395A-354	Sequence 354, App
6	423.5	36.1	247	US-09-130-491-15	Sequence 15, App
7	411.5	35.1	202	US-09-205-258-344	Sequence 344, App
8	407.5	34.7	211	US-09-130-491-4	Sequence 4, App
9	407.5	34.7	211	US-09-603-552-12	Sequence 12, App
10	407.5	34.7	211	US-09-886-683A-4	Sequence 4, App
11	378	32.2	218	US-09-130-491-14	Sequence 14, App
12	378	32.2	218	US-09-489-847-209	Sequence 209, App
13	314.5	26.8	228	US-09-603-552-1	Sequence 1, App
14	275	23.4	264	US-09-724-864-64	Sequence 64, App
15	223.5	19.0	137	US-09-188-930-174	Sequence 174, App
16	223.5	19.0	137	US-09-312-283C-174	Sequence 174, App
17	222	18.9	42	US-09-282-029A-7	Sequence 7, App
18	222	18.9	42	US-09-185-908-7	Sequence 7, App
19	210	17.9	113	US-09-621-976-5695	Sequence 5695, App
20	185.5	15.8	207	US-08-557-917A-2	Sequence 2, App
21	185.5	15.8	207	US-09-084-153-2	Sequence 2, App
22	185.5	15.8	207	US-09-084-079-2	Sequence 2, App
23	179	15.2	99	US-09-084-079-5	Sequence 5, App
24	174.5	14.9	99	US-09-621-976-4220	Sequence 4220, App
25	128	10.9	72	US-09-489-847-366	Sequence 366, App
26	128	10.9	73	US-09-489-847-241	Sequence 241, App
27	117	10.0	42	US-09-282-029A-6	Sequence 6, App

28	117	10.0	42	US-09-282-029A-11	Sequence 11, App
29	117	10.0	42	US-09-185-908-6	Sequence 6, App
30	117	10.0	42	US-09-185-908-11	Sequence 11, App
31	113	9.6	42	US-09-282-029A-8	Sequence 8, App
32	113	9.6	42	US-09-282-029A-10	Sequence 10, App
33	113	9.6	42	US-09-185-908-8	Sequence 8, App
34	113	9.6	42	US-09-185-908-10	Sequence 10, App
35	112	9.5	42	US-09-282-029A-9	Sequence 9, App
36	112	9.5	42	US-09-185-908-9	Sequence 9, App
37	105	8.9	32	US-09-205-258-872	Sequence 872, App
38	104.5	8.9	41	US-09-282-029A-12	Sequence 12, App
39	104.5	8.9	41	US-09-185-908-12	Sequence 12, App
40	101.5	8.6	323	US-09-123-030-8	Sequence 8, App
41	100	8.5	30	US-09-489-039A-8166	Sequence 8166, App
42	100	8.5	443	US-09-252-991A-10883	Sequence 10883, App
43	99	8.4	634	US-09-540-236-2483	Sequence 2483, App
44	98	8.3	160	US-08-600-430-5	Sequence 5, App
45	91	7.8	3		

ALIGNMENTS

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RESULT 1
US-09-663-600A-186
; Sequence 186, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Ducleit, Aymeric
; APPLICANT: Bouguerelet, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31 US3 CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 186
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -24..-1
; US-09-663-600A-186

Query Match      100.0%; Score 1174; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 3e-121;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MASLGLVGYITGLGLGLTIVAMLLPSWKTSYVGASIVTAVGFSKGLIMECATHTSG 60
DB      1 MASLGLVGYITGLGLGLTIVAMLLPSWKTSYVGASIVTAVGFSKGLIMECATHTSG 60
QY      61 ITQCDYVSTLGLPATIOAQAAMMTSSAISLACTIIVGRCCTVFCQESPAKDXVAVYA 120
DB      61 ITQCDYVSTLGLPATIOAQAAMMTSSAISLACTIIVGRCCTVFCQESPAKDXVAVYA 120
QY      121 GGVFTIIGLGLFIPVAMMLHGILRDFYSLVDKSKFEIGELALYGLIISLFLIAGII 180
DB      121 GGVFTIIGLGLFIPVAMMLHGILRDFYSLVDKSKFEIGELALYGLIISLFLIAGII 180
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 344
LENGTH: 202
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (202)
OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-344
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Query Match 35.1%; Score 411.5; DB 4; Length 202;
Best local Similarity 38.0%; Pred. No. 3e-37;
Matches 76; Conservative 49; Mismatches 70; Indels 5; Gaps 1;
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9 VGIILGLGLGLVLMALPSWKTSSYVGAISYTVANGFSGLMNECATHTSTGTTCDDIYS 68
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Db 1 MGIALAVLGLMVLMLCCALPMNRVTAFISGNTVTSQTIIEGLMNCVOSTGOMCKRYD 60
Qy 69 TLGLPADIQAAQMMVTSSAISLACIISVGMRCVFCOSRANRVAVAGVFILG 128
Db 61 SILALPQDQAAALVYIISIIYVAALGVLLSVGCKTNLEBESAKMTMIVAGVFLLA 120
Qy 129 GLIGFIPVAMNTHGILRDYSPVPSMKEFEGEALYLGIIISLFLINGIILCRSCSQ 188
Db 121 GLMIVIPVSWTAMNIIQDFYNPVLSGQREMGASLYVMAASGLLLGGLCCNCPPR 180
Qy 189 RNSNYYDAYOAOPLATRSS 208
Db 181 TDK-----PYSAKYSAAKSA 195
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```
RESULT 8
US-09-130-491-4
Sequence 4, Application US/09130491
Patent No. 6416974
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodheart, Andrew D.J.
TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
FILE REFERENCE: 09404/041001
CURRENT APPLICATION NUMBER: US/09/130,491
EARLIER FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: US 60/058,108
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: US 60/054,961
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 211
TYPE: PRT
ORGANISM: Homo sapiens
US-09-130-491-4
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Query Match 34.7%; Score 407.5; DB 4; Length 211;
Best local Similarity 37.3%; Pred. No. 8.8e-37;
Matches 81; Conservative 41; Mismatches 78; Indels 17; Gaps 2;
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Qy 1 MASLGIVGYIIGLGLGLVLMALPSWKTSSYVGAISYTVANGFSKGLMNECATHTSTG 60
Db 1 MANAGQLGLGFILAFGWIQALVSTLPMRITYVAGDNIIVAOAMVEGLMNSCVSQSTG 60
Qy 61 ITQCDDYSTLGLPADIQAAQMMVTSSAISLACIISVGMRCVFCQESRA-KORVAV 119
Db 61 QIQCKVFDLSLNSSTLQATRALMVGILGVIAIVATVGMCKCLEDEDEVQKRMAY 120
Qy 120 AGGVFPIGLGLGFIPVAMNTHGILRDYSPVPSMKEFEGEALYLGIIISLFLIAGI 179
Db 121 IGGAIIFLAGLAIIVATVANGNRIVGEFDPMTPVARAREFQGLFTGMAAASLCLGGA 180
Qy 180 ILCFSCSQRNSNYYDAYOAOPLATRSSPPRCQPPK 216
Db 181 LILCCSC-----PRKTSYTPRPYK 201
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RESULT 9
US-09-603-552-12
Sequence 12, Application US/09603552
Patent No. 6590089
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: RVP-1 VARIANT DIFFERENTIALLY EXPRESSED IN CROHN'S DISEASE
FILE REFERENCE: PC-0016 US
CURRENT APPLICATION NUMBER: US/09/603,552
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PERL Program
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; SEQ ID NO 12
; LENGTH: 211
; TYPE: PR
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: incycle ID No. 6590089 2057608CD1
US-09-603-552-12

Query Match      34.7%; Score 407.5; DB 4; Length 211;
Best Local Similarity 37.3%; Pred. No. 8.8e-37;
Matches 81; Conservative 41; Mismatches 78; Indels 17; Gaps 2;

QY 1 MASIGLQVGYIIIGLGLTLVAMLLPSWKTSSYVAGSIYTAAGFSGKLMGECATHTSG 60
D 1 MANAGLQDLFLAFLMIGWIGIVSTALPQWRIVYADNDIVTAQAMVEGIMSCVSGSTG 60
QY 61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIISVGMCTVFCQESRA-KDRVAV 119
D 61 QIQCKVDSLNTLSSTLQATRALMVVGILLGVIAIFVATVGMCKMCKLEDDEVQKRMMAV 120
QY 120 AGGVFFILGLGRIIPVAMNHLGRDPSGLVDSKMFRIEGLALYGIISLSFLAGI 179
D 121 IGGAFILLAGIALLVATWYGNRIYQEPDPTVNAHYEFQALFTGMAASICLLIGA 180
QY 180 ILFCSSQRNRSNYDAYQAQPLATRSSPPGQPK 216
D 181 LILCCSC-----PDKTSTYPRPRYPK 201

RESULT 10
US-09-886-683A-4
; Sequence 4; Application US/09886683A
; PATENT No. 6627439
; GENERAL INFORMATION:
; APPLICANT: Hoevel, Thorsten
; APPLICANT: Koch, Stefan
; APPLICANT: Kubbies, Manfred
; APPLICANT: Mundigsl, Olaf
; APPLICANT: Rueger, Petra
; TITLE OF INVENTION: Antibodies against SEMP1 (p23)
; FILE REFERENCE: Case 20692
; CURRENT APPLICATION NUMBER: US/09/886,683A
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: EP01107799.7
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 211
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-886-683A-4

Query Match      34.7%; Score 407.5; DB 4; Length 211;
Best Local Similarity 37.3%; Pred. No. 8.8e-37;
Matches 81; Conservative 41; Mismatches 78; Indels 17; Gaps 2;
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D 181 LILCCSC-----PDKTSTYPRPRYPK 201

RESULT 11
US-09-130-491-14
; Sequence 14; Application US/09130491
; Patent No. 6416974
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/09/130,491
; PRIOR FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: US 60/058,108
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: US 60/054,961
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 218
; TYPE: PR
; ORGANISM: Rattus rattus
US-09-130-491-14

Query Match      32.2%; Score 378; DB 4; Length 218;
Best Local Similarity 36.2%; Pred. No. 1.6e-33;
Matches 76; Conservative 52; Mismatches 76; Indels 6; Gaps 3;

QY 1 MASIGLQVGYIIIGLGLTLVAMLLPSWKTSSYVAGSIYTAAGFSGKLMGECATHTSG 60
D 1 MGSALIEILGLVLCVWGGLILACGLPMWQVAFIDHNIVTAQTMKGLMNSCVSGSTG 60
QY 61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIISVGMCTVFCQESRAKDRYVA 120
D 61 HMCKVDSVLTALSTEVQARALTVASAVLLAFVALLFVTLAQCCTCVAPGPAKARVALT 120
QY 121 GGVFFILGLGRIIPVAMNHLGRDPSGLVDSKMFRIEGLALYGIISLSFLAGI 180
D 121 GGVLYLFCGLIALLVPLCFWPNIVYREYDPSVSKTEIGALLYTGMAATLALLMVGGCL 180
QY 181 LC---FSCSSQRNRSNYDAYQA--OPLAT 205
D 181 LCCGANVCTGRPDL--FPVYISAPRRPRAT 209

RESULT 12
US-09-489-847-209
; Sequence 209; Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; PRIOR FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 209
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LENGTH: 218
TYPE: PRT
ORGANISM: Homo sapiens
US-09-489-847-209

Query Match 32.2%; Score 378; DB 4; Length 218;
Best Local Similarity 36.2%; Pred. No. 1.6e-33;
Matches 76; Conservative 52; Mismatches 76; Indels 6; Gaps 3;

1 MASLGOLVYIIGLIGLITLVAMLLPSKTSYVGAIVTAVGSKGLMCAHSTG 60
1 MGSALFELVCLVGMGGLIACGIPMOTAFEDHNVITQTTKGLMGCVVOSTG 60
61 ITCCDIYTLGLPADIOAAMWTSASISLACIISVGMCTVFCQESRAKDRVAV 120
61 HMCKYVDSVIALSTEQABALTVSAVLAPVALFVTLAAGCTTCVAPAKARVALT 120
121 GGVFFILGLIGLIPVAMNHLGILRDPYSPVDSMKFEIGELALYIGIISLSLAGIT 180
121 GGVLYIFCGILALVPLCMFANIVREFPSVPVSOKEIGALYIGMATALLMVGGL 180
181 LC---FSCSGQRNSNYDAYQA--OPLAT 205
181 LCCGANVCTGRPLS-FPVKYSAPRRPTAT 209

RESULT 13
US-09-603-552-1
Sequence 1, Application US/09603552
Patent No. 6590089
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: RVP-1 VARIANT DIFFERENTIALLY EXPRESSED IN CROHN'S DISEASE
FILE REFERENCE: PC-0016 US
CURRENT APPLICATION NUMBER: US/09/603,552
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 228
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6590089 1456746CD1
US-09-603-552-1

Query Match 26.8%; Score 314.5; DB 4; Length 228;
Best Local Similarity 32.5%; Pred. No. 1.8e-26;
Matches 78; Conservative 47; Mismatches 90; Indels 25; Gaps 10;
3 SLGLQVGYIIGLIGLITLVAMLLPS--WKTSSVGAIVTAVGSKGLMCAHSTG 60
2 SMAVEFFGFMAVYGLL--MLGVTLPSYVRVST-VHGANITNTJTFENLWFCADSLG 58
61 ITCCDIYTLGLPADIOAAMWTSASISLACIISVGMCTVFCQESRAKDRVAV 120
59 VYMCWEPSPMLASGYIACRALMTAILGLGLIGLIGLACTN--GGLBSKRYQA 116
121 GG---VFFILGLIGLIPVAMNHLGILRDPYSPVDSMKFEIGELALYIGIISLSLAGIT 177
117 GGRRAHLLIAGICGWAIAISVAFNITRDFDPLYPGT-KYELGALYILMWSASLSILG 175
178 GILLCBSC---SSGRNSNYDAYQA---QPLATRSPPRGQPKKSEFNYSLSLGYV 230
176 GLCLCSACCGSDPDAASARPPYQAPVSVMPVAT--SDQEGD-----SSFGKYGNNAYV 228

RESULT 14
US-09-724-864-64
Sequence 64, Application US/09724864

Patent No. 6380362
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Murison, James G.
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
TITLE OF INVENTION: by the polynucleotides and methods for their use.
FILE REFERENCE: 11000.105001
CURRENT APPLICATION NUMBER: US/09/724,864
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO 64
LENGTH: 264
TYPE: PRT
ORGANISM: Mouse
US-09-724-864-64

Query Match 23.4%; Score 275; DB 3; Length 264;
Best Local Similarity 27.3%; Pred. No. 4.9e-22;
Matches 62; Conservative 48; Mismatches 101; Indels 16; Gaps 4;

1 MASLGOLVYIIGLIGLITLVAMLLPSKTSYVGAIVTAVGSKGLMCAHSTG 60
1 MATTCQVVGILSLIGLICTAATGMDWSTQDLYD-NPVTAVFQHEGLMRSVQOQSG 59
61 ITCCDIYTLGLPADIOAAMWTSASISLACIISVGMCTVFCQESRAKDRVAV 119
60 FTBCREYFIIIGLIPALQVRAVMIVGIVIGLIVSIFALKICRIGMDSDAKAKMTL 119
120 AGGVFFILGLIGLIPVA-----W-----NLGILRDPYSPVDSMKFEIGELALY 165
120 TSGILFIIGLIGLIGLIPVAMNHLGILRDPYSPVDSMKFEIGELALY 179
166 LGIISLSFSLIAGLIGLIFSCSGQRNSNYDAYQAQPLATRSPPRG 212
180 VGVNAGGLTILIGVMMICRGLTTPDSNFKAVSYHASQNVAYIRPG 226

RESULT 15
US-09-188-930-174
Sequence 174, Application US/09188930A
Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
TITLE OF INVENTION: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FaastSeq for Windows Version 3.0
SEQ ID NO 174
LENGTH: 137
TYPE: PRT
ORGANISM: Human
US-09-188-930-174

Query Match 19.0%; Score 223.5; DB 3; Length 137;
Best Local Similarity 35.7%; Pred. No. 9.1e-17;
Matches 41; Conservative 30; Mismatches 43; Indels 1; Gaps 1;

67 YSTLGLPADIOAAMWTSASISLACIISVGMCTVFCQESRAKQ-RVAVAGGVFF 125
7 YDSVIALSALQTRALMVSVSLVGLFAMFVATMGKCTRCGGDDRYKARIAMGGIIF 66
126 ILGGLIGLIPVAMNHLGILRDPYSPVDSMKFEIGELALYIGIISLSLAGIT 180

Db 67 IVAGLAALVACSWYGHQIVTDFYNPLIPTNIKYEFGPAIFIGWAGSALVILGAL 121

Search completed: October 27, 2004, 07:22:34
Job time : 41 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 27, 2004, 07:11:11 ; Search time 38 Seconds
(without alignments)
582.365 Million cell updates/sec

Title: US-09-787-677A-3
Perfect score: 1174
Sequence: 1 MASLGLVGVILGLLGLG.....PGQPKVKSSEFNSYLTVY 230

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_79:.*
2: PIR1:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	423.5	36.1	280	A39484	androgen-withdrawn
2	100	8.5	400	AG2866	MPS permease [drug]
3	100	8.5	400	D97643	probable efflux pr
4	99.5	8.5	330	C69648	2-keto-3-deoxygluc
5	99.5	8.5	463	F90285	metabolite transpo
6	97.5	8.1	484	C75609	amino acid ABC tra
7	95.5	8.1	458	H71657	NADH2 dehydrogenas
8	93	7.9	523	T11916	NADH2 dehydrogenas
9	91	7.8	160	UN0503	peripheral myelin
10	90.5	7.7	487	T19237	hypothetical prote
11	90.5	7.5	619	F71019	hypothetical prote
12	88.5	7.5	429	A97241	permease [imported
13	88.5	7.5	521	A99549	amino acid permeas
14	88.5	7.5	593	H71283	conserved hypothet
15	88	7.5	160	A41144	growth arrest-tela
16	88	7.5	421	A99309	membrane transport
17	88	7.5	906	G90281	conserved hypothet
18	87.5	7.5	268	A71086	hypothetical prote
19	87.5	7.5	420	H96534	probable Na+/H+ an
20	87.5	7.5	519	T15364	hypothetical prote
21	87.5	7.5	690	S35251	tumor-associated m
22	87	7.4	157	G02355	probable membrane
23	87	7.4	160	S21721	growth arrest-spec
24	87	7.4	223	B87654	hypothetical prote
25	87	7.4	318	AG3576	iron(III) dicitrat
26	87	7.4	414	B85970	probable transport
27	87	7.4	414	C91125	probable transport
28	87	7.4	414	C91125	probable transport
29	86.5	7.4	255	B64604	conserved hypothet

30	86.5	7.4	402	A11853	sodium-dependent n
31	86.5	7.4	432	A70714	hypothetical prote
32	86.5	7.4	428	D97799	NADH2 dehydrogenas
33	86.5	7.4	497	AD3525	amino acid permeas
34	86.5	7.4	547	B64963	membrane protein y
35	86	7.3	388	UQ0113	2-keto-3-deoxygluc
36	86	7.3	409	S29124	membrane glycoprot
37	86	7.3	562	T52481	cytochrome-c oxida
38	85.5	7.3	216	I38474	olfactory receptor
39	85.5	7.3	371	D75266	cell division prot
40	85.5	7.3	414	AG0894	probable membrane
41	85.5	7.3	445	T11097	NADH2 dehydrogenas
42	85	7.2	233	T31865	hypothetical prote
43	85	7.2	502	B70845	probable sugar tra
44	85	7.2	531	T11074	NADH2 dehydrogenas
45	84.5	7.2	454	C86766	hypothetical prote

ALIGNMENTS

RESULT 1

A39484 androgen-withdrawal apoptosis protein RVPI, prostatic - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 04-Mar-2000

C/Accession: A39484

R/Brieh, M.M.; Miesfeld, R.L.

Mol. Endocrinol. 5, 1381-1388, 1991

A/Title: Isolation and characterization of transcripts induced by androgen withdrawal and

A/Reference number: A39484; MUID:92130987; PMID:1723140

A/Accession: A39484

A/Molecule type: mRNA

A/Residues: 1-280 <BRI>

A/Cross-references: GB:W74067; NID:G205857; PIDN:AAA1760.1; PID:G205858

A/Genetics:

A/Gene: RVP.1

C/Superfamily: rat androgen-withdrawal apoptosis protein RVPI

Query Match	36.1%	Score 423.5;	DB 2;	Length 280;
Best Local Similarity	37.7%	Pred. No. 2.4e-28;		
Matches	84;	Conservative	50;	Mismatches 74;
				Indels 15;
				Gaps 3;
Qy	3	SLGLVGVILGLLGLTVA	MLPSMKTSSVYGASIV	AVGFSKLAAMECATSHGIT 62
Db	2	SMSLRTGTSIAVGLWCT	IVCCALPMKVSARIGSS	ITRQITWEGIAVNC-VQSTGQM 60
Qy	63	QCDIYSTLGLPADIQAAQ	AMVYSSAISLACTISV	GNRCVFCQESRAKDRVAVAG 122
Db	61	QCKMYDSLALPQDLQAR	ALIVSILAAFGLLVLA	VGACINVCVDETAKAKITVAG 120
Qy	123	VPTLGLGLFIPYANMLH	GLDFFSPLVPDSMKPF	IGALVIGTISLSFLIAGITLC 182
Db	121	VLFLAAVLTLPVPSWANT	IRDFVNPVPEAQKREMG	GLVGMMAAQLDLGALLC 180
Qy	183	FSCSSORNSRNYDAYAO	PLAT-----RSSPRG	212
Db	181	CSCPPREKVAPTKILYSA	-PRSTGPGTGTATDRKTS	SRPG 222

RESULT 2

AG2866 MPS permease [drug] [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C/Species: Agrobacterium tumefaciens

C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C/Accession: AG2866

R/Wood, D.W.; Secubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McCellie

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E

ster, E.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A/Reference number: AB2577; MUID:21608550; PMID:11743193
A/Accession: AG2866
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-400 <KUR>
A/Cross-references: UNIPROT:Q8UCX2; GB:AE006688; P1DN:AA43349.1; P1D:G17740844; GSPDB:C
A/Experimental source: strain C58 (Dupont)
A/Genetics:
A/Map position: circular chromosome

Query Match 8.5%; Score 100; DB 2; Length 400;
Best Local Similarity 21.2%; Pred. No. 0.56;
Matches 44; Conservative 31; Mismatches 67; Indels 66; Gaps 7;

QY 8 LVGVIILGLGLGVVAMLLPSWKTSSVGSATVAVFGSKGLMECATSTGTGQDIY 67
DB 243 VAGYATGIFMLAGLMA--LSFGRLRARIGVTYLLAAGL-----VLMATGF----- 286
QY 68 STLGLPADIOAMQMMVTSASISLACTISVVG-----MRCVFCQESRARDV 117
DB 287 -----ALATAGGLSSMLALAVGAGLGAWVPSIMSTTLMALPLRLRGRI 332
QY 118 A--VAGVFPILGLGLGFIVANMLHGLIDFYSPLVPDSMKKEIGALYIGTISLFSL 175
DB 333 AGIVTASMF-----LGHFISPLVSQPMIARFGPATYRDIALVFAV 373
QY 176 IAGIILCFSCSSQRRNSNYDAYOAPL 203
DB 374 MAGLAATATIFORT-----GIRKQPL 396

RESULT 3
D97643
probable efflux protein cjl687 (imported) - Agrobacterium tumefaciens (strain C58, Cerec
C/Species: Agrobacterium tumefaciens
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C/Accession: D97643
R/Gooder, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Gurolo, B.; Goldman,
A.; Liu, F.; Mollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A/Reference number: A97359; MUID:21608551; PMID:11743194
A/Accession: D97643
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-400 <KUR>
A/Cross-references: UNIPROT:Q8UCX2; GB:AE007869; P1DN:AAK8101.1; P1D:G15157533; GSPDB:C
A/Genetics:
A/Map position: circular chromosome

Query Match 8.5%; Score 100; DB 2; Length 400;
Best Local Similarity 21.2%; Pred. No. 0.56;
Matches 44; Conservative 31; Mismatches 67; Indels 66; Gaps 7;

QY 8 LVGVIILGLGLGVVAMLLPSWKTSSVGSATVAVFGSKGLMECATSTGTGQDIY 67
DB 243 VAGYATGIFMLAGLMA--LSFGRLRARIGVTYLLAAGL-----VLMATGF----- 286
QY 68 STLGLPADIOAMQMMVTSASISLACTISVVG-----MRCVFCQESRARDV 117
DB 287 -----ALATAGGLSSMLALAVGAGLGAWVPSIMSTTLMALPLRLRGRI 332
QY 118 A--VAGVFPILGLGLGFIVANMLHGLIDFYSPLVPDSMKKEIGALYIGTISLFSL 175
DB 333 AGIVTASMF-----LGHFISPLVSQPMIARFGPATYRDIALVFAV 373
QY 176 IAGIILCFSCSSQRRNSNYDAYOAPL 203
DB 374 MAGLAATATIFORT-----GIRKQPL 396

RESULT 4
C69648
2-keto-3-deoxygluconate permease kdgT - Bacillus subtilis
C/Species: Bacillus subtilis
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: C69648
R/Kunst, F.; Ogaawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertec
C./Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A./Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A/Authors: Foulger, D.; Fultz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallazzi, A.; Gallie
Jech, J.; Harwood, C.R.; Hanaul, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lepidus, A.; Leduc, J.
A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mueel,
Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,
A/Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero,
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Teopetra, P.; Tognoni, A.; Tosato, V.; Uchiyama, K.
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A/Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: A69580; MUID:98044033; PMID:9384377
A/Accession: C69648

A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-330 <KUN>
A/Cross-references: UNIPROT:P50847; GB:Z99115; GB:AL009126; NID:G2634478; P1DN:CAB14126.J
A/Experimental source: strain 168
A/Genetics:
A/Map position: circular chromosome

Query Match 8.5%; Score 99.5; DB 2; Length 330;
Best Local Similarity 24.4%; Pred. No. 0.51;
Matches 51; Conservative 30; Mismatches 77; Indels 51; Gaps 11;

QY 2 ASIGLQVGYI-----LGLGLGLGVVAMLLP--SWKTSSVGSATVAVG-- 46
DB 60 ATIDFSSGTYARKGTTLLGKIGFALGVINAQPIPDGIGSGFAGLSVATVAVMN 119
QY 47 --SKGLMECATSTGTGQDIYTLGLPADIOAMQMMVTSASISLACTISVGMRC 104
DB 120 ETMGGLYALMNR-----MGRKED--AGAFAPSTSGPFMTVTGCVGL-- 163
QY 105 TVFCQESRARDVAVAGVFPILGLGLGFIVANMLHGLIDFYSPLVP--DSMKKEIG 161
DB 164 AAFPWETLA-----ATVIFPLIGCILG-----NDDHLDLDFSKVPAIIFFAFSLG 211
QY 162 EALYVGI--SPLSLAGI--ILCFSCSS 167
DB 212 NTLNFGMLIQSGLGLGIFGVSVILSGSS 240

Query Match 8.5%; Score 99.5; DB 2; Length 463;
Best Local Similarity 24.4%; Pred. No. 0.51;
Matches 51; Conservative 30; Mismatches 77; Indels 51; Gaps 11;

RESULT 5
F90285
metabolite transport related protein SSO1305 (imported) - Sulfolobus solfataricus
C/Species: Sulfolobus solfataricus
C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C/Accession: F90285
R/She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyze, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sersen, C.W.; Van der Oost, J.
Submitted to Genbank, April 2001
A/Description: Sulfolobus solfataricus complete genome.
A/Reference number: A99139
A/Accession: F90285
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-463 <KUR>
A/Cross-references: UNIPROT:Q97YU8; GB:AE006641; NID:G13814507; P1DN:AAK41541.1; GSPDB:G
A/Genetics:
A/Map position: circular chromosome

Best Local Similarity 23.8%; Pred. No. 0.71;
Matches 44; Conservative 35; Mismatches 59; Indels 47; Gaps 10;
QY 6 LQVVGITGLGTLVAMLLPSMKTSSVYGVASIVTAVGSGKLMW 56
DB 288 VQIAFPVTAITGVGVVQMSDKVRRLVAVSSLCIAGPILGPFILVWALFNVF 347
QY 57 -----HSTGI--TCDDIYTLGLPADIQ-AAQ-----AMVTSASISLACTISV 100
DB 348 LPEFGHMLMPQTRVSTEL--PTEIRNTRAGVWGMWMAIALGINSIFVPS---ITTVI 403
QY 101 GMRCTVFCQESRAKRVAVAGVFFILGLGFIPIVAMNLHG-----ILRDFYSPVLD 155
DB 404 GY-----SALAAVATSEFIIITLGLL--VQPDTHGKSLAEVVIDFYGKVPVS 450
QY 156 MKFEI 160
DB 451 KVEV 455
RESULT 6
C75609
amino acid ABC transporter, permease protein - Deinococcus radiodurans (strain R1)
C/Species: Deinococcus radiodurans
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: C75609
R/White, O.; Eichen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
S/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A/Reference number: A75250; MUID:20036896; PMID:10567266
A/Accession: C75609
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-484 <MW>
A/Cross-references: UNIPROT:Q9R217; GB:AE001862; GB:AE001825; NID:G6460468; PIDN:AAF1222
A/Experimental source: strain R1
C/Genetics:
A/Gene: DRA0136
A/Map position: 2
Query Match 8.3%; Score 97.5; DB 2; Length 484;
Best Local Similarity 26.1%; Pred. No. 1.1;
Matches 55; Conservative 25; Mismatches 84; Indels 47; Gaps 9;
QY 14 GLLGLGTLVAMLLPSMKTSSVYGVASIVTAVGSGKLMWCAHSTGITCDDIYTLGL 73
DB 164 GVAGALFAVAPPLGKNTLGLVQYRNVADTF---WPQIGTHAALSVIALLLAALLGL 219
QY 74 PADIQAAQAMVTSAL---SSLACTISV--GMRCTVFCQESRAK----- 115
DB 220 PLGIAAARNRTRLAGVGFASFLQITIPSVALLGILLPVFSALGVSAGVAFLANSGAALL 279
QY 116 -----RVAVAGVFFILG-----GLGFIPIVAM--NLHGILRDFYS---PLV 152
DB 280 LGLALTRVRLALPGLIALGLAQLALLAGLGLVQLQAGMFGGDSLRDAPSLAPLA 339
QY 153 PDSMKFEIGALVYGIISLPSLIAGITLCP 183
DB 340 SMGVR-GTGAAPLFLAL-TLYALLPIVNTF 368
RESULT 7
H71657
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain N RP537 - Rickettsia prowazekii
C/Species: Rickettsia prowazekii
C/Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C/Accession: H71657
R/Anderson, S.G.B.; Zomorodipour, A.; Anderson, J.O.; Sichteritz-Ponten, T.; Almaraz, U
A/Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A/Reference number: A71630; MUID:39039499; PMID:9823893

A/Accession: H71657
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-458 <ND>
A/Cross-references: UNIPROT:Q9ZD13; GB:AJ235272; GB:AJ235269; NID:93861033; PIDN:CAA14986
A/Experimental source: strain Madrid B
C/Genetics:
A/Gene: nuon1, RP537
A/Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C/Keywords: membrane-associated complex; NAD; oxidoreductase
Query Match 8.1%; Score 95.5; DB 2; Length 458;
Best Local Similarity 23.6%; Pred. No. 1.5;
Matches 59; Conservative 33; Mismatches 73; Indels 85; Gaps 12;
QY 13 LGLGLGTLVAMLLP-----SMKTSSVYGVASIVTAVGSGKLMW 52
DB 10 LTVIALGQCFALMIDNKNRIYIVILCTIISIFLTFKYSI-----EGIWA 57
QY 53 ECAT-HSTGITQCDI-----YSTLLGLPADIQAAQAMVTSASISLA 94
DB 58 SPATERNIGISKIILLFTVSLIYRDYSILVGETLKEFTLMLSLIVGIFVALISSN 117
QY 95 CIISVVGMRCTVFCQESRA---KDRVAVAGV-FPIIGLGLFIPIVAMNLHGI----- 143
DB 118 FLPLFGCMELTALTSYALAGFKLNDIKSEGALKYFILGSLVSCV---SLFGISFIYGF 173
QY 144 -----ILRDFYSPVLDPSMKFEIGALVYGI---SSLFSLIAGIILCFSCSSGRNSNY 195
DB 174 GSGIQFDLILQNLNDS---EIKPGLIGIVLFSIFPKLSSPLHFWIP----- 221
QY 196 DAYAQOPLAT 205
DB 222 DVEGSPIS 231
RESULT 8
T11916
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Prototheca wickerhamii mitochondrion
C/Species: mitochondrion Prototheca wickerhamii
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T11916
R/Molff, G.; Planke, I.; Lang, B.F.; Kueck, U.; Burger, G.
J. Mol. Biol. 237, 75-86, 1994
A/Title: Complete sequence of the mitochondrial DNA of the chlorophyte alga Prototheca w
A/Reference number: Z17373; MUID:94180393; PMID:8133522
A/Accession: T11916
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-523 <MW>
A/Cross-references: UNIPROT:Q37617; EMBL:U02970; NID:9467843; PID:9467848; PIDN:AAJ12635
A/Experimental source: strain HB-8
C/Genetics:
A/Gene: mitochondrion
A/Note: nad4
C/Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C/Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
Query Match 7.9%; Score 93; DB 2; Length 523;
Best Local Similarity 24.2%; Pred. No. 2.8;
Matches 45; Conservative 37; Mismatches 50; Indels 54; Gaps 11;
QY 8 LVGTYLGLG--LLGTLVAMLLPSMKTSSV---VGASIVTAVGSGKLMWCAHST-- 59
DB 24 IMSYIEVNTAIPILGIALLEVPSMKTQTRINIALNSSLTFL--ISLLWTFBDSALF 82
QY 60 -----GITQCDDIYTLGLPADIQAAQAMVTSASISLACTISVGMCTVFCQESRAKD 115
DB 83 QPFDGVSPIVVS-----DVTLAKA--ASSSSFALNALGVDGI----- 120
QY 116 RVAVAGVFFITGLGFIPIVAMNLHG-----ILRDFYSPVLDPSMKFEIGALVYGIIS 170
DB 121 -----SLFPIILITTL-LVPICTIVSWNNIEVYKEY-----CIAFVLFTLMLTVFS 166

Qy	171	SLESLI	176
		:	
Db	167	VLDLL	172

RESULT 9

peripheral myelin protein 22 - human
N/Alternate names: Charcot-Marie-Tooth; GAS-3 protein; growth arrest-specific protein 3;
C/Species: Homo sapiens (man)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: JN0503; JCI1190; A56697; S25357
R/Edoml, P.; Martinotti, A.; Colombo, M.P.; Schneider, C.
Gene 126, 289-290, 1993
A/Title: Sequence of human GAS3/PMP22 full-length cDNA.
A/Reference number: JN0503; MUID:93246261; PMID:8482547
A/Accession: JN0503
A/Molecule type: mRNA
A/Residues: 1-160 <EDO>
R/Access-references: UNIPROT:Q01453; GB:L03203; NID:G182984; PID:AAA58495.1; PID:G182985
R/Hayaoka, K.; Himoto, M.; Nanao, K.; Sato, W.; Mura, M.; Uyemura, K.; Takahashi, E.;
Biochem. Biophys. Res. Commun. 186, 827-831, 1992
A/Title: Isolation and sequence determination of cDNA encoding PMP-22 (PAs-II/SR13/GAS-3
A/Reference number: JCI1190; MUID:92360032; PMID:1497668

Query Match	7.8%	Score 91;	DB 2;	length 160;
Best Local Similarity	21.7%	Pred. No. 1.3;		
Matches 41;	Conservative 33;	Mismatches 69;	Indels 46;	Gaps 8

[illegible]

QY	172	LFSLIAGII	180
		: :: :	
Db	144	PLALLSGVI	152

RESULT 10

hypothetical protein C37A7.6 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Dates: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19237, T19502

A:Cross-references: UNIPROT:001932; EMBL:Z32825; P1DN:CA807317.1; GSPDB:GN00023; CESP:C27A7.6
A:Experimental source: clone C13C4
R:Harrie, B.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19132
A:Accession: T19502
A:Stratus: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-487 <W12>
A:Cross-references: EMBL:Z81041; P1DN:CA802792.1; GSPDB:GN00023; CESP:C27A7.6
A:Experimental source: clone C27A7
C:Genetics:
A:Gene: CESP:C27A7.6
A:Map position: 5
A:Intons: 30/3; 51/3; 87/3; 109/3; 183/1; 215/3; 264/2; 302/2; 330/3; 349/3; 372/1; 433.

```

QY      5  GQLGVYIIIGLIGLGTIVAMLLP--SMKTSYVGASIVTVAGSKG---LMEGCATNST  59
Db      297 GYEMAGPPRAVCAIVGTLITSLAGHIADTRFKFKIIRVCTVGSVCYITLRLMPLNPRT  356
QY      60  GIGQCIIYSTLIGLPADIDIAQAQAMVMTSASISLACISY-VGMRCTVFCQESBAKQVA  118
Db      297 GYEMAGPPRAVCAIVGTLITSLAGHIADTRFKFKIIRVCTVGSVCYITLRLMPLNPRT  356
QY      357 GLPDSIIIVTLGC-----CIGAFSIPQPIGVELGVETTPPVME-----A  396
Db      357 GLPDSIIIVTLGC-----CIGAFSIPQPIGVELGVETTPPVME-----A  396
QY      119 VAGGVFFILGSLIGLGF-IPVAMNHLGILNDFVSPLPVDSMKRFEIGBALGIISLSFSH  175
Db      397 TSSGVLIVTGSLSFMFIIPPAQNYTEKHLFYA---QSMKALDVTGSLIVSIVYLSL  450

```

RESULT 11

hypothetical protein PH1451 - Pyrococcus horikoshii
C1:species: Pyrococcus horikoshii
C1:date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004

R:Kawarabayashi,Y.; Sawada,M.; Horikawa,H.; Halkawa,Y.; Hino,Y.; Yamamoto,S.; Sekino,M.; Ohfuku,Y.; Funahashi,T.; Tanaka,T.; Kudoh,Y.; Yamazaki,J.; Kushida,N.; Oguchi,DNA Res. 5, 55-76, 1998
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeal
 A:Reference number: A71000; MUID:98344137; PMID:9679194
 A:Accession: F71019
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-617 <KAM>
 A:Cross-references: UNIPROT:O59120; GB:AF000006; NID:g3236133; PIDD:BAA30558.1; PID:g325
 A:Experimental source: strain OT3
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C:Genetics:
 A:Gene: PHL451

Query Match	7.7%	Score 90.5;	DB 2;	Length 617;
Best Local Similarity	24.4%;	Pred. No. 5.4;		
Matches 52;	Conservative 33;	Mismatches 81;	Indels 47;	Gaps 9

Qy 5 GLQVGYILGLL-----GLVAMLLPSMKTSSY-----VGASIVTAVGFS-- 47
Db 273 GTPLFGITIAFLGGLITIIIGSVLAALQEDIRKLFASISISQVYIIVGLDGIIGSLIEA 332
Qy 48 -----KGL-WMECAT--HSTGITQCDIYSTLGLPADIOAQAAMVTS-----AI 90
Db 333 IYNAISHALPKFGFLVAVATIIYRTGKTEFDFGGL-----AKMPEFTPMARIAI 383
Qy 91 SSLACIISVGMCTVCCQSRADRVAVAGVFFIIGLGLFIPVAMNHLGILRDYSP 150
Db 384 LSLAGLPPLVGFASKWLIIFRAVISQKPLILGGMFL-PSAIGFVYLLRFTYAVAFGGRPS 442
Qy 151 LVPSDMKEIGALYGLISSL--FSLIAGII 180
Db 443 DIEDTKDAPLPLAIGMIIIGLITANVFGVAPGLV 475

RESULT 12

A97241
permease (imported) - Clostridium acetobutylicum
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C/Accession: A97241
R;Nolling, J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Bacteriol. 183, 4823-4838, 2001
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: A97241
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-429 <KUR>
A;Cross-references: UNIPROT:Q9JFG7; GB:AF001437; PIDN:AAK80716.1; PID:915025810; GSPDB:C
A;Experimental source: Clostridium acetobutylicum ATCC824
C/Genetics:
A;Gene: CAC2772
C;Superfamily: conserved hypothetical protein H1025

Query Match 7.5%; Score 88.5; DB 2; Length 429;
Best Local Similarity 22.8%; Pred. No. 5.6;
Matches 41; Conservative 38; Mismatches 76; Indels 25; Gaps 8;

Qy 13 LGLLGLLG-TLVAMLLPSMKTSSYVGASIVTAVG-----SKGLWMECATH-----S 58
Db 79 MGLNALFTYITICIGLHSMKTA--LAASLIGITFLVLANPKRIQLIDSPQTLKXAIS 136
Qy 59 TGITQCDIYSTLGL--PADIOAQAAMVTSAISLACIISVGMCTVCCQSRADR 116
Db 137 IGI---GFRTIFGLQAGIIVGSKGLVTLASLKPVALAVIGVLLIIVLKNKIGS 193
Qy 117 VAVAGVFFIIGLGLFIPVAMNHLGILRDYSPLVPSDMKEIGALYGLISSLFSLI 176
Db 194 FVIGMIVYVIGIFG--VAKAPSGIV-SPPPSVAVFLOFDPKSAVAVIGIVEVITML 249

RESULT 13

A99549
amino acid permease (imported) - Mycoplasma pulmonis (strain UAB CTIP)
C/Species: Mycoplasma pulmonis
C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C/Accession: A99549
R;Chambaud, I.; Hellig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallison, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: A99549
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-521 <KUR>
A;Cross-references: UNIPROT:Q960R4; GB:AF445566; PID:g14089711; PIDN:CAIC13470.1; GSPDB:C
A;Experimental source: strain UAB CTIP
C/Genetics:
A;Gene: MYPV_2970

A;Genetic code: SGC3

Query Match 7.5%; Score 88.5; DB 2; Length 521;
Best Local Similarity 21.2%; Pred. No. 6.7;
Matches 50; Conservative 38; Mismatches 63; Indels 85; Gaps 11;

Qy 1 MASLQVGYIIGLGLITLVAMLL-----PSWKTSSYGA--SIVTA 43
Db 1 MSEKTRKXGFFALSMGLGSVVGIGIFPKNGSVRAVEHNGTSMILAWFGGIIISLA 60
Qy 44 VGRSK-----GLWMECATSTG-----ITQCDIYSTLGL----- 72
Db 61 INFSEISFLNKTIXAGIWN--SHKVGDKRGEVVISFTLPYSGIIQIILGFTAEI 116
Qy 73 -----LPADIOAQA--AMVTSAISLACIISVGMCTVCCQSRADRVAVAGV 124
Db 117 FPHMLNLGANNIKEMKHSILVGLTIVISFTIINIVSIK-----ASGVF 160
Qy 125 FILGLGLFIP-VAMNHLGI-----LRDYSPLVPSDMKEIGALYGLISSL 172
Db 161 QVITTIKKPLPLATIIIVGLIFVSTHTLEDGANAAPVFNKTK-KIGFSPANVIAL 215

RESULT 14

H71283
conserved hypothetical integral membrane protein TP0771 - syphilis spirochete
C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C/Accession: H71283
R;Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo
rney, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-386, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: H71283
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-593 <COL>
A;Cross-references: UNIPROT:O83750; GB:AF001248; GB:AE000520; NID:93323074; PIDN:AA6573;
A;Experimental source: strain Nichols
C/Genetics:
A;Gene: TP0771

Query Match 7.5%; Score 88.5; DB 2; Length 593;
Best Local Similarity 23.2%; Pred. No. 7.7;
Matches 45; Conservative 36; Mismatches 72; Indels 41; Gaps 8;

Qy 4 LGLQVGYIIGL-----LGLGLTLVAMLLPSMKTSSYV-----GASIVTAVGFSKGLWMEC 54
Db 177 LGSIMGF--GLFTGLGLSSLIPL--SVEELSPLKTAVERALSVPFGLLSFVLTV 232
Qy 55 ATHSTGITQCDIYSTLGLPADIOAQAAMVTSAISLACIISVGMCTVCCQSRAR 114
Db 233 ILHSSATTAIVLTMAFGVIGVEFAAASVIGSNVSTIDALIAIG-----SKLN 283
Qy 115 DRVAVAGVFFIIGLGLFIPVAMNHLGILRDYSP-----LVPSDMKEIGALYGL 167
Db 284 ARRAAAVHVLFFNFGALVFLM-----FFHVALLLCVLTPEKNSGFD-NITVRLA 331
Qy 168 IISLPLFELIAGIIL 181
Db 332 LFHSMRIVAVITIV 345

RESULT 15

A41144
growth arrest-related myelin protein precursor, sciatic nerve - rat
N/Alternate names: Schwann cell membrane glycoprotein, SAG
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C/Accession: A41144; S18550; A44826
R;Welcher, A.A.; Suter, U.; De Leon, M.; Snipes, G.J.; Shooter, E.M.

Proc. Natl. Acad. Sci. U.S.A. 88, 7195-7199, 1991
 A/Title: A myelin protein is encoded by the homologue of a growth arrest-specific gene.
 A/Reference number: A41144; MUID:91334432; PMID:1714591
 A/Accession: A41144
 A/Molecule type: mRNA
 A/Residues: 1-160 <HEL>
 A/Cross-references: UNIPROT:P25094; GB:M69139; NID:G207063; PID:AAA73063.1; PID:G207064
 R/Spreyer, P.; Kuhn, G.; Hanemann, C.O.; Gyllen, C.; Schaal, H.; Kuhn, R.; Lemke, G.; Mu
 EMO J. 10, 3661-3668, 1991
 A/Title: Axon-regulated expression of a Schwann cell transcript that is homologous to a
 A/Reference number: S18550; MUID:92037527; PMID:1935894
 A/Accession: S18550
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-29, 'E', 31-160 <SPR>
 A/Cross-references: EMBL:X62431; NID:G55903; PIDN:CAA44297.1; PID:G55904
 R/Dieperink, M.E.; O'Neill, A.; Magnoni, G.; Wolmann, R.L.; Heinrichson, R.L.; Zucher-Ne
 U. Neurosci. 12, 2177-2185, 1992
 A/Title: SAG: a Schwann cell membrane glycoprotein.
 A/Reference number: A44826; MUID:92300442; PMID:1376775
 A/Accession: A44826
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-21, 'K', 23-25, 'K', 27, 'R', 29-30 <DIE>
 A/Note: Sequence extracted from NCBI backbone (NCBIP:106581)
 C/Comment: The predicted signal sequence may not be cleaved in some cell types.
 C/Superfamily: growth arrest-specific protein
 C/Keywords: glycoprotein; Schwann cell; transmembrane protein

Query Match 7.58; Score 88; DB 2; Length 160;
 Best Local Similarly 25.84; Pred. No. 2.3;
 Matches 46; Conservative 26; Mismatches 70; Indels 36; Gaps 8;

QY 12 ILGLGLGLVLMLEPSMTSSVGSISYTAVGFSKGLMMECATSTGTCDDYSTLL 71
 Db 2 LHLGLGLFLHNLVLLF-VSTIVSQMLV-GNGHRTDLMQNTTSMAGAVQ-HCYSS-- 56
 QY 72 GLPADIQAAQAMWVTSSAISLACIISVGMRCIVFCQ-ESRAKDRVAVAGVFFIIGL 130
 Db 57 SVSEMWQSVQATWILSVTFVLSLFL-----FFCQLFTLTKGRFRYITGVFQILAGL 108
 QY 131 LGFIPVA-----NNLHGLLRDFISPLVPDSMKFEIGALYIGIISLPSLAGIT 180
 Db 109 CWSAAAIYTVRHSSEWVNN-----DYSYGFAYILAWVAFPLALISGIT 152

Search completed: October 27, 2004, 07:21:49
 Job time : 40 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: October 27, 2004, 06:56:41 ; Search time 196 Seconds
(without alignments)

675.185 Million cell updates/sec

Title: US-09-787-677a-3

Perfect score: 1174

Sequence: 1 MASIGLQVGVIGLGLG.....PGQPKVSEFNSLYTGYV 230

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1174	100.0	230	1 CLD2_HUMAN	P57739 homo sapien
2	1174	100.0	230	2 BAC11575	Bac11575 homo sapi
3	1174	100.0	230	3 AAH71747	Aah71747 homo sapi
4	1119	95.3	230	1 CLD4_CANFA	Q95K66 canis fami
5	1114	94.9	230	2 Q765F1	Q765F1 bos tauru
6	1114	94.9	230	2 BAD01111	Bad01111 bos tauru
7	1096	93.4	230	1 CLD2_MOUSE	O68552 mus musculu
8	1096	93.4	230	2 BAB23725	Bab23725 mus muscu
9	571	48.6	239	1 CLD6_HUMAN	O95500 homo sapien
10	571	48.6	239	2 AAR05858	Aar05858 homo sapi
11	571	48.6	239	2 AAR05859	Aar05859 homo sapi
12	571	48.6	239	2 CAD97762	Cad97762 homo sapi
13	571	48.6	239	2 CAD97763	Cad97763 homo sapi
14	561.5	47.8	239	1 CLD6_MOUSE	O92063 mus musculu
15	514	43.8	266	2 O6E5T4	O6e5t4 figu rubrip
16	507.5	43.2	236	2 O6GME4	O6gme4 xenopus lae
17	461.5	39.3	216	2 O6E5G0	O6e5g0 figu rubrip
18	460.5	39.2	210	2 O6E5R5	O6e5r5 figu rubrip
19	459.5	39.1	208	1 CLD4_BRARE	O6y9h1 brachydanc
20	459.5	39.1	213	2 O6D3J2	O6d3j2 xenopus tro
21	456	38.8	218	2 O90XR2	O90xr2 brachydanc
22	456	38.8	218	2 AAH65424	Aah65424 brachydanc
23	455	38.8	219	2 Q765N9	Q765n9 bos tauru
24	455	38.8	219	2 BAD01113	Bad01113 bos tauru
25	453	38.5	211	2 O6E5T5	O6e5t5 figu rubrip
26	452	38.5	213	2 O7ZS22	O7zsz2 xenopus lae
27	451	38.4	210	2 O6E5Q4	O6e5q4 figu rubrip
28	450.5	38.4	218	1 CLD3_CANFA	Q95K66 canis fami
29	450.5	38.4	223	1 O6E5R9	O6e5r9 figu rubrip
30	450	38.3	220	1 CLD3_HUMAN	O15551 homo sapien
31	450	38.3	220	2 AAH07555	Aah07555 homo sapi

32	448.5	38.2	219	2 Q81019	Q81019 mus musculu
33	448	38.2	213	2 Q805G0	Q805g0 xenopus lae
34	447.5	38.1	211	2 O6E5R7	O6e5r7 figu rubrip
35	446	38.0	210	1 CLD4_MOUSE	O35054 mus musculu
36	446	38.0	215	2 O90XR8	O90xr8 brachydanc
37	444.5	37.9	209	2 O90XR9	O90xr9 brachydanc
38	444.5	37.9	209	2 AAH62846	Aah62846 brachydanc
39	443.5	37.8	209	1 CLD4_CERAE	O19005 cercopithe
40	443.5	37.8	214	2 O6PBE4	O6pbe4 xenopus tro
41	443.5	37.8	214	2 AAH59750	Aah59750 xenopus t
42	443	37.7	219	1 CLD6_MOUSE	O92262 mus musculu
43	442.5	37.7	209	1 CLD6_HUMAN	O14493 homo sapien
44	442.5	37.7	209	1 AAP35635	Aap35635 homo sapi
45	442.5	37.7	209	2 AAH07555	Aah07555 homo sapi

ALIGNMENTS

RESULT 1
ID CLD2_HUMAN STANDARD; PRT; 230 AA.
AC P57739;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Claudin-2 (UNQ705/PRO1356) (SP82).
GN Name=CLD2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epithelium;
RA Reinecker H.-C., Sakaguchi T., Golden H.M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
RA Yu J., Han L.H.;
RT "Novel human cDNA clones with function of inhibiting cancer cell growth."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA MEDLINE=22867296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu O., Hase P.B., Heidens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Lao D., Mark W., Robble E., Sanchez C., Schoenfeld J.,
RA Seehagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vanden R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
RN [4]
RP SEQUENCE FROM N.A.
RA Heath P.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon, and Kidney;
RA MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Deje J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedín T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallatón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schmeich A., Schein J.E., Jones S.J.W., Maier M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences." ;
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Component of tight junction (TJ) strands.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the Claudin family.
CC -----
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DR EMBL: AF250558; AAF98151.1; -
DR EMBL: AF177340; AAG17984.1; -
DR EMBL: AY358474; AA088838.1; -
DR EMBL: AL158821; CAD23055.1; -
DR EMBL: BC015252; AAH15252.1; -
DR EMBL: BC014424; AAH14424.1; -
DR Genbank: HGNC:2041; CUDN2.
DR InterPro: IPR006187; Claudin.
DR InterPro: IPR005411; Claudin.
DR InterPro: IPR006188; Claudin reg.
DR InterPro: IPR004031; PMP22 Claudin.
DR Pfam: PF00882; PMP22 Claudin; 1.
DR PRINTS: PRO1077; CLAUDIN.
DR PRINTS: PRO1589; CLAUDIN2.
DR PROSITE: PS01346; CLAUDIN; 1.
DR K1: Tight junction; Transmembrane.
DR TRANSMEM 8 28 Potential.
DR TRANSMEM 82 102 Potential.
DR TRANSMEM 117 137 Potential.
DR TRANSMEM 163 183 Potential.
DR TRANSMEM 230 AA; 24548 MW; 52CA642DA62B70D CRC64;
SQ SEQUENCE

Query Match 100.0%; Score 1174; DB 1; Length 230;
Best Local Similarity 100.0%; Pred. No. 1,3e-90;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASIGLQVGYIIGLIGLGLTVAMLLPSMKTSSYVGASIVTAVGFSKGLMECATHTSG 60
DB 1 MASIGLQVGYIIGLIGLGLTVAMLLPSMKTSSYVGASIVTAVGFSKGLMECATHTSG 60

QY 61 ITQCDIYSTLGLPADIOAQAAMVTSASISLACIISVGMKCTVFCQESRAKDRVAVA 120
DB 61 ITQCDIYSTLGLPADIOAQAAMVTSASISLACIISVGMKCTVFCQESRAKDRVAVA 120

QY 121 GGVFFILGGLGIFPVAMNHLGIRDFYSPPLVDSKMFEGEALYLGIISSLSFLAGII 180
DB 121 GGVFFILGGLGIFPVAMNHLGIRDFYSPPLVDSKMFEGEALYLGIISSLSFLAGII 180

QY 181 LCFSCSSQRRNSNYDAYQAQPLATRSSPRGQPPKVKSEFNSYSLTGYV 230
DB 181 LCFSCSSQRRNSNYDAYQAQPLATRSSPRGQPPKVKSEFNSYSLTGYV 230

RESULT 2
BAC11575

ID BAC11575 PRELIMINARY; PRT; 230 AA.
AC BAC11575;
DT 02-MAR-2004 (TEMBLrel. 27, Created)
DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
DE CNNA PSEC0059 f1s, clone NT2RP200601, highly similar to Mus musculus
DE claudin-2 mRNA.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ota T., Nishikawa T., Suzuki Y., Kawaj-Hio Y., Hayashi K., Iehi S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahari K., Sugano S., Isogai T.;
RT "FRI human cDNA sequencing project."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK075371; BAC11575.1; -
SQ SEQUENCE 230 AA; 24548 MW; 52CA642DA62B70D CRC64;
Query Match 100.0%; Score 1174; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 1,3e-90;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASIGLQVGYIIGLIGLGLTVAMLLPSMKTSSYVGASIVTAVGFSKGLMECATHTSG 60
DB 1 MASIGLQVGYIIGLIGLGLTVAMLLPSMKTSSYVGASIVTAVGFSKGLMECATHTSG 60

QY 61 ITQCDIYSTLGLPADIOAQAAMVTSASISLACIISVGMKCTVFCQESRAKDRVAVA 120
DB 61 ITQCDIYSTLGLPADIOAQAAMVTSASISLACIISVGMKCTVFCQESRAKDRVAVA 120

QY 121 GGVFFILGGLGIFPVAMNHLGIRDFYSPPLVDSKMFEGEALYLGIISSLSFLAGII 180
DB 121 GGVFFILGGLGIFPVAMNHLGIRDFYSPPLVDSKMFEGEALYLGIISSLSFLAGII 180

QY 181 LCFSCSSQRRNSNYDAYQAQPLATRSSPRGQPPKVKSEFNSYSLTGYV 230
DB 181 LCFSCSSQRRNSNYDAYQAQPLATRSSPRGQPPKVKSEFNSYSLTGYV 230

RESULT 3
AAH71747
ID AAH71747 PRELIMINARY; PRT; 230 AA.
AC AAH71747;
DT 01-JUN-2004 (TEMBLrel. 27, Created)
DT 01-JUN-2004 (TEMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TEMBLrel. 27, Last annotation update)
DE CUDN2 protein.
GN CUDN2.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Stemann C.M., Schaller G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedín T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallatón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywniński M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP SEQUENCE FROM N.A.
RC TISSUE=Skin and meninges pool- skin;
RA Strauberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC071747; AAH1747.1;
SQ SEQUENCE 230 AA; 24548 MW; 52CA642D4A62B70D CRC64;

Query Match 100.0%; Score 1174; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 1,3e-90;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASIGLVGYIIGLGLGLTVAMLLPSWKTSYVGAIVTVAVGFSKGLMECATHTSG 60
DB 1 MASIGLVGYIIGLGLGLTVAMLLPSWKTSYVGAIVTVAVGFSKGLMECATHTSG 60
QY 61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACTISVGMCTVFCQESRAKDRVAVA 120
DB 61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACTISVGMCTVFCQESRAKDRVAVA 120
QY 121 GGVFFIIGLGLFIPVAMNHLGILRDYSPPLVPDSMKFEIGALYIGTISLFLSLAGII 180
DB 121 GGVFFIIGLGLFIPVAMNHLGILRDYSPPLVPDSMKFEIGALYIGTISLFLSLAGII 180
QY 181 LCFSSCSQRNRSNYYDAYOAOPLATRSSPRGQPPKXSEFNSYSLTGYV 230
DB 181 LCFSSCSQRNRSNYYDAYOAOPLATRSSPRGQPPKXSEFNSYSLTGYV 230

RESULT 4

ID CLD2_CANFA STANDARD; PRT; 230 AA.

AC Q95KM6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Claudin-2.
GN Name=CLDN2;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21206012; PubMed=11309408;
RA Furness M., Furness K., Saeki H., Tsukita S.;
RT "Conversion of zonulae occludentes from tight to leaky strand type by
RT introducing claudin-2 into Madin-Darby canine kidney I cells";
RL J. Cell Biol. 153:263-272(2001).
CC -1- FUNCTION: Component of tight junction (TJ) strands.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the claudin family.

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CC EMBL: AF358907; AKS1433.1;
DR InterPro: IPR006187; Claudin.
DR InterPro: IPR005411; Claudin.
DR InterPro: IPR006188; Claudin_reg.
DR InterPro: IPR004031; BMP22_Claudin.

DR Pfam; PF00822; BMP22_Claudin.1.
DR PRINTS; PRO1077; CLAUDIN.
DR PRINTS; PRO1589; CLAUDIN2.
DR PROSITE; PS01346; CLAUDIN.1.
KW Tight junction; Transmembrane.
FT TRANSMEM 8 28 Potential.
FT TRANSMEM 82 102 Potential.
FT TRANSMEM 117 137 Potential.
FT TRANSMEM 163 183 Potential.
SQ SEQUENCE 230 AA; 24502 MW; 91B71C1B5C0C4BE9 CRC64;

Query Match 95.3%; Score 1119; DB 1; Length 230;
Best Local Similarity 93.5%; Pred. No. 5.3e-86;
Matches 215; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 MASIGLVGYIIGLGLGLTVAMLLPSWKTSYVGAIVTVAVGFSKGLMECATHTSG 60
DB 1 MASIGLVGYIIGLGLGLTVAMLLPSWKTSYVGAIVTVAVGFSKGLMECATHTSG 60
QY 61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACTISVGMCTVFCQESRAKDRVAVA 120
DB 61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACTISVGMCTVFCQESRAKDRVAVA 120
QY 121 GGVFFIIGLGLFIPVAMNHLGILRDYSPPLVPDSMKFEIGALYIGTISLFLSLAGII 180
DB 121 GGVFFIIGLGLFIPVAMNHLGILRDYSPPLVPDSMKFEIGALYIGTISLFLSLAGII 180
QY 181 LCFSSCSQRNRSNYYDAYOAOPLATRSSPRGQPPKXSEFNSYSLTGYV 230
DB 181 LCFSSCSQRNRSDYDYSOAOPLATRGSPRGQPPKXSEFNSYSLTGYV 230

RESULT 5

ID O76SP1 PRELIMINARY; PRT; 230 AA.

AC O76SP1;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Claudin 2.
GN Name=CLDN2;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Ohta H., Takiguchi M., Inaba M.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB115779; BAD0111.1;
DR InterPro: IPR006187; Claudin.
DR InterPro: IPR005411; Claudin.
DR InterPro: IPR006188; Claudin_reg.
DR InterPro: IPR004031; BMP22_Claudin.
DR Pfam; PF00822; BMP22_Claudin.1.
DR PRINTS; PRO1077; CLAUDIN.
DR PRINTS; PRO1589; CLAUDIN2.
DR PROSITE; PS01346; CLAUDIN.1.
KW Transmembrane.
SQ SEQUENCE 230 AA; 24533 MW; ED241778B0E541CA CRC64;

Query Match 94.9%; Score 1114; DB 2; Length 230;
Best Local Similarity 93.9%; Pred. No. 1.4e-85;
Matches 216; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 MASIGLVGYIIGLGLGLTVAMLLPSWKTSYVGAIVTVAVGFSKGLMECATHTSG 60
DB 1 MASIGLVGYIIGLGLGLTVAMLLPSWKTSYVGAIVTVAVGFSKGLMECATHTSG 60
QY 61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACTISVGMCTVFCQESRAKDRVAVA 120
DB 61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACTISVGMCTVFCQESRAKDRVAVA 120

```

Db      61 ITCCDIYSTLGLPADIOAAQAMWVTSSAMSLACIVSVGMCTVFFQESRAKDRVAVV 120
Qy      121 GGVFFILGGLGFIPIVAMNHLGILRDPYSPVPSDKMFEIGALYGIISLSFLIAGIT 180
      121 GGVFFILGGLGFIPIVAMNHLGILRDPYSPVPSDKMFEIGALYGIISLSFLIAGIT 180
Db      181 LCFSCSGQRNRSNYYDAYOAOPLATRSSPRPGQPKKSEFNSYSILGYV 230
      181 LCFSCSGQRNRSNYYDAYOAOPLATRSSPRPGQPKKSEFNSYSILGYV 230
Qy      181 LCFSCSGQRNRSNYYDAYOAOPLATRSSPRPGQPKKSEFNSYSILGYV 230
      181 LCFSCSGQRNRSNYYDAYOAOPLATRSSPRPGQPKKSEFNSYSILGYV 230
Db      181 LCFSCSGQRNRSNYYDAYOAOPLATRSSPRPGQPKKSEFNSYSILGYV 230
      181 LCFSCSGQRNRSNYYDAYOAOPLATRSSPRPGQPKKSEFNSYSILGYV 230

RESULT 6
BAD01111
ID      BAD01111      PRELIMINARY;      PRT;      230 AA.
AC      BAD01111
DT      02-MAR-2004 (TEMBLrel. 27, Created)
DT      02-MAR-2004 (TEMBLrel. 27, Last sequence update)
DT      02-MAR-2004 (TEMBLrel. 27, Last annotation update)
DE      Claudin 2.
GN      Bos taurus (Bovine).
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX      Bovidae; Bovinae; Bos.
RN      NCBI_TaxID=9913;
RP      [1]
RS      SEQUENCE FROM N.A.
RC      TISSUE=Kidney;
RA      Ohta H., Takiguchi M., Inaba M.;
RT      "Localization of claudin proteins in bovine kidneys.";
RL      Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RD      EMBL; AB115779; BAD01111.1; -.
SQ      SEQUENCE 230 AA; 24533 MW; ED241778B0E541CA CRC64;

Query Match      94.9%; Score 1114; DB 2; Length 230;
Best Local Similarity 93.9%; Pred. No. 1,4e-85;
Matches 216; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy      1 MASLGLQVGYIIGLIGLGLTVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60
      1 MASLGLQVGYIIGLIGLGLTVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60
Db      61 ITCCDIYSTLGLPADIOAAQAMWVTSSAMSLACIVSVGMCTVFFQESRAKDRVAVV 120
      61 ITCCDIYSTLGLPADIOAAQAMWVTSSAMSLACIVSVGMCTVFFQESRAKDRVAVV 120
Qy      61 ITCCDIYSTLGLPADIOAAQAMWVTSSAMSLACIVSVGMCTVFFQESRAKDRVAVV 120
      61 ITCCDIYSTLGLPADIOAAQAMWVTSSAMSLACIVSVGMCTVFFQESRAKDRVAVV 120
Db      61 ITCCDIYSTLGLPADIOAAQAMWVTSSAMSLACIVSVGMCTVFFQESRAKDRVAVV 120
      61 ITCCDIYSTLGLPADIOAAQAMWVTSSAMSLACIVSVGMCTVFFQESRAKDRVAVV 120
Qy      121 GGVFFILGGLGFIPIVAMNHLGILRDPYSPVPSDKMFEIGALYGIISLSFLIAGIT 180
      121 GGVFFILGGLGFIPIVAMNHLGILRDPYSPVPSDKMFEIGALYGIISLSFLIAGIT 180
Db      121 GGVFFILGGLGFIPIVAMNHLGILRDPYSPVPSDKMFEIGALYGIISLSFLIAGIT 180
      121 GGVFFILGGLGFIPIVAMNHLGILRDPYSPVPSDKMFEIGALYGIISLSFLIAGIT 180
Qy      121 GGVFFILGGLGFIPIVAMNHLGILRDPYSPVPSDKMFEIGALYGIISLSFLIAGIT 180
      121 GGVFFILGGLGFIPIVAMNHLGILRDPYSPVPSDKMFEIGALYGIISLSFLIAGIT 180
Db      121 GGVFFILGGLGFIPIVAMNHLGILRDPYSPVPSDKMFEIGALYGIISLSFLIAGIT 180
      121 GGVFFILGGLGFIPIVAMNHLGILRDPYSPVPSDKMFEIGALYGIISLSFLIAGIT 180
Qy      181 LCFSCSGQRNRSNYYDAYOAOPLATRSSPRPGQPKKSEFNSYSILGYV 230
      181 LCFSCSGQRNRSNYYDAYOAOPLATRSSPRPGQPKKSEFNSYSILGYV 230
Db      181 LCFSCSGQRNRSNYYDAYOAOPLATRSSPRPGQPKKSEFNSYSILGYV 230
      181 LCFSCSGQRNRSNYYDAYOAOPLATRSSPRPGQPKKSEFNSYSILGYV 230

RESULT 7
CLD2_MOUSE
ID      CLD2_MOUSE      STANDARD;      PRT;      230 AA.
AC      O88552;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Claudin-2.
GN      Name=Clnd2;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RS      SEQUENCE FROM N.A.
RC      MEDLINE=98311639; PubMed=9647647;
RA      Furue M., Fujita K., Hiraagi T., Fujimoto K., Tsukita S.;
RT      "Claudin-1 and -2: novel integral membrane proteins localizing at

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RT      tight junctions with no sequence similarity to occludin.";
RL      J. Cell Biol. 141:1539-1550(1998).
CC      -1- FUNCTION: Component of tight junction (TJ) strands.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- SIMILARITY: Belongs to the claudin family.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF072128; AAC27079.1; -.
DR      MGD; MG1:1276110; Clnd2.
DR      InterPro; IPR006187; Claudin.
DR      InterPro; IPR005411; Claudin2.
DR      InterPro; IPR006188; Claudin2_reg.
DR      InterPro; IPR004031; PMP22_Claudin.
DR      Pfam; PF00822; PMP22_Claudin; 1.
DR      PRINTS; PR01077; CLAUDIN.
DR      PRINTS; PR01598; CLAUDIN2.
DR      PROSITE; PS01346; CLAUDIN; 1.
KW      Tight junction; Transmembrane.
FT      TRANSMEM 8..28
FT      TRANSMEM 82..102
FT      TRANSMEM 117..137
FT      TRANSMEM 163..183
FT      TRANSMEM 163..183
SQ      SEQUENCE 230 AA; 24483 MW; 38A7C074A1E0D5D2 CRC64;

Query Match      93.4%; Score 1096; DB 1; Length 230;
Best Local Similarity 91.3%; Pred. No. 4,5e-94;
Matches 210; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

Qy      1 MASLGLQVGYIIGLIGLGLTVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60
      1 MASLGLQVGYIIGLIGLGLTVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60
Db      61 ITCCDIYSTLGLPADIOAAQAMWVTSSAMSLACIVSVGMCTVFFQESRAKDRVAVV 120
      61 ITCCDIYSTLGLPADIOAAQAMWVTSSAMSLACIVSVGMCTVFFQESRAKDRVAVV 120
Qy      61 ITCCDIYSTLGLPADIOAAQAMWVTSSAMSLACIVSVGMCTVFFQESRAKDRVAVV 120
      61 ITCCDIYSTLGLPADIOAAQAMWVTSSAMSLACIVSVGMCTVFFQESRAKDRVAVV 120
Db      61 ITCCDIYSTLGLPADIOAAQAMWVTSSAMSLACIVSVGMCTVFFQESRAKDRVAVV 120
      61 ITCCDIYSTLGLPADIOAAQAMWVTSSAMSLACIVSVGMCTVFFQESRAKDRVAVV 120
Qy      121 GGVFFILGGLGFIPIVAMNHLGILRDPYSPVPSDKMFEIGALYGIISLSFLIAGIT 180
      121 GGVFFILGGLGFIPIVAMNHLGILRDPYSPVPSDKMFEIGALYGIISLSFLIAGIT 180
Db      121 GGVFFILGGLGFIPIVAMNHLGILRDPYSPVPSDKMFEIGALYGIISLSFLIAGIT 180
      121 GGVFFILGGLGFIPIVAMNHLGILRDPYSPVPSDKMFEIGALYGIISLSFLIAGIT 180
Qy      121 GGVFFILGGLGFIPIVAMNHLGILRDPYSPVPSDKMFEIGALYGIISLSFLIAGIT 180
      121 GGVFFILGGLGFIPIVAMNHLGILRDPYSPVPSDKMFEIGALYGIISLSFLIAGIT 180
Db      121 GGVFFILGGLGFIPIVAMNHLGILRDPYSPVPSDKMFEIGALYGIISLSFLIAGIT 180
      121 GGVFFILGGLGFIPIVAMNHLGILRDPYSPVPSDKMFEIGALYGIISLSFLIAGIT 180
Qy      181 LCFSCSGQRNRSNYYDAYOAOPLATRSSPRPGQPKKSEFNSYSILGYV 230
      181 LCFSCSGQRNRSNYYDAYOAOPLATRSSPRPGQPKKSEFNSYSILGYV 230
Db      181 LCFSCSGQRNRSNYYDAYOAOPLATRSSPRPGQPKKSEFNSYSILGYV 230
      181 LCFSCSGQRNRSNYYDAYOAOPLATRSSPRPGQPKKSEFNSYSILGYV 230

RESULT 8
BAB23725
ID      BAB23725      PRELIMINARY;      PRT;      230 AA.
AC      BAB23725;
DT      14-APR-2004 (TEMBLrel. 27, Created)
DT      14-APR-2004 (TEMBLrel. 27, Last sequence update)
DT      14-APR-2004 (TEMBLrel. 27, Last annotation update)
DE      Adult male liver cDNA, RIKEN full-length enriched library,
      clone:1300013G06 product:claudin 2, full insert sequence.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RS      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Liver;
RX      MEDLINE=22354683; PubMed=12466851;
RA      The FANTOM Consortium.
RA      the RIKEN Genome Exploration Research Group Phase I & II Team;
RT      "Analysis of the mouse transcriptome based on functional annotation of
      60,770 full-length cDNAs.";

```


RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Caminici P., Prange C.,
 RA Raba S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
 RA Scherach A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences." J.
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6].
 RP VARIANT MET-4.
 RX MEDLINE=22675606; PubMed=12791041;
 RA Uyguner O., Emiroglu M., Uzuncu A., Hafiz G., Ghanbari A., Baeer N.,
 RA Yiksel-Apak M., Wollnik B.;
 RT "Frequencies of gap- and tight-junction mutations in Turkish families
 RT with autosomal-recessive non-syndromic hearing loss." J.
 RL Clin. Genet. 64:65-69(2003).
 CC -1- FUNCTION: Component of tight junction (TJ) strands.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Liver, kidney. Also found in ear.
 CC -1- DISEASE: Defects in CLDN14 are the cause of an autosomal recessive
 CC form of nonsyndromic sensorineural deafness (DFNB29) [MIM:605608].
 CC -1- SIMILARITY: Belongs to the claudin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@ebi.ac.uk).

DR EMBL: AJ132445; CA10669.1; -;
 DR EMBL: AF114090; AA660052.1; -;
 DR EMBL: AY358533; AA088987.1; -;
 DR EMBL: AP001726; BA955509.1; -;
 DR EMBL: BC012126; AA112126.1; -;
 DR Genew; HGNC:2035; CLDN14.
 DR MIM; 605608; -;
 DR GO; GO:000461; P:Protein complex assembly; TAS.
 DR Interpro; IPR006187; Claudin.
 DR Interpro; IPR006188; Claudin_reg.
 DR Interpro; IPR004031; PMP22_Claudin.
 DR Pfam; PF00822; PMP22_Claudin; 1.
 DR PRINTS; PR01077; CLAUDIN.
 DR PROSITE; PS01346; CLAUDIN; 1.
 KM Deafness; Disease mutation; Polymorphism; Tight junction;
 KM Transmembrane.
 FT TRANSMEM 8 28 Potential.
 FT TRANSMEM 82 102 Potential.
 FT TRANSMEM 116 136 Potential.
 FT TRANSMEM 163 183 Potential.
 FT VARIANT 4 4 T->M.
 FT VARIANT 85 85 /FTID=VAR_017227.
 FT VARIANT V->D (in DFNB29).
 FT VARIANT /FTID=VAR_010738.
 SQ SEQUENCE 239 AA; 25699 MW; DD41652F7FD0E09A CRC64;

Query Match 48.6%; Score 571; DB 1; Length 239;
 Best Local Similarity 46.8%; Pred. No. 6e-40; Indels 12; Gaps 3;
 Matches 11; Conservative 44; Mismatches 70;

QY 1 MASTGLQVYIGLGLGLTLVAMLLPSMKTSSYVGSIVTAVGFSKGLMECATSTG 60
 DB 1 MASTAVQLGLGLFLGVMGTLITLLPHMRRHAGVTNLTAVSYKGLMECVHSTG 60
 QY 61 ITQCDIYSTLLGLPADIQAAMVNTSSAISLACIISVGMRICTVFCQSRAXDRVVA 120
 DB 61 ITQCDIYSTLLGLPADIQAAMVNTSSAISLACIISVGMRICTVFCQSRAXDRVVA 120
 QY 121 GGVPFLLGLGLGFIPIAMNHLGIRDFYSPVLVDSKFEIGALYLGIIISLFLIAGII 180
 DB 121 GGVLFIAGLGLCMVAVSWTTNDVQNFYPLPSGKFEIGALYLGFISSLSLIGTL 180
 QY 61 IYCCQIYRSLALPDLQARALMTVISCILSGIACAVIGMKCTFCAGTPAKTTFALL 120
 DB 61 IYCCQIYRSLALPDLQARALMTVISCILSGIACAVIGMKCTFCAGTPAKTTFALL 120
 QY 121 GGVPFLLGLGLGFIPIAMNHLGIRDFYSPVLVDSKFEIGALYLGIIISLFLIAGII 180
 DB 121 GGVLFIAGLGLCMVAVSWTTNDVQNFYPLPSGKFEIGALYLGFISSLSLIGTL 180
 QY 181 LCFSCSSQRRNSNYDAYQAQPLATRSSPPG---QPRVKSEFNSYLT---GY 229
 DB 181 LCLSCQDEAP---YRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSY 233

RESULT 11
 AAR05859 PRELIMINARY; PRT; 239 AA.
 AC AAR05859;
 DT 02-MAR-2004 (T-EMBLrel. 27, Created)
 DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
 DE Claudin 14 epsilon isoform.
 GN CLDN14.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primata; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wattenhofer M., Falciola V., Charollais A., Caille D., Borel C.,
 RA Bectivill X., Petersen M.B., Antonarakis S.E., Meda P., Raymond A.,
 RT "Claudin 14 and deafness." J.
 SQ SEQUENCE 239 AA; 25699 MW; DD41652F7FD0E09A CRC64;

Query Match 48.6%; Score 571; DB 2; Length 239;
 Best Local Similarity 46.8%; Pred. No. 6e-40; Indels 12; Gaps 3;
 Matches 11; Conservative 44; Mismatches 70;

QY 1 MASTGLQVYIGLGLGLTLVAMLLPSMKTSSYVGSIVTAVGFSKGLMECATSTG 60
 DB 1 MASTAVQLGLGLFLGVMGTLITLLPHMRRHAGVTNLTAVSYKGLMECVHSTG 60
 QY 61 ITQCDIYSTLLGLPADIQAAMVNTSSAISLACIISVGMRICTVFCQSRAXDRVVA 120
 DB 61 ITQCDIYSTLLGLPADIQAAMVNTSSAISLACIISVGMRICTVFCQSRAXDRVVA 120
 QY 121 GGVPFLLGLGLGFIPIAMNHLGIRDFYSPVLVDSKFEIGALYLGIIISLFLIAGII 180
 DB 121 GGVLFIAGLGLCMVAVSWTTNDVQNFYPLPSGKFEIGALYLGFISSLSLIGTL 180
 QY 61 IYCCQIYRSLALPDLQARALMTVISCILSGIACAVIGMKCTFCAGTPAKTTFALL 120
 DB 61 IYCCQIYRSLALPDLQARALMTVISCILSGIACAVIGMKCTFCAGTPAKTTFALL 120
 QY 121 GGVPFLLGLGLGFIPIAMNHLGIRDFYSPVLVDSKFEIGALYLGIIISLFLIAGII 180
 DB 121 GGVLFIAGLGLCMVAVSWTTNDVQNFYPLPSGKFEIGALYLGFISSLSLIGTL 180
 QY 181 LCFSCSSQRRNSNYDAYQAQPLATRSSPPG---QPRVKSEFNSYLT---GY 229
 DB 181 LCLSCQDEAP---YRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSY 233

RESULT 11
 AAR05859 PRELIMINARY; PRT; 239 AA.
 AC AAR05859;
 DT 02-MAR-2004 (T-EMBLrel. 27, Created)
 DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
 DE Claudin 14 epsilon isoform.
 GN CLDN14.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primata; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wattenhofer M., Falciola V., Charollais A., Caille D., Borel C.,
 RA Bectivill X., Petersen M.B., Antonarakis S.E., Meda P., Raymond A.,
 RT "Claudin 14 and deafness." J.
 SQ SEQUENCE 239 AA; 25699 MW; DD41652F7FD0E09A CRC64;

RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY55349; AAR0589.1; -
 SQ SEQUENCE 239 AA; 25699 MW; DD41652F7DDE09A CRC64;

Query Match 48.6%; Score 571; DB 2; Length 239;
 Best Local Similarity 46.8%; Pred. No. 6e-40;
 Matches 111; Conservative 44; Mismatches 70; Indels 12; Gaps 3;

QY 1 MASIGQLVGYIIGLGLGLTIVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60
 DB 1 MASTAVQLGLGFLSPFGMVGTLITTLPHMRRTAHVGNITLTAVSYLKGLMECVMHSTG 60
 QY 61 ITCCDIYSTLLGLPADIOAAQAMWVTSASISLACIISVGMKCTVFCQESRANRYAVA 120
 DB 61 IYCCQIRSLALPQDIOAARALMVISCLISGACAVIGMCKTRCAKGTPTTFAIL 120
 QY 121 GGVFFILGLGFLPVAAMNHLGILRDPYSPVPSMKFEIGALYIGIISLSFLINGII 180
 DB 121 GGTFLPILAGLGMVAWSMTTNDVQNFYPLPSGMKFEIGQALYIGIISLSLIGTL 180
 QY 181 LCFSCSSQRRNSNYDAYOAPLATRSSPRG---QPPKVSFNYSYSLT-----GY 229
 DB 181 LCISQCEAP---YRPYQAPPRATTTTANTAPAYQPPAAYKONRAPSVTSATHSY 233

RESULT 12

CAD97762 PRELIMINARY; PRT; 239 AA.

ID CAD97762; PRELIMINARY; PRT; 239 AA.
 AC CAD97762; (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DE Claudin 14.
 GN CLDN14.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primata; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Placenta;
 RA Wattenhofer M., Falciola V., Charollais A., Caille D., Borel C.,
 RA Berville X., Petersen M.B., Antonarakis S.E., Meda P., Raymond A.;
 RT "Claudin 14 and deafness";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ56765; CAD97762.1; -
 SQ SEQUENCE 239 AA; 25699 MW; DD41652F7DDE09A CRC64;

Query Match 48.6%; Score 571; DB 2; Length 239;
 Best Local Similarity 46.8%; Pred. No. 6e-40;
 Matches 111; Conservative 44; Mismatches 70; Indels 12; Gaps 3;

QY 1 MASIGQLVGYIIGLGLGLTIVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60
 DB 1 MASTAVQLGLGFLSPFGMVGTLITTLPHMRRTAHVGNITLTAVSYLKGLMECVMHSTG 60
 QY 61 ITCCDIYSTLLGLPADIOAAQAMWVTSASISLACIISVGMKCTVFCQESRANRYAVA 120
 DB 61 IYCCQIRSLALPQDIOAARALMVISCLISGACAVIGMCKTRCAKGTPTTFAIL 120
 QY 121 GGVFFILGLGFLPVAAMNHLGILRDPYSPVPSMKFEIGALYIGIISLSFLINGII 180
 DB 121 GGTFLPILAGLGMVAWSMTTNDVQNFYPLPSGMKFEIGQALYIGIISLSLIGTL 180
 QY 181 LCFSCSSQRRNSNYDAYOAPLATRSSPRG---QPPKVSFNYSYSLT-----GY 229
 DB 181 LCISQCEAP---YRPYQAPPRATTTTANTAPAYQPPAAYKONRAPSVTSATHSY 233

RESULT 13
 CAD97763 PRELIMINARY; PRT; 239 AA.
 ID CAD97763; PRELIMINARY; PRT; 239 AA.
 AC CAD97763;

DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE Claudin 14.

GN CLDN14.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primata; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Testis;
 RA Wattenhofer M., Falciola V., Charollais A., Caille D., Borel C.,
 RA Berville X., Petersen M.B., Antonarakis S.E., Meda P., Raymond A.;
 RT "Claudin 14 and deafness";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ56766; CAD97763.1; -
 SQ SEQUENCE 239 AA; 25699 MW; DD41652F7DDE09A CRC64;

Query Match 48.6%; Score 571; DB 2; Length 239;
 Best Local Similarity 46.8%; Pred. No. 6e-40;
 Matches 111; Conservative 44; Mismatches 70; Indels 12; Gaps 3;

QY 1 MASIGQLVGYIIGLGLGLTIVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60
 DB 1 MASTAVQLGLGFLSPFGMVGTLITTLPHMRRTAHVGNITLTAVSYLKGLMECVMHSTG 60
 QY 61 ITCCDIYSTLLGLPADIOAAQAMWVTSASISLACIISVGMKCTVFCQESRANRYAVA 120
 DB 61 IYCCQIRSLALPQDIOAARALMVISCLISGACAVIGMCKTRCAKGTPTTFAIL 120
 QY 121 GGVFFILGLGFLPVAAMNHLGILRDPYSPVPSMKFEIGALYIGIISLSFLINGII 180
 DB 121 GGTFLPILAGLGMVAWSMTTNDVQNFYPLPSGMKFEIGQALYIGIISLSLIGTL 180
 QY 181 LCFSCSSQRRNSNYDAYOAPLATRSSPRG---QPPKVSFNYSYSLT-----GY 229
 DB 181 LCISQCEAP---YRPYQAPPRATTTTANTAPAYQPPAAYKONRAPSVTSATHSY 233

RESULT 14

CLDN_MOUSE STANDARD; PRT; 239 AA.

ID CLDN_MOUSE STANDARD; PRT; 239 AA.
 AC 092053; 092054;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Claudin-14.
 GN Name=Clndn14;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Liver;
 RA Motika K., Furness M., Tsukita S.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

QY 1 MASIGQLVGYIIGLGLGLTIVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60
 DB 1 MASTAVQLGLGFLSPFGMVGTLITTLPHMRRTAHVGNITLTAVSYLKGLMECVMHSTG 60
 QY 61 ITCCDIYSTLLGLPADIOAAQAMWVTSASISLACIISVGMKCTVFCQESRANRYAVA 120
 DB 61 IYCCQIRSLALPQDIOAARALMVISCLISGACAVIGMCKTRCAKGTPTTFAIL 120
 QY 121 GGVFFILGLGFLPVAAMNHLGILRDPYSPVPSMKFEIGALYIGIISLSFLINGII 180
 DB 121 GGTFLPILAGLGMVAWSMTTNDVQNFYPLPSGMKFEIGQALYIGIISLSLIGTL 180
 QY 181 LCFSCSSQRRNSNYDAYOAPLATRSSPRG---QPPKVSFNYSYSLT-----GY 229
 DB 181 LCISQCEAP---YRPYQAPPRATTTTANTAPAYQPPAAYKONRAPSVTSATHSY 233

QY 181 LCFSCSSQRRNSNYDAYOAPLATRSSPRG---QPPKVSFNYSYSLT-----GY 229
 DB 181 LCISQCEAP---YRPYQAPPRATTTTANTAPAYQPPAAYKONRAPSVTSATHSY 233

RESULT 15
 CAD97763 PRELIMINARY; PRT; 239 AA.
 ID CAD97763; PRELIMINARY; PRT; 239 AA.
 AC CAD97763;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 27, 2004, 07:36:34 ; Search time 128 Seconds
(without alignments)
582.575 Million cell updates/sec

Title: US-09-787-677A-3

Perfect score: 230

Sequence: 1 MASLGLQVGYITGLGLG.....PCGPPKYSRFSNYSITGVY 230

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1370721 seqs, 324215800 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: Published Applications_AA:*
2: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubppaa/PCT_NEW_PUB.pep:*
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18: /cgn2_6/prodata/1/pubppaa/US11_NEW_PUB.pep:*
19: /cgn2_6/prodata/1/pubppaa/US60_NEW_PUB.pep:*
20: /cgn2_6/prodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	230	100.0	230	9	US-09-998-598-2590 Sequence 2590, App
2	230	100.0	230	10	US-09-888-257A-6 Sequence 6, Appl
3	230	100.0	230	10	US-09-946-374-134 Sequence 134, Appl
4	230	100.0	230	11	US-09-833-245-1256 Sequence 1256, App
5	230	100.0	230	11	US-09-978-360A-698 Sequence 698, Appl
6	230	100.0	230	13	US-10-006-867-80 Sequence 80, Appl
7	230	100.0	230	13	US-10-063-547-80 Sequence 80, Appl
8	230	100.0	230	13	US-10-063-551-80 Sequence 80, Appl
9	230	100.0	230	14	US-10-028-072-492 Sequence 492, Appl
10	230	100.0	230	14	US-10-063-616-80 Sequence 80, Appl
11	230	100.0	230	14	US-10-140-808-492 Sequence 492, Appl
12	230	100.0	230	14	US-10-063-569-80 Sequence 80, Appl
13	230	100.0	230	14	US-10-063-513-80 Sequence 80, Appl

14	230	100.0	230	14	US-10-063-515-80	Sequence 80, Appl
15	230	100.0	230	14	US-10-063-512-80	Sequence 80, Appl
16	230	100.0	230	14	US-10-121-049-492	Sequence 492, Appl
17	230	100.0	230	14	US-10-123-904-492	Sequence 492, Appl
18	230	100.0	230	14	US-10-140-470-492	Sequence 492, Appl
19	230	100.0	230	14	US-10-063-502-80	Sequence 80, Appl
20	230	100.0	230	14	US-10-175-746-492	Sequence 492, Appl
21	230	100.0	230	14	US-10-176-918-492	Sequence 492, Appl
22	230	100.0	230	14	US-10-176-921-492	Sequence 492, Appl
23	230	100.0	230	14	US-10-063-549-80	Sequence 80, Appl
24	230	100.0	230	14	US-10-137-865-492	Sequence 492, Appl
25	230	100.0	230	14	US-10-142-419-492	Sequence 492, Appl
26	230	100.0	230	14	US-10-142-431-492	Sequence 492, Appl
27	230	100.0	230	14	US-10-143-114-492	Sequence 492, Appl
28	230	100.0	230	14	US-10-140-002-492	Sequence 492, Appl
29	230	100.0	230	14	US-10-063-554-80	Sequence 80, Appl
30	230	100.0	230	14	US-10-006-856A-134	Sequence 134, Appl
31	230	100.0	230	14	US-10-142-419-492	Sequence 492, Appl
32	230	100.0	230	14	US-10-063-553-80	Sequence 80, Appl
33	230	100.0	230	14	US-10-063-518-80	Sequence 80, Appl
34	230	100.0	230	14	US-10-123-262-492	Sequence 492, Appl
35	230	100.0	230	14	US-10-142-423-492	Sequence 492, Appl
36	230	100.0	230	14	US-10-063-598-80	Sequence 80, Appl
37	230	100.0	230	14	US-10-227-693-80	Sequence 80, Appl
38	230	100.0	230	14	US-10-006-818A-134	Sequence 134, Appl
39	230	100.0	230	14	US-10-121-050-492	Sequence 492, Appl
40	230	100.0	230	14	US-10-141-755-492	Sequence 492, Appl
41	230	100.0	230	14	US-10-143-037-492	Sequence 492, Appl
42	230	100.0	230	14	US-10-063-563-80	Sequence 80, Appl
43	230	100.0	230	14	US-10-006-485A-134	Sequence 134, Appl
44	230	100.0	230	14	US-10-013-907A-134	Sequence 134, Appl
45	230	100.0	230	14	US-10-015-499A-134	Sequence 134, Appl

ALIGNMENTS

US-09-998-598-2590	RESULT 1	US-09-998-598-2590
Sequence 2590, Application US/0998598		
Patent No. US20020150922A1		
GENERAL INFORMATION:		
APPLICANT: Stolk, John A.		
APPLICANT: Xu, Jiangchun		
APPLICANT: Chenault, Ruth A.		
APPLICANT: Meagher, Madelein Joy		
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND		
FILE REFERENCE: 210121.561		
CURRENT APPLICATION NUMBER: US/09/998,598		
CURRENT FILING DATE: 2001-11-16		
NUMBER OF SEQ. ID NOS: 2606		
SOFTWARE: Corixa Invention Disclosure Database		
SEQ. ID NO 2590		
LENGTH: 230		
TYPE: PRT		
ORGANISM: Homo sapiens		
US-09-998-598-2590		
Query Match	100.0%;	Score 230; DB 9; Length 230;
Best Local Similarity	100.0%;	Pred. No. 1.8e-207;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
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DB	1	MASLGLQVGYITGLGLGLTIVAMLLPWSKTSYVGASITVAVGFSKGLMECATHTG 60
QY	61	ITGCDISTLGLPADIOAQAAMVTSSAISLACTISVGMKCTVFCQESRAXDVAVA 120
DB	61	ITGCDISTLGLPADIOAQAAMVTSSAISLACTISVGMKCTVFCQESRAXDVAVA 120
QY	121	GGVFITGLGLGFIPIVAMNIGIILDFYSPPLVDSMKFEIGALYGIISLPSLIAGII 180

Db 121 GGVFLLGLGLGTFPAMNHLGRDFYSLVPSDKMKEFGALYIGIISLFSLIAGII 180
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Db 181 LCFSSCSQRNRSNYYDAYQAQPLATRSSPRPGQPPKVSSEFNSYSLTGYV 230

RESULT 2

US-09-888-257A-6
; Sequence 6, Application US/09888257A
; Publication No. US20030060612A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Polakis, Paul
; APPLICANT: Smith, Victoria
; APPLICANT: Wood, William I.
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5002R1
; CURRENT APPLICATION NUMBER: US/09/888,257A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/063,540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: US 60/089,653
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; PRIOR APPLICATION NUMBER: US 60/103,678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: US 60/235,451
; PRIOR FILING DATE: 2000-09-26
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; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US00/04342
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
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; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 6
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-888-257A-6

Query Match 100.0%; Score 230; DB 10; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.8e-207;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASIGLQVGVYIIGLGLGLTLVAMLLPSKMTSSYVASIVTVAGFSKGLMBCATHTSG 60
Db 1 MASIGLQVGVYIIGLGLGLTLVAMLLPSKMTSSYVASIVTVAGFSKGLMBCATHTSG 60
QY 61 ITCCDIYSTLLGLPADIOAAQAMVNTSSAISLACTISVYGMCTVCGESRAKDRAVA 120
Db 61 ITCCDIYSTLLGLPADIOAAQAMVNTSSAISLACTISVYGMCTVCGESRAKDRAVA 120

QY 121 GGVFLLGLGLGTFPAMNHLGRDFYSLVPSDKMKEFGALYIGIISLFSLIAGII 180
Db 121 GGVFLLGLGLGTFPAMNHLGRDFYSLVPSDKMKEFGALYIGIISLFSLIAGII 180
QY 181 LCFSSCSQRNRSNYYDAYQAQPLATRSSPRPGQPPKVSSEFNSYSLTGYV 230
Db 181 LCFSSCSQRNRSNYYDAYQAQPLATRSSPRPGQPPKVSSEFNSYSLTGYV 230

RESULT 3

US-09-946-374-134
; Sequence 134, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tomas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
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 PRIOR FILING DATE: 1998-10-26
 PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 230; DB 10; Length 230;
 Best Local Similarity 100.0%; Pred. No. 1.8e-207;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASIQLVGYITIGLIGLIGTIVAMLLPSMKTSYVGSIVTVAVGSKGLMBCATHSTG 60
 DB 1 MASIQLVGYITIGLIGLIGTIVAMLLPSMKTSYVGSIVTVAVGSKGLMBCATHSTG 60

QY 61 ITGCDIYSTLLGHPADIOAAMWTSLSLACIIISVGMCTVFCQESRAKDRVAVA 120
DB 61 ITGCDIYSTLLGHPADIOAAMWTSLSLACIIISVGMCTVFCQESRAKDRVAVA 120
QY 121 GGVFFLIGLGLGHPVAMNHLGILRDFYSPVDPDSMKFEIGALYLGIIISLFLIAGII 180
DB 121 GGVFFLIGLGLGHPVAMNHLGILRDFYSPVDPDSMKFEIGALYLGIIISLFLIAGII 180
QY 181 LCFSSCSQRKRSNYDAYOAOPLATRSSPRGQPPKVKSEFNYSILGTIV 230
DB 181 LCFSSCSQRKRSNYDAYOAOPLATRSSPRGQPPKVKSEFNYSILGTIV 230

RESULT 4

US-09-833-245-1256
Sequence 1256, Application US/09833245
Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PFS46PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256,931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1256
LENGTH: 230
TYPE: PRT
ORGANISM: Homo sapiens
US-09-833-245-1256

Query Match 100.0%; Score 230; DB 11; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.8e-207;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGIQVGYIIGLIGLGLTIVAMLLPSWKTSSYVGASIVTAVGFSKGLMMECATHTSG 60
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QY 181 LCFSSCSQRKRSNYDAYOAOPLATRSSPRGQPPKVKSEFNYSILGTIV 230
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RESULT 5

US-09-978-360A-698
Sequence 698, Application US/09978360A
Publication No. US20040110939A1
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste Dumas Milne
APPLICANT: Duclet, Aymeric
APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: 56 USA CIP
CURRENT APPLICATION NUMBER: US/09/978,360A
CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: US 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: US 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: US 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: US 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 60/099,273
PRIOR FILING DATE: -09-04
PRIOR APPLICATION NUMBER: US 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: US 09/215,435
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: PCT/IB98/02122
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: US 09/247,155
PRIOR FILING DATE: 1999-02-09
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 810
SOFTWARE: Patent.pm
SEQ ID NO 698
LENGTH: 230
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -24..-1
US-09-978-360A-698

Query Match 100.0%; Score 230; DB 11; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.8e-207;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGIQVGYIIGLIGLGLTIVAMLLPSWKTSSYVGASIVTAVGFSKGLMMECATHTSG 60
DB 1 MASLGIQVGYIIGLIGLGLTIVAMLLPSWKTSSYVGASIVTAVGFSKGLMMECATHTSG 60
QY 61 ITGCDIYSTLLGHPADIOAAMWTSLSLACIIISVGMCTVFCQESRAKDRVAVA 120
DB 61 ITGCDIYSTLLGHPADIOAAMWTSLSLACIIISVGMCTVFCQESRAKDRVAVA 120
QY 121 GGVFFLIGLGLGHPVAMNHLGILRDFYSPVDPDSMKFEIGALYLGIIISLFLIAGII 180
DB 121 GGVFFLIGLGLGHPVAMNHLGILRDFYSPVDPDSMKFEIGALYLGIIISLFLIAGII 180
QY 181 LCFSSCSQRKRSNYDAYOAOPLATRSSPRGQPPKVKSEFNYSILGTIV 230
DB 181 LCFSSCSQRKRSNYDAYOAOPLATRSSPRGQPPKVKSEFNYSILGTIV 230

RESULT 6

US-10-006-867-80
Sequence 80, Application US/10006867
Publication No. US20020119130A1
GENERAL INFORMATION:
APPLICANT: Baton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerltisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Matanabe, Colin K.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/006,867
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 60/063435

PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/064215
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/082797
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Query Match 100.0%; Score 230; DB 13; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.8e-207;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MASLGQLVGYITLGLGLGLTIVAMLLPSWKTSYVGAIVTAVGSKGLMECAHSTG 60
DB 1 MASLGQLVGYITLGLGLGLTIVAMLLPSWKTSYVGAIVTAVGSKGLMECAHSTG 60
QY ITCCDIYSTLLGLPADIOAQAAMWTSASISLACIISVGMKCTVFCQESRAKORVAVA 120
DB 61 ITCCDIYSTLLGLPADIOAQAAMWTSASISLACIISVGMKCTVFCQESRAKORVAVA 120
QY 121 GGVFFILGGLGFIPIVAMNLHGILRDPFSPVLPDSMKFEIGALYGIISLPSLIAGII 180
DB 121 GGVFFILGGLGFIPIVAMNLHGILRDPFSPVLPDSMKFEIGALYGIISLPSLIAGII 180
QY 181 LCPSCSSQRNRSNYDAYQAOPLATRSSPPQGPVKSEFNSYSLTGYV 230
DB 181 LCPSCSSQRNRSNYDAYQAOPLATRSSPPQGPVKSEFNSYSLTGYV 230

```

RESULT 7

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US-10-063-547-80
; Sequence 80, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerltisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

```

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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,547
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 80
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-063-547-80

```

```

Query Match 100.0%; Score 230; DB 13; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.8e-207;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MASLGQLVGYITLGLGLGLTIVAMLLPSWKTSYVGAIVTAVGSKGLMECAHSTG 60
DB 1 MASLGQLVGYITLGLGLGLTIVAMLLPSWKTSYVGAIVTAVGSKGLMECAHSTG 60
QY ITCCDIYSTLLGLPADIOAQAAMWTSASISLACIISVGMKCTVFCQESRAKORVAVA 120
DB 61 ITCCDIYSTLLGLPADIOAQAAMWTSASISLACIISVGMKCTVFCQESRAKORVAVA 120
QY 121 GGVFFILGGLGFIPIVAMNLHGILRDPFSPVLPDSMKFEIGALYGIISLPSLIAGII 180
DB 121 GGVFFILGGLGFIPIVAMNLHGILRDPFSPVLPDSMKFEIGALYGIISLPSLIAGII 180
QY 181 LCPSCSSQRNRSNYDAYQAOPLATRSSPPQGPVKSEFNSYSLTGYV 230
DB 181 LCPSCSSQRNRSNYDAYQAOPLATRSSPPQGPVKSEFNSYSLTGYV 230

```

RESULT 8

```

US-10-063-551-80
; Sequence 80, Application US/10063551
; Publication No. US20020183494A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerltisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,551
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 80
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-063-551-80

```

```

Query Match 100.0%; Score 230; DB 13; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.8e-207;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MASLGQLVGYITLGLGLGLTIVAMLLPSWKTSYVGAIVTAVGSKGLMECAHSTG 60
DB 1 MASLGQLVGYITLGLGLGLTIVAMLLPSWKTSYVGAIVTAVGSKGLMECAHSTG 60
QY ITCCDIYSTLLGLPADIOAQAAMWTSASISLACIISVGMKCTVFCQESRAKORVAVA 120
DB 61 ITCCDIYSTLLGLPADIOAQAAMWTSASISLACIISVGMKCTVFCQESRAKORVAVA 120
QY 121 GGVFFILGGLGFIPIVAMNLHGILRDPFSPVLPDSMKFEIGALYGIISLPSLIAGII 180
DB 121 GGVFFILGGLGFIPIVAMNLHGILRDPFSPVLPDSMKFEIGALYGIISLPSLIAGII 180

```

Db 121 GGVFFILGGLGFLPVMNLHGILRDFYSPFLVPDSMFEIGEMALYGLIISLFSLLIAGII 180
Qy 181 LCPSCSSQRNRSNYDAYOAOPLATRSSPRGCPKXKSEFNYSYLTGYV 230
Db 181 LCPSCSSQRNRSNYDAYOAOPLATRSSPRGCPKXKSEFNYSYLTGYV 230

RESULT 9

US-10-028-072-492
Sequence 492, Application US/10028072
Publication No. US2003004311A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Gudney, Austin J.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028, 072
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059836
PRIOR FILING DATE: 1997-09-24
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062285
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062814
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/062816
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063045
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063082
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/063127
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063327

PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063329
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063550
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063561
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063704
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063733
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063735
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063738
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063755
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064248
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064809
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065846
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066453
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066511
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069212
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069278
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069334
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069694
PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 60/072320
PRIOR FILING DATE: 1998-01-23
PRIOR APPLICATION NUMBER: 60/073612
PRIOR FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/074092
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081695
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081818
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082999
PRIOR FILING DATE: 1998-04-24

PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/083545
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084627
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084637
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/085149
 PRIOR FILING DATE: 1998-05-12
 PRIOR APPLICATION NUMBER: 60/085323
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085338
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085339
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/086414
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/086430
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/087106
 PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/088026
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088720
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088741
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088810
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088858
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/089532
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089599
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089907
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089947
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/090349
 PRIOR FILING DATE: 1998-06-23
 PRIOR APPLICATION NUMBER: 60/090429
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090445
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090538
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090863
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091360
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07

Query Match 100.0%; Score 230; DB 14; Length 230;
 Best Local Similarity 100.0%; Pred. No. 1.8e-207;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASIGLQVGYITGLGLGTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60
 DB 1 MASIGLQVGYITGLGLGTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60

QY 61 ITQCDIYSTLLGLPADIOAAMTSSAISLACTIISVVGRCCTVFCQESRAKRVAVA 120
 DB 61 ITQCDIYSTLLGLPADIOAAMTSSAISLACTIISVVGRCCTVFCQESRAKRVAVA 120
 QY 121 GGVFFITGLGLGTFIPVAMNLHGILRDFYSPPLVDSMKFEIGALYIGTISLPSLIAGII 180
 DB 121 GGVFFITGLGLGTFIPVAMNLHGILRDFYSPPLVDSMKFEIGALYIGTISLPSLIAGII 180
 QY 181 LCFSCSSQNRNSRYDYAYOAPLATRSSPRGQPPVKSEFNSYSITGYV 230
 DB 181 LCFSCSSQNRNSRYDYAYOAPLATRSSPRGQPPVKSEFNSYSITGYV 230

RESULT 10
 US-10-063-616-80
 Sequence 80, Application US/10063616
 Publication No. US20030013855A1
 GENERAL INFORMATION:
 APPLICANT: Baton, Dan L.
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gerltisen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Abecia L.
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3230R1C1
 CURRENT APPLICATION NUMBER: US/10/063,616
 PRIOR FILING DATE: 2002-05-03
 PRIOR APPLICATION REMOVED - See file wrapper or Palm
 NUMBER OF SEQ ID NOS: 170
 SEQ ID NO 80
 LENGTH: 230
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-063-616-80

Query Match 100.0%; Score 230; DB 14; Length 230;
 Best Local Similarity 100.0%; Pred. No. 1.8e-207;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASIGLQVGYITGLGLGTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60
 DB 1 MASIGLQVGYITGLGLGTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60
 QY 61 ITQCDIYSTLLGLPADIOAAMTSSAISLACTIISVVGRCCTVFCQESRAKRVAVA 120
 DB 61 ITQCDIYSTLLGLPADIOAAMTSSAISLACTIISVVGRCCTVFCQESRAKRVAVA 120
 QY 121 GGVFFITGLGLGTFIPVAMNLHGILRDFYSPPLVDSMKFEIGALYIGTISLPSLIAGII 180
 DB 121 GGVFFITGLGLGTFIPVAMNLHGILRDFYSPPLVDSMKFEIGALYIGTISLPSLIAGII 180
 QY 181 LCFSCSSQNRNSRYDYAYOAPLATRSSPRGQPPVKSEFNSYSITGYV 230
 DB 181 LCFSCSSQNRNSRYDYAYOAPLATRSSPRGQPPVKSEFNSYSITGYV 230

RESULT 11
 US-10-140-808-492
 Sequence 492, Application US/10140808
 Publication No. US20030017563A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Beresini, Maureen
 APPLICANT: Deforge, Laura
 APPLICANT: Desnoyers, Luc
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerltisen, Mary E.

```

; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumaer, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C182
; CURRENT APPLICATION NUMBER: US/10/140,808
; PRIOR APPLICATION removed - See File Wrapper or Palm
; SEQ ID NO 492
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-808-492

Query Match      100.0%; Score 230; DB 14; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.8e-207;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MASLGQLVGYITIGLGLGTLVAMLLPSWKTSYVGASIVTVAGFSKGLMMECAHTSTG 60
DB      1 MASLGQLVGYITIGLGLGTLVAMLLPSWKTSYVGASIVTVAGFSKGLMMECAHTSTG 60

QY      61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120
DB      61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120

QY      121 GGVFFILGLGLGFIPIVAMNHGILRDFYSPVDSMKFEIGALYIGIISLPSLGIIT 180
DB      121 GGVFFILGLGLGFIPIVAMNHGILRDFYSPVDSMKFEIGALYIGIISLPSLGIIT 180

QY      181 LCFSCSSQRRNSNYDAYOQOPLATRSSPPRGQPPVKSEFNSYSLTGYV 230
DB      181 LCFSCSSQRRNSNYDAYOQOPLATRSSPPRGQPPVKSEFNSYSLTGYV 230

RESULT 12
US-10-063-569-80
; Sequence 80, Application US/10063569
; Publication No. US20030018168A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,569
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 80
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-569-80

Query Match      100.0%; Score 230; DB 14; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.8e-207;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MASLGQLVGYITIGLGLGTLVAMLLPSWKTSYVGASIVTVAGFSKGLMMECAHTSTG 60
DB      1 MASLGQLVGYITIGLGLGTLVAMLLPSWKTSYVGASIVTVAGFSKGLMMECAHTSTG 60

QY      61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120
DB      61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120

QY      121 GGVFFILGLGLGFIPIVAMNHGILRDFYSPVDSMKFEIGALYIGIISLPSLGIIT 180
DB      121 GGVFFILGLGLGFIPIVAMNHGILRDFYSPVDSMKFEIGALYIGIISLPSLGIIT 180

QY      181 LCFSCSSQRRNSNYDAYOQOPLATRSSPPRGQPPVKSEFNSYSLTGYV 230
DB      181 LCFSCSSQRRNSNYDAYOQOPLATRSSPPRGQPPVKSEFNSYSLTGYV 230
```

```

Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MASLGQLVGYITIGLGLGTLVAMLLPSWKTSYVGASIVTVAGFSKGLMMECAHTSTG 60
DB      1 MASLGQLVGYITIGLGLGTLVAMLLPSWKTSYVGASIVTVAGFSKGLMMECAHTSTG 60

QY      61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120
DB      61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120

QY      121 GGVFFILGLGLGFIPIVAMNHGILRDFYSPVDSMKFEIGALYIGIISLPSLGIIT 180
DB      121 GGVFFILGLGLGFIPIVAMNHGILRDFYSPVDSMKFEIGALYIGIISLPSLGIIT 180

QY      181 LCFSCSSQRRNSNYDAYOQOPLATRSSPPRGQPPVKSEFNSYSLTGYV 230
DB      181 LCFSCSSQRRNSNYDAYOQOPLATRSSPPRGQPPVKSEFNSYSLTGYV 230

RESULT 13
US-10-063-513-80
; Sequence 80, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,513
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 80
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-513-80

Query Match      100.0%; Score 230; DB 14; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.8e-207;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MASLGQLVGYITIGLGLGTLVAMLLPSWKTSYVGASIVTVAGFSKGLMMECAHTSTG 60
DB      1 MASLGQLVGYITIGLGLGTLVAMLLPSWKTSYVGASIVTVAGFSKGLMMECAHTSTG 60

QY      61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120
DB      61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120

QY      121 GGVFFILGLGLGFIPIVAMNHGILRDFYSPVDSMKFEIGALYIGIISLPSLGIIT 180
DB      121 GGVFFILGLGLGFIPIVAMNHGILRDFYSPVDSMKFEIGALYIGIISLPSLGIIT 180

QY      181 LCFSCSSQRRNSNYDAYOQOPLATRSSPPRGQPPVKSEFNSYSLTGYV 230
DB      181 LCFSCSSQRRNSNYDAYOQOPLATRSSPPRGQPPVKSEFNSYSLTGYV 230

RESULT 14
US-10-063-515-80
; Sequence 80, Application US/10063515
; Publication No. US20030018173A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,515
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 80
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-515-80

Query Match      100.0%; Score 230; DB 14; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.8e-207;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MASLGQLVGYITIGLGLGTLVAMLLPSWKTSYVGASIVTVAGFSKGLMMECAHTSTG 60
DB      1 MASLGQLVGYITIGLGLGTLVAMLLPSWKTSYVGASIVTVAGFSKGLMMECAHTSTG 60

QY      61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120
DB      61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120

QY      121 GGVFFILGLGLGFIPIVAMNHGILRDFYSPVDSMKFEIGALYIGIISLPSLGIIT 180
DB      121 GGVFFILGLGLGFIPIVAMNHGILRDFYSPVDSMKFEIGALYIGIISLPSLGIIT 180

QY      181 LCFSCSSQRRNSNYDAYOQOPLATRSSPPRGQPPVKSEFNSYSLTGYV 230
DB      181 LCFSCSSQRRNSNYDAYOQOPLATRSSPPRGQPPVKSEFNSYSLTGYV 230
```

```

; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,515
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 80
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-515-80

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Query Match 100.0%; Score 230; DB 14; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.8e-207;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MASLGQLVGYILGLIGLGLTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECAHSTG 60
DB 1 MASLGQLVGYILGLIGLGLTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECAHSTG 60
QY 61 ITQCDIYSTLLGLPADIOAAMMTSSAISLACTISVGNRCCTVFCQESRAKDRVAVA 120
DB 61 ITQCDIYSTLLGLPADIOAAMMTSSAISLACTISVGNRCCTVFCQESRAKDRVAVA 120
QY 121 GGVPFILGGLGRIPVAMNLHGILRDFSPVLPDSMKFEIGALYLGIIISLFSLIAGII 180
DB 121 GGVPFILGGLGRIPVAMNLHGILRDFSPVLPDSMKFEIGALYLGIIISLFSLIAGII 180
QY 181 LCFSSCSQRNRNSNYDAYQAOPLATRSSPRGQPPKVKSEFNSYSLTGYV 230
DB 181 LCFSSCSQRNRNSNYDAYQAOPLATRSSPRGQPPKVKSEFNSYSLTGYV 230

```

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RESULT 15
US-10-063-512-80
; Sequence 80, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 80
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-512-80

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Query Match 100.0%; Score 230; DB 14; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.8e-207;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MASLGQLVGYILGLIGLGLTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECAHSTG 60
DB 1 MASLGQLVGYILGLIGLGLTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECAHSTG 60
QY 61 ITQCDIYSTLLGLPADIOAAMMTSSAISLACTISVGNRCCTVFCQESRAKDRVAVA 120
DB 61 ITQCDIYSTLLGLPADIOAAMMTSSAISLACTISVGNRCCTVFCQESRAKDRVAVA 120
QY 121 GGVPFILGGLGRIPVAMNLHGILRDFSPVLPDSMKFEIGALYLGIIISLFSLIAGII 180
DB 121 GGVPFILGGLGRIPVAMNLHGILRDFSPVLPDSMKFEIGALYLGIIISLFSLIAGII 180
QY 181 LCFSSCSQRNRNSNYDAYQAOPLATRSSPRGQPPKVKSEFNSYSLTGYV 230
DB 181 LCFSSCSQRNRNSNYDAYQAOPLATRSSPRGQPPKVKSEFNSYSLTGYV 230

```

Search completed: October 27, 2004, 07:50:58
Job time : 129 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 27, 2004, 07:21:57 ; Search time 155 Seconds

(without alignments)
532.308 Million cell updates/sec

Title: US-09-787-677A-3

Perfect score: 230

Sequence: 1 MASIGQLVYLIGLGLG.....PGQPKVSEFNSYLGYV 230

Scoring table: OLIGO

Gapex 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729239 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*\n2: geneseqp1980s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	230	100.0	230	2	AAV36181 Human sec
2	230	100.0	230	3	AAV84609 A human m
3	230	100.0	230	3	AAV9378 Human PRO
4	230	100.0	230	4	AAV66127 Protein o
5	230	100.0	230	4	AAE04207 Human gen
6	230	100.0	230	4	AAU12417 Human PRO
7	230	100.0	230	4	AAU09178 Human PRO
8	230	100.0	230	4	AAV87565 Human PRO
9	230	100.0	230	4	AAV88342 Human mem
10	230	100.0	230	5	ABP67991 Human COL
11	230	100.0	230	5	ABG95890 Human sec
12	230	100.0	230	5	ABH84912 Human PRO
13	230	100.0	230	5	AAU76534 Tuncour-as
14	230	100.0	230	5	ABG64507 Human alb
15	230	100.0	230	5	ABH04707 Human SP8
16	230	100.0	230	5	ABH95518 Human ang
17	230	100.0	230	6	ABO17861 Novel hum
18	230	100.0	230	6	ABU81115 Human PRO
19	230	100.0	230	6	ABU90915 Novel hum
20	230	100.0	230	6	ABO33974 Human sec
21	230	100.0	230	6	ABU71991 Novel hum
22	230	100.0	230	6	ABU66815 Human PRO
23	230	100.0	230	6	ABU71545 Human sec
24	230	100.0	230	6	ABU47946 Human sec
25	230	100.0	230	6	ABU59896 Novel sec

26	230	100.0	230	6	ABU72326 Human PRO
27	230	100.0	230	6	ABU90999 Human PRO
28	230	100.0	230	6	ABO27320 Human sec
29	230	100.0	230	6	ABO25086 Human sec
30	230	100.0	230	6	ABR00178 Human gen
31	230	100.0	230	6	ABU92515 Human sec
32	230	100.0	230	6	ABU81185 Human sec
33	230	100.0	230	6	ABO53299 Novel hum
34	230	100.0	230	6	ABU67091 Human sec
35	230	100.0	230	6	ABU98302 Novel hum
36	230	100.0	230	6	ABU89307 Novel hum
37	230	100.0	230	6	ABU82514 Novel hum
38	230	100.0	230	6	ABU96478 Human PRO
39	230	100.0	230	6	ABU72148 Human PRO
40	230	100.0	230	6	ADA46011 Novel hum
41	230	100.0	230	6	ADA76442 Human PRO
42	230	100.0	230	6	ADBI7137 Human tra
43	230	100.0	230	6	ADA19092 Human PRO
44	230	100.0	230	6	ADA61715 Homo sapi
45	230	100.0	230	6	ADBI9500 Novel hum

ALIGNMENTS

RESULT 1
ID AAV36181 standard; protein; 230 AA.

AC AAV36181;

DT 23-SEP-1999 (first entry)

DE Human secreted protein #53.

KW Secreted protein; human; cytosolic; thrombotic; osteopathic; forensic;

KM diagnostic; gene therapy; chromosome mapping; secretion vector.

XX Homo sapiens.

XX WO9925825-A2.

XX PD 27-MAY-1999.

XX PF 13-NOV-1998; 98MO-IB001862.

XX PR 13-NOV-1997; 97US-0066677P.

XX PR 17-DEC-1997; 97US-0069957P.

XX PR 09-FEB-1998; 98US-0074121P.

XX PR 13-APR-1998; 98US-0081563P.

XX PR 10-AUG-1998; 98US-0096116P.

XX PR 04-SEP-1998; 98US-0099273P.

XX PA (GENST) GENSET.

XX PI Bougueleret L, Duclert A, Dumas Milne Edwards J;

XX PS WPI; 1999-347472/29.

XX DR N-PSDB; AAX97865.

XX XX Extended cDNAs encoding secreted proteins.

XX PT Claim 7, Page 289; 307PP; English.

AAV36129-Y36222 represent novel human secreted proteins encoded by the extended cDNA sequences represented in AAX97813-X97906. The proteins of the invention have cytosolic, thrombotic and osteopathic activity. The extended cDNAs can be used to express secreted proteins or parts of them or to obtain antibodies capable of binding to the secreted proteins. They may also be used in diagnostic, forensic, gene therapy and chromosome mapping procedures. Uses also include design of expression vectors and secretion vectors

XX WO200012708-A2.
 XX 09-MAR-2000.
 PD
 XX
 PF 01-SEP-1999; 99WO-US020111.
 XX
 PR 01-SEP-1998; 98US-0098716P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 01-SEP-1998; 98US-0098750P.
 PR 02-SEP-1998; 98US-0098803P.
 PR 02-SEP-1998; 98US-0098821P.
 PR 02-SEP-1998; 98US-0098843P.
 PR 09-SEP-1998; 98US-0099536P.
 PR 09-SEP-1998; 98US-0099596P.
 PR 09-SEP-1998; 98US-0099598P.
 PR 09-SEP-1998; 98US-0099602P.
 PR 09-SEP-1998; 98US-0099642P.
 PR 10-SEP-1998; 98US-0099741P.
 PR 10-SEP-1998; 98US-0099754P.
 PR 10-SEP-1998; 98US-0099763P.
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 PR 10-SEP-1998; 98US-0099808P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98US-0099815P.
 PR 10-SEP-1998; 98US-0099816P.
 PR 15-SEP-1998; 98US-0100385P.
 PR 15-SEP-1998; 98US-0100388P.
 PR 15-SEP-1998; 98US-0100390P.
 PR 16-SEP-1998; 98US-0100584P.
 PR 16-SEP-1998; 98US-0100627P.
 PR 16-SEP-1998; 98US-0100627P.
 PR 16-SEP-1998; 98US-0100661P.
 PR 16-SEP-1998; 98US-0100662P.
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 PR 17-SEP-1998; 98US-0100683P.
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 PR 17-SEP-1998; 98US-0100710P.
 PR 17-SEP-1998; 98US-0100711P.
 PR 17-SEP-1998; 98US-0100919P.
 PR 17-SEP-1998; 98US-0100930P.
 PR 18-SEP-1998; 98US-0100848P.
 PR 18-SEP-1998; 98US-0100849P.
 PR 18-SEP-1998; 98US-0101014P.
 PR 18-SEP-1998; 98US-0101068P.
 PR 18-SEP-1998; 98US-0101071P.
 PR 22-SEP-1998; 98US-0101279P.
 PR 23-SEP-1998; 98US-0101471P.
 PR 23-SEP-1998; 98US-0101472P.
 PR 23-SEP-1998; 98US-0101474P.
 PR 23-SEP-1998; 98US-0101475P.
 PR 23-SEP-1998; 98US-0101477P.
 PR 23-SEP-1998; 98US-0101479P.
 PR 24-SEP-1998; 98US-0101738P.
 PR 24-SEP-1998; 98US-0101741P.
 PR 24-SEP-1998; 98US-0101743P.
 PR 24-SEP-1998; 98US-0101915P.
 PR 24-SEP-1998; 98US-0101916P.
 PR 29-SEP-1998; 98US-0102207P.
 PR 29-SEP-1998; 98US-0102240P.
 PR 29-SEP-1998; 98US-0102307P.
 PR 29-SEP-1998; 98US-0102330P.
 PR 29-SEP-1998; 98US-0102331P.
 PR 30-SEP-1998; 98US-0102484P.
 PR 30-SEP-1998; 98US-0102487P.
 PR 30-SEP-1998; 98US-0102570P.
 PR 30-SEP-1998; 98US-0102571P.
 PR 01-OCT-1998; 98US-0102684P.
 PR 01-OCT-1998; 98US-0102687P.
 PR 02-OCT-1998; 98US-0102965P.
 PR 06-OCT-1998; 98US-0103258P.
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 PR 07-OCT-1998; 98US-0103395P.
 PR 07-OCT-1998; 98US-0103396P.
 PR 07-OCT-1998; 98US-0103401P.
 PR 08-OCT-1998; 98US-0103633P.
 PR 08-OCT-1998; 98US-0103678P.
 PR 08-OCT-1998; 98US-0103679P.
 PR 08-OCT-1998; 98US-0103711P.
 PR 14-OCT-1998; 98US-0104257P.
 PR 20-OCT-1998; 98US-0104887P.
 PR 20-OCT-1998; 98US-0105000P.
 PR 20-OCT-1998; 98US-0105002P.
 PR 21-OCT-1998; 98US-0105104P.
 PR 21-OCT-1998; 98US-0105169P.
 PR 22-OCT-1998; 98US-0105266P.
 PR 26-OCT-1998; 98US-0105593P.
 PR 26-OCT-1998; 98US-0105594P.
 PR 26-OCT-1998; 98US-0105807P.
 PR 27-OCT-1998; 98US-0105810P.
 PR 27-OCT-1998; 98US-0105822P.
 PR 27-OCT-1998; 98US-0106062P.
 PR 28-OCT-1998; 98US-0106023P.
 PR 28-OCT-1998; 98US-0106029P.
 PR 28-OCT-1998; 98US-0106030P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 28-OCT-1998; 98US-0106033P.
 PR 28-OCT-1998; 98US-0106178P.
 PR 29-OCT-1998; 98US-0106248P.
 PR 29-OCT-1998; 98US-0106384P.
 PR 29-OCT-1998; 98US-0108500P.
 PR 30-OCT-1998; 98US-0106464P.
 PR 03-NOV-1998; 98US-0106856P.
 PR 03-NOV-1998; 98US-0106902P.
 PR 03-NOV-1998; 98US-0106905P.
 PR 03-NOV-1998; 98US-0106919P.
 PR 03-NOV-1998; 98US-0106932P.
 PR 03-NOV-1998; 98US-0106934P.
 PR 10-NOV-1998; 98US-0107783P.
 PR 17-NOV-1998; 98US-0108775P.
 PR 17-NOV-1998; 98US-0108779P.
 PR 17-NOV-1998; 98US-0108787P.
 PR 17-NOV-1998; 98US-0108801P.
 PR 17-NOV-1998; 98US-0108818P.
 PR 17-NOV-1998; 98US-0108820P.
 PR 17-NOV-1998; 98US-0108806P.
 PR 17-NOV-1998; 98US-0108807P.
 PR 17-NOV-1998; 98US-0108867P.
 PR 17-NOV-1998; 98US-0108867P.
 PR 18-NOV-1998; 98US-0108848P.
 PR 18-NOV-1998; 98US-0108849P.
 PR 18-NOV-1998; 98US-0108850P.
 PR 18-NOV-1998; 98US-0108851P.
 PR 18-NOV-1998; 98US-0108852P.
 PR 18-NOV-1998; 98US-0108858P.
 PR 18-NOV-1998; 98US-0108904P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WT;
 XX WPI; 2000-237871/20.
 DR N-PSDB; AAA37060.
 XX
 PT New mammalian DNA sequences encoding transmembrane, receptor or secreted
 PT PRO polypeptides, useful for screening of potential peptide or small
 XX molecule inhibitors of the relevant receptor/ligand interactions.
 PS Claim 12; Fig 78; 773pp; English.
 XX
 CC AAA37022 to AAA37144 encode the new isolated human transmembrane,
 CC receptor or secreted PRO polypeptides given in AAY93340 to AAY93462. The
 CC transmembrane and receptor PRO proteins can be used for screening of

CC potential peptide or small molecule inhibitors of the relevant
CC receptor/ligand interactions. The polypeptides and nucleotide sequences
CC encoding them have various industrial applications, including uses as
CC pharmaceutical and diagnostic agents. AAs3145 to AAs3730 represent PCR
CC primers and hybridisation probes used in the isolation of the PRO
CC polypeptides from the present invention

XX Sequence 230 AA;

Query Match 100.0%; Score 230; DB 3; Length 230;
Best Local Similarity 100.0%; Pred. No. 3.9e-210;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGLQVGYIIGLGLGLTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60
DB 1 MASLGLQVGYIIGLGLGLTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60
QY 61 ITQCDIYSTLLGLPADIOAAMMTSSAISLACTISVGMKCTVFCQESRAKDRVAVA 120
DB 61 ITQCDIYSTLLGLPADIOAAMMTSSAISLACTISVGMKCTVFCQESRAKDRVAVA 120
QY 121 GGVFTLLGLGLFIPVAMNHLGILRDFYSPVLPDSMKFEIGEALYIGIISLFSLIAGII 180
DB 121 GGVFTLLGLGLFIPVAMNHLGILRDFYSPVLPDSMKFEIGEALYIGIISLFSLIAGII 180
QY 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPPRGQPPVKSEFNSYSLTGYV 230
DB 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPPRGQPPVKSEFNSYSLTGYV 230

RESULT 4
AAB66127
ID AAB66127 standard; protein; 230 AA.

XX AAB66127;

XX 02-APR-2001 (first entry)

XX Protein of the invention #39.

XX Secreted; transmembrane; gene therapy.

XX Unidentified.

XX WO200078961-A1.

XX 28-DEC-2000.

XX 18-FEB-2000; 2000WO-US0004342.

XX 23-JUN-1999; 99US-0141037P.

XX 20-JUL-1999; 99US-0144758P.

XX 26-JUL-1999; 99US-0145698P.

XX 01-SEP-1999; 99WO-US020111.

XX 29-OCT-1999; 99US-0162506P.

XX 30-NOV-1999; 99WO-US028313.

XX 02-DEC-1999; 99WO-US028551.

XX 16-DEC-1999; 99WO-US030095.

XX 05-JAN-2000; 2000WO-US000219.

XX 06-JAN-2000; 2000WO-US000376.

XX (GETH) GENENTECH INC.

XX Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
XX Geo W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Williams PM, Wood WI;
XX WPI; 2001-071395/08.
XX Secreted and transmembrane proteins and nucleic acids designated PRO,
XX PT useful as hybridization probes, in chromosome and gene mapping and gene
XX therapy.

XX Claim 1; Fig 78; 787p; English.

XX The present invention relates to secreted and transmembrane proteins.
XX These proteins and the DNA encoding them may be used as hybridization
XX probes, in chromosome and gene mapping and in the generation of anti-
XX sense RNA and DNA. They may also be used to generate either
XX transgenic animals or knockout animals which are in turn useful for
XX development and screening of therapeutically useful reagents. The nucleic
XX acids may also be used in gene therapy

XX Sequence 230 AA;

Query Match 100.0%; Score 230; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 3.9e-210;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGLQVGYIIGLGLGLTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60
DB 1 MASLGLQVGYIIGLGLGLTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60
QY 61 ITQCDIYSTLLGLPADIOAAMMTSSAISLACTISVGMKCTVFCQESRAKDRVAVA 120
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DB 121 GGVFTLLGLGLFIPVAMNHLGILRDFYSPVLPDSMKFEIGEALYIGIISLFSLIAGII 180
QY 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPPRGQPPVKSEFNSYSLTGYV 230
DB 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPPRGQPPVKSEFNSYSLTGYV 230

RESULT 5
AAB04207

ID AAB04207 standard; protein; 230 AA.

XX AAB04207;

XX 09-AUG-2001 (first entry)

XX Human gene 10 encoded secreted protein HRP183, SEQ ID NO:62.

XX Human; secreted protein; proliferative disorder; cancer; tumour;
XX foetal abnormality; developmental abnormality; haematopoietic disorder;
XX immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
XX inflammation; allergy; neurological disorder; Alzheimer's disease;
XX Parkinson's disease; cognitive disorder; schizophrenia; asthma;
XX skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
XX cardiovascular disorder; angiotensin disorder; kidney disorder;
XX gastrointestinal disorder; pregnancy-related disorder; gene therapy;
XX endocrine disorder; infection; wound healing; vulnerability; cell culture;
XX chemotaxis; food additive; binding partner identification.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..24 /label= signal_peptide

FT Protein 25..230 /note="Mature secreted protein"

XX WO200136432-A2.

XX 25-MAY-2001.

XX 15-NOV-2000; 2000WO-US031162.

XX 19-NOV-1999; 99US-0166415P.

XX 30-JUN-2000; 2000US-0215136P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Komatsoulis GA, Baker KP, Young PE;
 XX WPI; 2001-343793/36.
 DR N-PSDB; AAD08497.
 XX
 PT Isolated nucleic acid molecule encoding a human secreted protein is used
 PT in preventing, treating or ameliorating a medical condition.
 XX
 PS Claim 11; Page 439; 509pp; English.
 CC AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted
 CC protein genes, and AAB04199-AAB04239 represent the proteins they encode.
 CC AAB04240-AAB04297 represent human secreted protein fragments or variants.
 CC The secreted proteins and their genes are useful for preventing, treating
 CC or ameliorating medical conditions, e.g., by protein or gene therapy.
 CC Pathological conditions can be diagnosed by determining the amount of the
 CC new protein in a sample or by determining the presence of mutations in
 CC the new genes. Specific uses are described for each of the 18 genes,
 CC based on the tissues in which they are most highly expressed, and include
 CC developing products for the diagnosis or treatment of proliferative
 CC disorders, cancer, tumors, foetal and developmental abnormalities,
 CC hematopoietic disorders, diseases of the immune system, AIDS, autoimmune
 CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
 CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
 CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
 CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
 CC angiogenic disorders, kidney disorders, gastrointestinal disorders,
 CC pregnancy-related disorders, endocrine disorders, and infections. The
 CC proteins can also be used to aid wound healing and epithelial cell
 CC proliferation, to prevent skin ageing due to sunburn, to maintain organs
 CC before transplantation, for supporting cell culture of primary tissues,
 CC to regenerate tissues, to identify their cognate ligands or binding
 CC partners, and in chemotaxis, and can be used as a food additive or
 CC preservative to modify storage properties. Antibodies specific for a
 CC protein of the invention can be used in alleviating symptoms associated
 CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
 CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The
 CC present sequence represents a human secreted protein of the invention
 XX
 XX Sequence 230 AA;
 SQ
 Query Match 100.0%; Score 230; DB 4; Length 230;
 Best Local Similarity 100.0%; Pred. No. 3.9e-210;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
 KW prostate; cervical; tumor necrosis factor-alpha; TNF-alpha; cartilage;
 KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
 KW A-peptide; factor VIIa; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200140466-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 01-DEC-2000; 2000MO-US032678.
 XX
 PR 01-DEC-1999; 99MO-US028301.
 PR 01-DEC-1999; 99MO-US028634.
 PR 02-DEC-1999; 99MO-US028551.
 PR 02-DEC-1999; 99MO-US028564.
 PR 02-DEC-1999; 99MO-US028565.
 PR 09-DEC-1999; 99US-0170262P.
 PR 16-DEC-1999; 99MO-US030095.
 PR 20-DEC-1999; 99MO-US030911.
 PR 20-DEC-1999; 99MO-US030999.
 PR 30-DEC-1999; 99MO-US031243.
 PR 30-DEC-1999; 99MO-US031274.
 PR 05-JAN-2000; 2000MO-US000219.
 PR 06-JAN-2000; 2000MO-US000277.
 PR 06-JAN-2000; 2000MO-US000376.
 PR 11-FEB-2000; 2000MO-US003565.
 PR 18-FEB-2000; 2000MO-US004341.
 PR 18-FEB-2000; 2000MO-US004342.
 PR 22-FEB-2000; 2000MO-US004414.
 PR 24-FEB-2000; 2000MO-US004914.
 PR 24-FEB-2000; 2000MO-US005004.
 PR 01-MAR-2000; 2000MO-US005601.
 PR 02-MAR-2000; 2000MO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 10-MAR-2000; 2000MO-US006319.
 PR 15-MAR-2000; 2000MO-US006884.
 PR 20-MAR-2000; 2000MO-US007377.
 PR 21-MAR-2000; 2000MO-US007532.
 PR 30-MAR-2000; 2000MO-US008439.
 PR 17-MAY-2000; 2000MO-US013705.
 PR 22-MAY-2000; 2000MO-US014042.
 PR 30-MAY-2000; 2000MO-US014941.
 PR 02-JUN-2000; 2000MO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000MO-US020710.
 PR 11-AUG-2000; 2000MO-US022031.
 PR 23-AUG-2000; 2000MO-US023522.
 PR 24-AUG-2000; 2000MO-US023328.
 PR 08-NOV-2000; 2000MO-US030952.
 PR 10-NOV-2000; 2000MO-US030873.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2001-408281/43.
 DR N-PSDB; AAS21489.
 XX
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
 PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
 PT breast, prostate, cervical.
 XX
 PS Claim 12; Fig 492; 813pp; English.
 CC AAI12172-AAI12446 represent novel human secretory and transmembrane PRO
 CC polypeptides. The PRO polypeptides are useful to detect other PRO
 CC polypeptides, to link bioactive molecules to cells expressing PRO
 CC polypeptides, to modulate biological activities of cells expressing PRO

CC polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample. Some
 CC of the 275 sequences are also useful to stimulate the release of tumour
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
 CC differentiation of chondrocytes, the proliferation or gene expression in
 CC pericyte cells, the release of proteoglycans from cartilage, the
 CC proliferation of inner ear utricular supporting cells or of T-
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes
 CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
 CC muscle cells or by adipocytes, or inhibit binding of A-peptide to factor
 CC VIIA. The PRO polypeptides can be used in assays to identify molecules
 CC involved in binding interactions. The polynucleotides encoding PRO
 CC polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy

XX Sequence 230 AA;

Query Match 100.0%; Score 230; DB 4; Length 230;
 Best Local Similarity 100.0%; Pred. No. 3.9e-210;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGLQVGYIIGLLGLGLTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60
 DB 1 MASLGLQVGYIIGLLGLGLTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60
 QY 61 ITCCDIYSTLLGLPADIQAAQAMWVTSSAISLACITISVVMRCCTVCOESRAKDRVAVA 120
 DB 61 ITCCDIYSTLLGLPADIQAAQAMWVTSSAISLACITISVVMRCCTVCOESRAKDRVAVA 120
 QY 121 GGVEFIIGLLGLFIPVAMNHLGILRDFYSPVPDSMKFEIGALYGIISLSFSLAGIT 180
 DB 121 GGVEFIIGLLGLFIPVAMNHLGILRDFYSPVPDSMKFEIGALYGIISLSFSLAGIT 180
 QY 181 LCRTSSGQRKRSNYDYAQOPLATRSSPRGQPPKXSEFNYSLTGYV 230
 DB 181 LCRTSSGQRKRSNYDYAQOPLATRSSPRGQPPKXSEFNYSLTGYV 230

RESULT 7

AAU09178 ID AAU09178 standard; protein; 230 AA.

XX AAU09178;

XX 16-JAN-2002 (first entry)

XX Human PRO1356 polypeptide.

XX Human; PRO1356; clone DNA64886-1601; immune-related disorder;
 KW inflammatory disorder; infectious disorder; immunodeficiency disorder;
 KW autoimmune disorder; renal disease; demyelinating disease; skin disease;
 KW neoplasia; transplantation associated disease; immunosuppressive;
 KW anti-inflammatory; antidiabetic; antidiabetic.

XX Homo sapiens.

XX Location/Qualifiers

FT Key 1..24 /label= Signal_peptide

FT Modified-site 17..23 /note= "N-myristoylation site"

FT Modified-site 20..26 /note= "N-myristoylation site"

FT Protein 25..230 /label= Mature_PRO1356_polypeptide

FT Region 46..60 /note= "Also found in FMP-22, EMP and MP20 family proteins"

FT Modified-site 60..66 /note= "N-myristoylation site"

FT Domain 82..102

FT /label= Transmembrane_domain
 FT 101..107 /note= "N-myristoylation site"
 FT Domain 117..140 /label= Transmembrane_domain
 FT Modified-site 128..134 /note= "N-myristoylation site"
 FT Domain 153..182 /label= Transmembrane_domain
 FT Modified-site 167..173 /note= "N-myristoylation site"
 FT Modified-site 178..184 /note= "N-myristoylation site"
 FT Modified-site 190..194 /note= "N-glycosylation site"
 FT Modified-site 216..225 /note= "Tyrosine kinase phosphorylation site"

FN WO200166740-A2.

PD 13-SEP-2001.

PF 01-MAR-2001; 2001MO-US006666.

XX 03-MAR-2000; 2000US-0187202P.
 PR 21-MAR-2000; 2000US-0191015P.
 PR 30-MAY-2000; 2000MO-US014941.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 24-AUG-2000; 2000MO-US023328.
 PR 01-DEC-2000; 2000MO-US032678.

XX (GETH) GENENTECH INC.

XX Eaton DU, Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
 PI Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WPI, 2001-625876/72.

DR N-PSDB; AAS15360.

XX Nucleic acids encoding PRO polypeptides, useful for detecting and
 PT treating immune related diseases and disorders in mammals including
 PT autoimmune diseases, inflammatory diseases and asthma.

XX Claim 10; Fig 2; 122pp; English.

XX The present invention relates to the isolation of 9 novel human PRO
 CC polypeptides and the cDNA sequences (AAS15360-AAS15368) encoding them.
 CC The novel PRO polypeptides include PRO1356, PRO1268, PRO1884, PRO3444,
 CC PRO3151, PRO4322, PRO3964, PRO10008 and PRO19598. The cDNA sequences
 CC encoding these PRO polypeptides have been designated as clones DNA64886-
 CC 1601, DNA64903-1553, DNA64318-2520, DNA87997, DNA89273, DNA92223-2567,
 CC DNA96973, DNA101921 and DNA145887 respectively. Compositions (e.g.
 CC vaccines) containing PRO polypeptides and methods of using these
 CC compositions are useful in the treatment and diagnosis of immune-related
 CC disorders. Such disorders include immune-mediated inflammatory disorders
 CC (e.g. osteoarthritis), non-immune-mediated inflammatory disorders (e.g.
 CC diabetes mellitus), infectious disorders (e.g. granulomatous hepatitis),
 CC immunodeficiency disorders (e.g. AIDS), autoimmune disorders (e.g.
 CC rheumatoid arthritis), immune-related renal diseases (e.g. cirrhosis),
 CC demyelinating diseases of the peripheral or central nervous system (e.g.
 CC Guillain-Barre syndrome), immune-mediated skin diseases (e.g. contact
 CC dermatitis), neoplasias and transplantation associated diseases. The
 CC polynucleotide sequences of the invention may be used in gene therapy.
 CC AAU09178-AAU09186 represent the novel human PRO polypeptides of the
 CC invention

XX Sequence 230 AA;

Query Match 100.0%; Score 230; DB 4; Length 230;
 Best Local Similarity 100.0%; Pred. No. 3.9e-210;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGLQVGYIIGLLGLGLTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60

```
Db 1 MASIGQLVGYIIGLGLGTLVAMLLPSWKTSSYVGASIVTVAGFSKGLMECATHTSTG 60
QY 61 ITQCDIYSTLLGLPADIQAAQAMMTSSAISLACIIISVGMCTVFCOESRAKDRVAVA 120
Db 61 ITQCDIYSTLLGLPADIQAAQAMMTSSAISLACIIISVGMCTVFCOESRAKDRVAVA 120
QY 121 GGVPFLLGLGLGFIPIVAMNHLGILRDFYSPVDPDSMKFEIGELALYIGIISLSFLAGII 180
Db 121 GGVPFLLGLGLGFIPIVAMNHLGILRDFYSPVDPDSMKFEIGELALYIGIISLSFLAGII 180
QY 181 LCFSSCSQRRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV 230
Db 181 LCFSSCSQRRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV 230

RESULT 8
AAB87565
ID AAB87565 standard; protein; 230 AA.
XX
AC AAB87565;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human PRO1356.
XX
KM Human; PRO protein; mapping.
XX
OS Homo sapiens.
XX
PN WO200116318-A2.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US023328.
XX
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 07-DEC-1999; 99US-0169495P.
PR 09-DEC-1999; 99US-0170262P.
PR 11-JAN-2000; 2000US-0175461P.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 03-MAR-2000; 2000US-0187282P.
PR 21-MAR-2000; 2000US-0191007P.
PR 30-MAR-2000; 2000WO-US008439.
PR 25-APR-2000; 2000US-0199397P.
PR 22-MAY-2000; 2000WO-US014042.
PR 05-JUN-2000; 2000US-0209832P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ,
PI Grimaldi CJ, Gurney AL, Matarabze CK, Wood WI,
XX
DR N-PSDB; AAF92097.
XX
WPI; 2001-183260/18.
XX
PT Bighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT biology, including use as hybridization probes, and in chromosome and
PT gene mapping.
XX
PS Claim 12; Fig 80; 278bp; English.
XX
CC The present sequence is a human PRO polypeptide (secreted and
CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC anti-PRO antibodies are useful for preparation of a medicament useful in
CC the treatment of a condition which is responsive to the PRO protein,
CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC employed as molecular weight markers for protein electrophoresis. The PRO
CC coding sequence has applications in molecular biology, including use as
```

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CC hybridisation probes, and in chromosome and gene mapping
XX
SQ Sequence 230 AA;
QY 100.0%; Score 230; DB 4; Length 230;
Db Best Local Similarity 100.0%; Pred. No. 3.9e-210; Indels 0; Gaps 0;
Matches 230; Conservative 0; Mismatches 0;
QY 1 MASIGQLVGYIIGLGLGTLVAMLLPSWKTSSYVGASIVTVAGFSKGLMECATHTSTG 60
Db 1 MASIGQLVGYIIGLGLGTLVAMLLPSWKTSSYVGASIVTVAGFSKGLMECATHTSTG 60
QY 61 ITQCDIYSTLLGLPADIQAAQAMMTSSAISLACIIISVGMCTVFCOESRAKDRVAVA 120
Db 61 ITQCDIYSTLLGLPADIQAAQAMMTSSAISLACIIISVGMCTVFCOESRAKDRVAVA 120
QY 121 GGVPFLLGLGLGFIPIVAMNHLGILRDFYSPVDPDSMKFEIGELALYIGIISLSFLAGII 180
Db 121 GGVPFLLGLGLGFIPIVAMNHLGILRDFYSPVDPDSMKFEIGELALYIGIISLSFLAGII 180
QY 181 LCFSSCSQRRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV 230
Db 181 LCFSSCSQRRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV 230

RESULT 9
AAB88342
ID AAB88342 standard; protein; 230 AA.
XX
AC AAB88342;
XX
DT 23-MAY-2001 (first entry)
XX
DE Human membrane or secretory protein clone PSRC0059.
XX
KM Human; secretory protein; membrane protein; vaccine; gene therapy;
KM rheumatoid arthritis; diabetes.
XX
OS Homo sapiens.
XX
PN EP1067182-A2.
XX
PD 10-JAN-2001.
XX
PF 07-JUL-2000; 2000EP-00114090.
XX
PR 08-JUL-1999; 99JP-00194179.
PR 11-JAN-2000; 2000JP-00118775.
PR 02-MAY-2000; 2000JP-00183766.
XX
PA (HELI-) HELIX RES INST.
XX
PI Oca T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
PI WPI; 2001-093989/11.
XX
DR N-PSDB; AAF93769.
XX
PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT gene therapy or as candidate target molecules in drug development.
XX
PS Claim 1; SEQ ID NO 52; 609pp + Sequence Listing; English.
XX
CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC which encode human secretory or membrane proteins represented by AAB88317
CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
CC invention. The invention also includes methods for the production of
CC antibodies directed against the proteins, and cDNA sequences, which can
CC be used in vaccines. The polynucleotide sequences can be used in gene
CC therapy. The polynucleotide sequences and the proteins they encode may be
CC used in the prevention, treatment and diagnosis of diseases associated
CC with inappropriate secretory protein/membrane protein expression. The
CC nucleic acids and complementary sequences may also be used as DNA probes
```

CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
CC and quantitate the presence of similar nucleic acid sequences in samples.
CC They may also be used to study the expression and function of secretory
CC proteins/membrane polypeptides and their role in metabolism. The
CC polypeptides may be used as antigens in the production of antibodies
CC against them and in assays to identify modulators (agonists and
CC antagonists) of expression and activity. The antibodies and antagonists
CC may also be used as therapeutic agents to down regulate expression and
CC activity. The antibodies may also be used as diagnostic agents for
CC detecting the presence of the polypeptides in samples (e.g. by enzyme
CC linked immunosorbent assay (ELISA). Examples of diseases which may be
CC treated include rheumatoid arthritis and diabetes

XX Sequence 230 AA;

Query Match 100.0%; Score 230; DB 4; Length 230;

Best Local Similarity 100.0%; Pred. No. 3.9e-210; Mismatches 0; Gaps 0;

Matches 230; Conservative 0; Indels 0; Gaps 0;

QY 1 MASLGLQVGYIIGLGLGLTVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60
DB 1 MASLGLQVGYIIGLGLGLTVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60
QY 61 ITCCDIYSTLLGLPADIOAAQAMWVTSASISLACIISVGMKCTVFCQESRAKDRVAVA 120
DB 61 ITCCDIYSTLLGLPADIOAAQAMWVTSASISLACIISVGMKCTVFCQESRAKDRVAVA 120
QY 121 GGVFFILGLGLGIPVAMNHLGILRDYSPVLDPSMKFEIGELALYIGIISLSFLIAGII 180
DB 121 GGVFFILGLGLGIPVAMNHLGILRDYSPVLDPSMKFEIGELALYIGIISLSFLIAGII 180
QY 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPPGQPPVKSEFNSYSLTGYV 230
DB 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPPGQPPVKSEFNSYSLTGYV 230

RESULT 10
ABP67991

ID ABP67991 standard; protein; 230 AA.

XX ABP67991;

XX 13-DEC-2002 (first entry)

XX Human colon cancer related polypeptide SEQ ID NO 2590.

XX Human; colon; cancer; cytostatic; tumour; gene therapy; vaccine.

XX Homo sapiens.

XX WO200258534-A2.

XX 01-AUG-2002.

XX 16-NOV-2001; 2001WO-US043704.

XX 20-NOV-2000; 2000US-0252222P.

XX 06-FEB-2001; 2001US-0267011P.

XX 28-MAR-2001; 2001US-0279670P.

XX 10-JUL-2001; 2001US-0304037P.

XX (CORI-) CORIXA CORP.

XX Stolk JA, Xu J, Chenault RA, Meagher MJ, Secretist H, King GE;

XX WPI; 2002-608400/65.

XX N-PSDB; ABV89278.

XX New isolated tumor colon polynucleotide and polypeptide, useful for the
XX diagnosis, prevention and/or treatment of cancer, in particular colon
XX cancer.

XX Claim 2; SEQ ID NO 2590; 266pp + Sequence Listing; English.

XX The invention relates to a human colon tumour expressed polynucleotide
CC (I) encoding a polypeptide (II, ABP67991-ABP67996) comprising: (i) any of
CC 2600 fully defined nucleotide sequences (ABV8669-ABV89289); (ii)
CC complements of (i); (iii) at least 20 contiguous residues of (i); (iv)
CC sequences that hybridize to (i), under moderately stringent conditions;
CC (v) sequences having at least 75% or 90% identity to (i); or (vi)
CC degenerate variants of (i). The compositions and methods of the present
CC invention are useful for the diagnosis, prevention and/or treatment of
CC cancer, particularly colon cancer. (i) can be used in gene therapy and
CC (i) and (ii) are useful in pharmaceutical compositions such as vaccines.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 230 AA;

Query Match 100.0%; Score 230; DB 5; Length 230;

Best Local Similarity 100.0%; Pred. No. 3.9e-210; Mismatches 0; Gaps 0;

Matches 230; Conservative 0; Indels 0; Gaps 0;

QY 1 MASLGLQVGYIIGLGLGLTVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60
DB 1 MASLGLQVGYIIGLGLGLTVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60
QY 61 ITCCDIYSTLLGLPADIOAAQAMWVTSASISLACIISVGMKCTVFCQESRAKDRVAVA 120
DB 61 ITCCDIYSTLLGLPADIOAAQAMWVTSASISLACIISVGMKCTVFCQESRAKDRVAVA 120
QY 121 GGVFFILGLGLGIPVAMNHLGILRDYSPVLDPSMKFEIGELALYIGIISLSFLIAGII 180
DB 121 GGVFFILGLGLGIPVAMNHLGILRDYSPVLDPSMKFEIGELALYIGIISLSFLIAGII 180
QY 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPPGQPPVKSEFNSYSLTGYV 230
DB 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPPGQPPVKSEFNSYSLTGYV 230

RESULT 11
ABG95890

ID ABG95890 standard; protein; 230 AA.

XX ABG95890;

XX 10-DEC-2002 (first entry)

XX Human secreted/transmembrane protein PRO1356.

XX Human; secreted protein; transmembrane protein; anti-rheumatic;

XX antiarthritic; osteopathic; sports-related joint problem;

XX articular cartilage defect; osteoarthritis; rheumatoid arthritis.

XX Homo sapiens.

XX US2002119130-A1.

XX 29-AUG-2002.

XX 06-DEC-2001; 2001US-00006867.

XX 29-OCT-1997; 97US-0063435P.

XX 29-OCT-1997; 97US-0064215P.

XX 29-APR-1998; 98US-0082797P.

XX 29-APR-1998; 98US-0083495P.

XX 15-MAY-1998; 98US-0085799P.

XX 02-JUN-1998; 98US-0087759P.

XX 04-JUN-1998; 98US-0088021P.

XX 04-JUN-1998; 98US-0088029P.

XX 04-JUN-1998; 98US-0088030P.

XX 10-JUN-1998; 98US-0088734P.

XX 10-JUN-1998; 98US-0088740P.

XX 10-JUN-1998; 98US-0088811P.

XX 10-JUN-1998; 98US-0088824P.

PR 10-JUN-1998; 98US-0088825P.
 PR 11-JUN-1998; 98US-0088863P.
 PR 12-JUN-1998; 98US-0089105P.
 PR 16-JUN-1998; 98US-0089514P.
 PR 17-JUN-1998; 98US-0089532P.
 PR 19-JUN-1998; 98US-0089552P.
 PR 22-JUN-1998; 98US-0090246P.
 PR 24-JUN-1998; 98US-0090444P.
 PR 25-JUN-1998; 98US-0090688P.
 PR 25-JUN-1998; 98US-0090696P.
 PR 26-JUN-1998; 98US-0090862P.
 PR 02-JUL-1998; 98US-0091628P.
 PR 10-AUG-1998; 98US-0096012P.
 PR 17-AUG-1998; 98US-0096757P.
 PR 18-AUG-1998; 98US-0096949P.
 PR 18-AUG-1998; 98US-0096959P.
 PR 26-AUG-1998; 98US-0097954P.
 PR 26-AUG-1998; 98US-0097971P.
 PR 26-AUG-1998; 98US-0097979P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 10-SEP-1998; 98US-0099741P.
 PR 10-SEP-1998; 98US-0099763P.
 PR 10-SEP-1998; 98US-0099792P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98US-0099815P.
 PR 16-SEP-1998; 98US-0100627P.
 PR 16-SEP-1998; 98US-0100652P.
 PR 16-SEP-1998; 98US-0100653P.
 PR 17-SEP-1998; 98US-0100683P.
 PR 17-SEP-1998; 98US-0100684P.
 PR 17-SEP-1998; 98US-0100930P.
 PR 22-SEP-1998; 98US-0101279P.
 PR 23-SEP-1998; 98US-0101475P.
 PR 24-SEP-1998; 98US-0101738P.
 PR 24-SEP-1998; 98US-0101743P.
 PR 30-SEP-1998; 98US-0101916P.
 PR 30-SEP-1998; 98US-0102570P.
 PR 06-OCT-1998; 98US-0103449P.
 PR 08-MAR-1999; 98US-0103502P.
 PR 14-MAY-1999; 98US-0103733P.
 PR 02-JUN-1999; 98US-0103733P.
 PR 01-SEP-1999; 99US-0103733P.
 PR 15-SEP-1999; 99US-0103733P.
 PR 15-SEP-1999; 99US-0103733P.
 PR 22-DEC-1999; 99US-0103733P.
 PR 18-FEB-2000; 2000US-0103733P.
 PR 18-FEB-2000; 2000US-0103733P.
 PR 22-FEB-2000; 2000US-0103733P.
 PR 01-MAR-2000; 2000US-0103733P.
 PR 30-MAR-2000; 2000US-0103733P.
 PR 02-JUN-2000; 2000US-0103733P.
 PR 23-AUG-2000; 2000US-0103733P.
 PR 24-AUG-2000; 2000US-0103733P.
 PR 10-NOV-2000; 2000US-0103733P.
 PR 10-DEC-2000; 2000US-0103733P.
 PR 20-DEC-2000; 2000US-0103733P.
 PR 28-FEB-2001; 2001US-0103733P.
 PR 01-MAR-2001; 2001US-0103733P.
 PR 30-MAY-2001; 2001US-0103733P.
 PR 01-JUN-2001; 2001US-0103733P.
 PR 20-JUN-2001; 2001US-0103733P.
 PR 29-JUN-2001; 2001US-0103733P.
 PR 09-JUL-2001; 2001US-0103733P.
 PR XX
 PA (GERTH) GENENTECH INC.
 PI Baton DL, Filvaroff E, Gerltsen ME, Goddard A, Godowski PJ,
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI,
 XX WPI; 2002-731348/79.
 DR N-PSDB; ABS74417.
 XX

PT New isolated secreted and transmembrane PRO polypeptide useful for
 PT modulating biological activity of a cell, or for treating sports-related
 PT joint problems, osteoarthritis or rheumatoid arthritis.
 PR
 PR Claim 20; Fig 80; 399pp; English.
 PS
 XX The invention relates to an isolated secreted and transmembrane PRO
 CC polypeptide having 80 % sequence identity to a sequence appearing as
 CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
 CC extracellular domain of the proteins with their associated signal peptide
 CC or lacking its associated signal peptide. Also included are the nucleic
 CC acids encoding the proteins, vectors, host cells, fusion proteins and
 CC antibodies which specifically bind to the proteins. The proteins are
 CC useful for detecting a polypeptide designated as A, B, C or D in a sample
 CC suspected of containing an A, B, C or D polypeptide, by contacting the
 CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
 CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
 CC conjugate in the sample, where the formation of the conjugate is
 CC indicative of the presence of an A, B, C or D polypeptide in the sample,
 CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
 CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
 CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
 CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
 CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
 CC H or I polypeptide is labeled with a detectable label or is attached to a
 CC solid support. The proteins are useful for linking a bioactive molecule
 CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
 CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
 CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
 CC or I, or antibodies against them are useful for modulating a biological
 CC activity of a cell expressing a polypeptide designated as A, B, C or D or
 CC E, F, G, H, or I. The cell is killed. The proteins are useful for
 CC identifying agonists or antagonists, for the preparation of a medicament
 CC useful in the treatment of a condition which is responsive to the
 CC proteins, as molecular weight markers for protein electrophoresis
 CC purposes, and as therapeutic agents for treating sports-related joint
 CC problems, articular cartilage defects, osteoarthritis or rheumatoid
 CC arthritis. Nucleic acids encoding the proteins are useful as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of anti-sense RNA and DNA, for the preparation of the proteins, to
 CC generate transgenic or knockout animals which are useful in the
 CC development and screening of therapeutic useful reagents, for chromosome
 CC identification, and in gene therapy. The antibody is useful as a
 CC therapeutic agent, in a diagnostic assay and for affinity purification of
 CC the protein from recombinant cell culture natural sources. The present
 CC sequence represents a novel secreted or transmembrane protein of the
 CC invention
 CC XX
 SQ Sequence 230 AA;
 Query Match 100.0%; Score 230; DB 5; Length 230;
 Best Local Similarity 100.0%; Pred. No. 3,9e-210; Indels 0; Gaps 0;
 Matches 230; Conservative 0; Mismatches 0;
 QY 1 MASIGLQVGIYIIGLGLTLVAMLLPSKTSYVGAIVTAVGFSKGLMECATHTSG 60
 Db 1 MASIGLQVGIYIIGLGLTLVAMLLPSKTSYVGAIVTAVGFSKGLMECATHTSG 60
 QY 61 ITQCDIYVTLGLPADIOAAMVNTSSAIISSIACTIISVGMKCTYVQESRAKDRYVA 120
 Db 61 ITQCDIYVTLGLPADIOAAMVNTSSAIISSIACTIISVGMKCTYVQESRAKDRYVA 120
 QY 121 GGVFFILGILGIFPVAAMNHGILRPYSPLVVDMSKFEIGELALYGIITSLSLAGIT 180
 Db 121 GGVFFILGILGIFPVAAMNHGILRPYSPLVVDMSKFEIGELALYGIITSLSLAGIT 180
 QY 181 LCFSSCSQRNRSNYDYAQOPLATRSSPRPGQPKVKSFEFNSYSLTGYV 230
 Db 181 LCFSSCSQRNRSNYDYAQOPLATRSSPRPGQPKVKSFEFNSYSLTGYV 230
 RESULT 12
 AB884912

ID ABB84912 standard; protein; 230 AA.
XX
AC ABB84912;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO1356 protein sequence SEQ ID NO:192.
XX
KW Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;
KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping.
XX
OS Homo sapiens.
XX
PN NC020020690-A2.
XX
PD 03-JAN-2002.
XX
PF 20-JUN-2001; 2001MO-US019692.
XX
PR 23-JUN-2000; 2000US-0213637P.
XX
PR 20-JUL-2000; 2000US-0219556P.
XX
PR 25-JUL-2000; 2000US-0220624P.
XX
PR 25-JUL-2000; 2000US-0220664P.
XX
PR 28-JUL-2000; 2000MO-US020710.
XX
PR 02-AUG-2000; 2000US-0222695P.
XX
PR 17-AUG-2000; 2000US-00643657.
XX
PR 23-AUG-2000; 2000MO-US023322.
XX
PR 07-SEP-2000; 2000US-0230978P.
XX
PR 18-SEP-2000; 2000US-00664510.
XX
PR 18-SEP-2000; 2000US-00665350.
XX
PR 24-OCT-2000; 2000US-0242922P.
XX
PR 08-NOV-2000; 2000US-00709238.
XX
PR 08-NOV-2000; 2000MO-US030952.
XX
PR 10-NOV-2000; 2000MO-US030873.
XX
PR 01-DEC-2000; 2000MO-US032578.
XX
PR 20-DEC-2000; 2000US-00747259.
XX
PR 20-DEC-2000; 2000MO-US034556.
XX
PR 22-JAN-2001; 2001US-00767609.
XX
PR 28-FEB-2001; 2001US-00796498.
XX
PR 28-FEB-2001; 2001MO-US006520.
XX
PR 01-MAR-2001; 2001MO-US006666.
XX
PR 09-MAR-2001; 2001US-00802706.
XX
PR 14-MAR-2001; 2001US-00808689.
XX
PR 22-MAR-2001; 2001US-00816744.
XX
PR 05-APR-2001; 2001US-00828366.
XX
PR 10-MAY-2001; 2001US-00854208.
XX
PR 25-MAY-2001; 2001US-00866034.
XX
PR 25-MAY-2001; 2001US-00866034.
XX
PR 30-MAY-2001; 2001MO-US017092.
XX
PR 30-MAY-2001; 2001US-00870574.
XX
PR 30-MAY-2001; 2001MO-US017443.
XX
PR 01-JUN-2001; 2001MO-US017800.
XX
PA (GETH) GENENTECH INC.
XX
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
XX Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
XX WPI; 2002-090516/12.
XX N-PSDB; ABL8167.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.

XX
PS Claim 11; Fig 192; 565bp; English.
XX
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiac, cytosolic,
CC antiangiogenic, hypotensive, vulnery and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The PRO polynucleotides have applications in molecular biology,
CC including use as hybridisation probes, and in chromosome and gene
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC exemplification of the present invention
XX
SQ Sequence 230 AA;
XX
Query Match 100.0%; Score 230; DB 5; Length 230;
Best Local Similarity 100.0%; Pred. No. 3.9e-210;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASLGQLVGYITGLGLGLTVMALLPSWKTSYVGAIVTVAVGSKLMECAHSTG 60
DB 1 MASLGQLVGYITGLGLGLTVMALLPSWKTSYVGAIVTVAVGSKLMECAHSTG 60
QY 61 ITQCDIYSTLLGLPADIOAAMMTSSAISLACIISVGNRCYFCQESRAKDRVANA 120
DB 61 ITQCDIYSTLLGLPADIOAAMMTSSAISLACIISVGNRCYFCQESRAKDRVANA 120
QY 121 GGVFFILGILGRIPIVAMNHLGIARDYSPVLPVDSMKFEIGALYGIISLPSLIAGII 180
DB 121 GGVFFILGILGRIPIVAMNHLGIARDYSPVLPVDSMKFEIGALYGIISLPSLIAGII 180
QY 181 LCFSCSSQRRNSRYDYOQAPLATSSPRPQPPVKSEFNSYSLTGYV 230
DB 181 LCFSCSSQRRNSRYDYOQAPLATSSPRPQPPVKSEFNSYSLTGYV 230
RESULT 13
AAU76534 standard; protein; 230 AA.
XX
XX AAU76534;
XX
DT 05-JUN-2002 (first entry)
XX
DE Tumour-associated antigenic target protein, TAT134.
XX
KW TAT134; Tumour-associated Antigenic Target; tumour; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer;
KW central nervous system cancer; liver cancer; bladder cancer; melanoma;
KW pancreatic cancer; leukaemia; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..24
FT Region 4..181
FT Modified-site /note="BMP-32/EMP/MP20/Claudin family (not defined)"
FT Modified-site /note="N-myristoylation site"
FT Modified-site /note="N-myristoylation site"
FT Protein /note="N-myristoylation site"
FT Protein /note="Mature TAT134"
FT Modified-site /note="N-myristoylation site"
FT Domain /note="82..102
/note="Transmembrane domain"

FT Modified-site 101..106
FT /note= "N-myristoylation site"
FT Domain 120..140
FT /note= "Transmembrane domain"
FT Modified-site 128..133
FT /note= "N-myristoylation site"
FT Domain 160..180
FT /note= "Transmembrane domain"
FT Modified-site 167..172
FT /note= "N-myristoylation site"
FT Modified-site 178..183
FT /note= "N-myristoylation site"
FT Modified-site 190..193
FT /note= "Aen is N-glycosylated"
FT Modified-site 216..224
FT /note= "Tyrosine kinase phosphorylation site"
PN WO200216429-A2.
PD 28-FEB-2002.
XX 22-JUN-2001; 2001WO-US020118.
XX 24-AUG-2000; 2000WO-US023328.
XX 26-SEP-2000; 2000US-0235451P.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
XX (GETH) GENENTECH INC.
XX Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Polakis P, Smith V;
PI Wood WI, Wu TD, Zhang Z;
XX WPI; 2002-280917/32.
DR N-PSDB; ABK11089.
XX
PT Novel isolated tumor-associated antigenic target polypeptides which are
PT useful as targets for cancer therapy and diagnosis in mammals.
XX
PS Claim 12; Fig 6; 121pp; English.
XX
XX The invention relates to an isolated tumour-associated antigenic target
CC polypeptide (TAT) (I), specifically TAT134-TAT138 polypeptides, and the
CC polynucleotides (II) encoding them. (II) is useful for diagnosing the
CC presence of a tumour in a mammal, where the level of expression of (II)
CC is indicative on the presence of tumour in the mammal from which the test
CC sample was obtained. Antibody to (I) is useful for killing a cancer cell
CC (e.g. breast cancer cell, a colorectal cancer cell, a lung cancer cell,
CC an ovarian cancer cell, a central nervous system (CNS) cancer cell, a
CC liver cancer cell, a bladder cancer cell, a pancreatic cancer cell, a
CC melanoma cell or a leukaemia cell) that expresses (I). Oligonucleotides
CC hybridising to (II) are useful as diagnostic probes, antisense
CC oligonucleotide probes or for encoding fragments of full length TAT
CC polypeptide. (II) is also useful in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA probes, for constructing
CC hybridisation probes for mapping the gene encoding TAT and for genetic
CC analysis of individuals with genetic disorders. (II) is also useful for
CC generating either transgenic animals or knockout animals, and in gene
CC therapy. The TAT polypeptides and nucleic acids may also be used for
CC tissue typing and the TAT polypeptides are useful for screening compounds
CC that mimic the TAT polypeptide (agonist) or prevent the effect of TAT
CC polypeptide (antagonist). The antibody is useful for staging TAT
CC polypeptide-expressing cancers, purifying or immunoprecipitating TAT
CC polypeptide from cells, for detection and quantitation of TAT polypeptide
CC in vitro, e.g., in an enzyme linked immunosorbent assay (ELISA) or
CC Western blot. The antibodies are also useful for treating a TAT-
CC expressing cancer or alleviating one or more symptoms of cancer in a
CC mammal. The present sequence represents the amino acid sequence of TAT134
XX
SQ Sequence 230 AA;
Query Match 100.0%; Score 230; DB 5; Length 230;

Best Local Similarity 100.0%; Pred. No. 3.9e-210;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASIGOLVGYITLGLGLGLTLVAMLLPSWKTSYVGASIVTAVGSKGLMECAHTSTG 60
D 1 MASIGOLVGYITLGLGLGLTLVAMLLPSWKTSYVGASIVTAVGSKGLMECAHTSTG 60
QY 61 ITDCDITSTLLGLPADIOAAQAMWVTSASISLACIIISVGMKCTVFCESRAKDRVAVA 120
D 61 ITDCDITSTLLGLPADIOAAQAMWVTSASISLACIIISVGMKCTVFCESRAKDRVAVA 120
QY 121 GGVPFLIGLGLGPIPVAMNHLGLRDPYSPVVDNSKPFRIGEALYIGITISLPSLLAGII 180
D 121 GGVPFLIGLGLGPIPVAMNHLGLRDPYSPVVDNSKPFRIGEALYIGITISLPSLLAGII 180
QY 181 LCFSCSSQRNRSMNYDAYOQOPLATRSSPPGQPPVKSEFNSYSLTGYV 230
D 181 LCFSCSSQRNRSMNYDAYOQOPLATRSSPPGQPPVKSEFNSYSLTGYV 230
RESULT 14
ID ABG64507 standard; protein; 230 AA.
XX
XX ABG64507;
AC
XX 27-AUG-2002 (first entry)
DT
XX
DE Human albumin fusion protein #1182.
XX
XX Albumin fusion protein; therapeutic protein X; human albumin; HA;
KW human serum albumin; HSA; cancer; reproductive disorder;
KW digestive disorder; immune disorder; endocrine disorder;
KW hematopoietic disorder; neural disorder; connective disorder;
KW cytoskeletal; antiinfectility; antiinflammatory; anticler;
KW immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
KW osteopathic; anticharctic.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200177137-A1.
XX
XX 18-OCT-2001.
PD
XX 12-APR-2001; 2001WO-US011988.
PF
XX 12-APR-2000; 2000US-0229358P.
PR 25-APR-2000; 2000US-0199384P.
PR 21-DEC-2000; 2000US-0256931P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Haseltine WA;
XX WPI; 2002-010886/01.
DR
XX New fusion protein for treating disease e.g. diabetes comprises an
PT albumin fused to a therapeutic protein.
XX
PS Claim 1; Page 1277-1278; 2102pp; English.
XX
XX The present invention relates to albumin fusion proteins comprising a
CC therapeutic protein X and human albumin (HA), also known as human serum
CC albumin, HSA). The proteins are useful for treating a disease or disorder
CC that may be modulated by therapeutic protein X. The albumin extends the
CC shelf-life of protein X, and may increase its biological in vitro/in vivo
CC activity. The protein is useful for treating and diagnosing disorders
CC such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's
CC disease, ulcerative colitis), immune disorders (e.g. acquired
CC immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),
CC hematopoietic disorders, neural disorders (e.g. Alzheimer's,

CC Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,
CC Schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).
CC ABG63326-ABG65518 represent albumin fusion proteins of the invention
XX
SQ Sequence 230 AA:

Query Match 100.0%; Score 230; DB 5; Length 230;
Best Local Similarity 100.0%; Pred. No. 3.9e-210;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYIIGLGLGLTLVAMLLPSMKTSSYVGSIVTAVGFSKGLMECATHTSTG 60
DB 1 MASLGQLVGYIIGLGLGLTLVAMLLPSMKTSSYVGSIVTAVGFSKGLMECATHTSTG 60
QY 61 ITQCDIYSTLLGLPADIQAAQAMMTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120
DB 61 ITQCDIYSTLLGLPADIQAAQAMMTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120
QY 121 GGVFFILGGLGFI PVAMNHLGILRDFSPPLVPDSMKFEIGALYIGIISLPSLIAGII 180
DB 121 GGVFFILGGLGFI PVAMNHLGILRDFSPPLVPDSMKFEIGALYIGIISLPSLIAGII 180
QY 181 LCFSSCSQRNRSNYDAYQAOPLATRSSPRPGQPPKVKSEFNSYSLTGYV 230
DB 181 LCFSSCSQRNRSNYDAYQAOPLATRSSPRPGQPPKVKSEFNSYSLTGYV 230

RESULT 15

ABB04707
ID ABB04707 standard; protein: 230 AA.

AC ABB04707;

DT 11-MAR-2002 (first entry)

DE Human SP82 protein SEQ ID NO:2.

XX Human, SP82; cancer suppression.

OS Homo sapiens.

XX CN1313315-A.

PD 19-SEP-2001.

PF 13-MAR-2000; 2000CN-00111989.

PR 13-MAR-2000; 2000CN-00111989.

PA (SHAN-) SHANGHAI INST ONCOLOGY.

PI Gu J, Yang S;

DR WPI; 2002-042191/06.

DR N-PSDB; ABA04424.

XX New human protein able to suppress growth of cancer cells and its
XX encoding polynucleotide sequence.

PS Claim 1; Page 12 (Disclosure); 42pp; Chinese.

CC The present sequence represents human SP82 protein, which has cancer-
CC suppressing activity. The present invention also describes a method for
CC the preparation of the protein by recombination, and the application of
CC the protein in treating diseases such as cancer

XX

SQ Sequence 230 AA;

Query Match 100.0%; Score 230; DB 5; Length 230;
Best Local Similarity 100.0%; Pred. No. 3.9e-210;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYIIGLGLGLTLVAMLLPSMKTSSYVGSIVTAVGFSKGLMECATHTSTG 60

DB 1 MASLGQLVGYIIGLGLGLTLVAMLLPSMKTSSYVGSIVTAVGFSKGLMECATHTSTG 60
QY 61 ITQCDIYSTLLGLPADIQAAQAMMTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120
DB 61 ITQCDIYSTLLGLPADIQAAQAMMTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120
QY 121 GGVFFILGGLGFI PVAMNHLGILRDFSPPLVPDSMKFEIGALYIGIISLPSLIAGII 180
DB 121 GGVFFILGGLGFI PVAMNHLGILRDFSPPLVPDSMKFEIGALYIGIISLPSLIAGII 180
QY 181 LCFSSCSQRNRSNYDAYQAOPLATRSSPRPGQPPKVKSEFNSYSLTGYV 230
DB 181 LCFSSCSQRNRSNYDAYQAOPLATRSSPRPGQPPKVKSEFNSYSLTGYV 230

Search completed: October 27, 2004, 07:35:43
Job time : 156 secs

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OM protein - protein search, using sw model

Run on: October 27, 2004, 07:30:58 ; Search time 41 Seconds
(without alignments)
372.028 Million cell updates/sec

Title: US-09-787-677a-3

Perfect score: 230

Sequence: 1 MASLGLQVGVYILGLGLTGLG.....PGQPPKVKSEFNSYSLTGYV 230

Scoring table: OLIGO

Searched: 478139 seqs, 66318000 residues

Word size: 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	230	100.0	230	US-09-663-600A-186	Sequence 186, App
2	230	100.0	230	US-10-140-002-492	Sequence 492, App
3	127	55.2	230	US-09-663-600A-92	Sequence 92, App
4	38	16.5	42	US-09-282-029A-7	Sequence 7, Appli
5	38	16.5	42	US-09-185-908-7	Sequence 7, Appli
6	9	3.9	208	US-09-252-991A-22641	Sequence 22641, A
7	8	3.5	31	US-08-525-539A-34	Sequence 34, Appli
8	8	3.5	58	US-09-275-252A-32	Sequence 32, Appli
9	8	3.5	138	US-09-252-991A-16828	Sequence 16828, A
10	8	3.5	335	US-09-248-796A-17661	Sequence 17661, A
11	8	3.5	341	US-09-190-965-3	Sequence 3, Appli
12	8	3.5	341	US-09-470-253-3	Sequence 3, Appli
13	8	3.5	487	US-09-252-991A-28079	Sequence 28079, A
14	8	3.5	673	US-09-091-725-13	Sequence 13, Appli
15	8	3.5	673	US-09-091-725-19	Sequence 19, Appli
16	8	3.5	673	US-09-091-725-23	Sequence 23, Appli
17	8	3.5	1196	US-09-275-252A-9	Sequence 9, Appli
18	8	3.5	4550	US-08-804-227C-8	Sequence 8, Appli
19	8	3.5	4550	US-08-804-158-2	Sequence 2, Appli
20	7	3.0	8	US-09-282-029A-131	Sequence 131, App
21	7	3.0	8	US-09-185-908-131	Sequence 131, App
22	7	3.0	30	US-09-282-029A-473	Sequence 473, App
23	7	3.0	31	US-08-525-539A-32	Sequence 32, Appli
24	7	3.0	37	US-08-789-333F-16	Sequence 16, Appli
25	7	3.0	37	US-09-133-944-16	Sequence 16, Appli
26	7	3.0	37	US-09-208-827-17	Sequence 17, Appli
27	7	3.0	37	US-08-787-738B-16	Sequence 16, Appli

28	7	3.0	37	4	US-09-157-748-19	Sequence 19, Appli
29	7	3.0	37	4	US-09-800-170-69	Sequence 69, Appli
30	7	3.0	37	4	US-10-043-074-17	Sequence 17, Appli
31	7	3.0	37	4	US-09-285-912A-79	Sequence 79, Appli
32	7	3.0	37	4	US-09-578-030-20	Sequence 20, Appli
33	7	3.0	37	4	US-09-916-940-16	Sequence 16, Appli
34	7	3.0	42	1	US-08-004-492-4	Sequence 4, Appli
35	7	3.0	42	1	US-08-004-492-7	Sequence 7, Appli
36	7	3.0	67	4	US-09-543-681A-7721	Sequence 7721, Ap
37	7	3.0	93	4	US-09-489-039A-7356	Sequence 7356, Ap
38	7	3.0	93	4	US-09-489-039A-11691	Sequence 11691, A
39	7	3.0	97	4	US-09-519-878-6	Sequence 6, Appli
40	7	3.0	102	1	US-08-282-951-2	Sequence 2, Appli
41	7	3.0	105	4	US-09-107-532A-5500	Sequence 5500, Ap
42	7	3.0	110	1	US-08-017-570-2	Sequence 2, Appli
43	7	3.0	110	1	US-08-471-426-2	Sequence 2, Appli
44	7	3.0	110	3	US-09-672-609-13	Sequence 13, Appli
45	7	3.0	110	4	US-09-025-403A-13	Sequence 13, Appli

ALIGNMENTS

```
RESULT 1
US-09-663-600A-186
; Sequence 186, Application US/09663600A
; Patent No. 6573068
;
GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Bouguerelet, Lydie
; TITLE OF INVENTION: EXTENDED CNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31. US3. CIP
; CURRENT APPLICATION NUMBER: US/09/663, 600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191, 997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066, 677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069, 957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074, 121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081, 563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096, 116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099, 273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 186
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -24...-1
; US-09-663-600A-186
;
Query Match 100.0%; Score 230; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 9.7e-208;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASLGLQVGVYILGLGLTGLVAMLPKWTSSYVGASITVAVGRSKGLMECAHSTG 60
Db 1 MASLGLQVGVYILGLGLTGLVAMLPKWTSSYVGASITVAVGRSKGLMECAHSTG 60
QY 61 ITCCDIYSTLLGLPADIQAAMMTSSAISLACTISVGMKCTVFCOSSRAKDRVAVA 120
Db 61 ITCCDIYSTLLGLPADIQAAMMTSSAISLACTISVGMKCTVFCOSSRAKDRVAVA 120
QY 121 GGVFFILGLGLGPIPAVMNLHGILRDFYSPPLVDSMKFEIGALYIGIISLPSLIAGII 180
```

Db 121 GGVEFIIIGLGLFIPVAMNHLGILRDFYSPVPDSKMEKEIGEAALYIIISLFSLLIIGII 180
QY 181 LCFSCSSQRNRNSNYDAYOAOPLATRSSPRPGOPPKYSEFNYSILGYV 230
Db 181 LCFSCSSQRNRNSNYDAYOAOPLATRSSPRPGOPPKYSEFNYSILGYV 230

RESULT 2

US-10-140-002-492
Sequence 492, Application US/10140002
Patent No. 6725730
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvarioff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS
FILE REFERENCE: P33081C59
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 492
LENGTH: 230
TYPE: PRT
ORGANISM: Homo sapien
US-10-140-002-492

Query Match 100.0%; Score 230; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 9.7e-208;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASIGLOLVGYIILGLIGLGLTVAMLLPSWKTSSYVGAIVTAVGFSKGLMECATHTSG 60
Db 1 MASIGLOLVGYIILGLIGLGLTVAMLLPSWKTSSYVGAIVTAVGFSKGLMECATHTSG 60
QY 61 ITGCDIYSTLLGLPADIOAQAAMWVTSSAISLACIISVVMRCCTVFCOESRAKORVAVA 120
Db 61 ITGCDIYSTLLGLPADIOAQAAMWVTSSAISLACIISVVMRCCTVFCOESRAKORVAVA 120
QY 121 GGVEFIIIGLGLFIPVAMNHLGILRDFYSPVPDSKMEKEIGEAALYIIISLFSLLIIGII 180
Db 121 GGVEFIIIGLGLFIPVAMNHLGILRDFYSPVPDSKMEKEIGEAALYIIISLFSLLIIGII 180
QY 181 LCFSCSSQRNRNSNYDAYOAOPLATRSSPRPGOPPKYSEFNYSILGYV 230
Db 181 LCFSCSSQRNRNSNYDAYOAOPLATRSSPRPGOPPKYSEFNYSILGYV 230

RESULT 3

US-09-663-600A-92
Sequence 92, Application US/09663600A
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bouguetieret, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS

FILE REFERENCE: 31.US3.CIP
CURRENT APPLICATION NUMBER: US/09/663,600A
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 92
LENGTH: 230
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -24..-1
NAME/KEY: UNSURE
LOCATION: 54,79
OTHER INFORMATION: Xaa = any one of the twenty amino acids
US-09-663-600A-92

Query Match 55.2%; Score 127; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 3.7e-111;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 CTYFCOESRAKORVAVAGVFPIIGLGRIPVAMNHLGILRDFYSPVPDSKMEKEIGEA 163
Db 104 CTYFCOESRAKORVAVAGVFPIIGLGRIPVAMNHLGILRDFYSPVPDSKMEKEIGEA 163
QY 164 LVYGIISLFSLLIIGLGLFIPVAMNHLGILRDFYSPVPDSKMEKEIGEA 223
Db 164 LVYGIISLFSLLIIGLGLFIPVAMNHLGILRDFYSPVPDSKMEKEIGEA 223
QY 224 YSLTGYV 230
Db 224 YSLTGYV 230

RESULT 4

US-09-282-029A-7
Sequence 7, Application US/09282029A
Patent No. 6723700
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gout, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
FILE REFERENCE: 100086,409C1
CURRENT APPLICATION NUMBER: US/09/282,029A
CURRENT FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 460
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 42
TYPE: PRT
ORGANISM: Mus musculus
US-09-282-029A-7

Query Match 16.5%; Score 38; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.1e-28;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 TSSYVGAIVTAVGFSKGLMECATHTSGITGCDIYST 69

Db 5 TSSYVGSIVTAVGFSKGLMECATSTGTTCDDYST 42

RESULT 5
US-09-185-908-7
Sequence 7, Application US/09185908A
Patent No. 6756356
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gaur, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
FILE REFERENCE: 100086.409
CURRENT APPLICATION NUMBER: US/09/185.908A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 269
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 42
TYPE: PRT
ORGANISM: Mus musculus
US-09-185-908-7

Query Match 16.5%; Score 38; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.1e-28;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 TSSYVGSIVTAVGFSKGLMECATSTGTTCDDYST 69
Db 5 TSSYVGSIVTAVGFSKGLMECATSTGTTCDDYST 42

RESULT 6
US-09-252-991A-22641
Sequence 22641, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22641
LENGTH: 208
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22641

Query Match 3.9%; Score 9; DB 4; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 204 ATRSSPPG 212
Db 20 ATRSSPPG 28

RESULT 7
US-08-525-539A-34
Sequence 34, Application US/08525539A
Patent No. 6309636
GENERAL INFORMATION:
APPLICANT: DO COUTO, FERNANDO J.R.
APPLICANT: CERIANI, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE

TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FORSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525.539A
FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 27633-20001.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELE: 706141
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-525-539A-34

Query Match 3.5%; Score 8; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 GTIVAMLL 27
Db 17 GTIVAMLL 24

RESULT 8
US-09-275-252A-32
Sequence 32, Application US/09275252A
Patent No. 6641997
GENERAL INFORMATION:
APPLICANT: The Rockefeller University
TITLE OF INVENTION: Assays for Screening Compounds which Interact with
TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
FILE REFERENCE: 018512-002901US
CURRENT APPLICATION NUMBER: US/09/275.252A
CURRENT FILING DATE: 1999-03-24
PRIOR APPLICATION NUMBER: US 09/045,529
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: US 09/054,347
PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: WO PCT/US99/06307
PRIOR FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 32
LENGTH: 58
TYPE: PRT
ORGANISM: Mus musculus
US-09-275-252A-32

Query Match 3.5%; Score 8; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 3.9;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 123 VFPIIGSL 130
|||
Db 33 VFPIIGSL 40

RESULT 9
US-09-252-991A-16828
; Sequence 16828, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16828
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16828

Query Match
Best Local Similarity 100.0%; Score 8; DB 4; Length 138;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 ILGLPADI 77
|||
Db 73 ILGLPADI 80

RESULT 10
US-09-248-796A-17661
; Sequence 17661, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248.796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17661
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (33)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
US-09-248-796A-17661

Query Match
Best Local Similarity 100.0%; Score 8; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 PLATRSSP 209
|||
Db 38 PLATRSSP 45

RESULT 11
US-09-190-965-3
; Sequence 3, Application US/09190965
; Patent No. 6071721
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Gorgone, Gina A.
; TITLE OF INVENTION: CALCIUM BINDING PROTEIN
; FILE REFERENCE: PF-0635 US
; CURRENT APPLICATION NUMBER: US/09/190,965
; CURRENT FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: g262934
US-09-190-965-3

Query Match
Best Local Similarity 100.0%; Score 8; DB 3; Length 341;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GLGLTLVA 24
|||
Db 78 GLGLTLVA 85

RESULT 12
US-09-470-253-3
; Sequence 3, Application US/09470253
; Patent No. 6365371
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Gorgone, Gina A.
; TITLE OF INVENTION: CALCIUM BINDING PROTEIN
; FILE REFERENCE: PF-0635 US
; CURRENT APPLICATION NUMBER: US/09/470,253
; CURRENT FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 09/190,965
; PRIOR FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: g262934
US-09-470-253-3

Query Match
Best Local Similarity 100.0%; Score 8; DB 3; Length 341;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GLGLTLVA 24
|||
Db 78 GLGLTLVA 85

RESULT 13
US-09-252-991A-28079
; Sequence 28079, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 31142
SEQ ID NO 28079
LENGTH: 487
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28079

Query Match 3.5%; Score 8; DB 4; Length 487;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 ILGLGL 82
DB 294 ADIQAQA 301

RESULT 14
US-09-091-725-13
Sequence 13, Application US/09091725
Patent No. 6329141
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Improved methods for transforming Phaffia
TITLE OF INVENTION: and recombinant DNA for use therein
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 2000 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: United States of America
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,725
FILING DATE: 23-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95203620.0
FILING DATE: 22-DEC-1995
APPLICATION NUMBER: EP 96200943.7
FILING DATE: 11-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: E. Victor Donahue
REGISTRATION NUMBER: 35,492
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-091-725-13

Query Match 3.5%; Score 8; DB 3; Length 673;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ILGLGL 19
DB 17 ILGLGL 24

RESULT 15
US-09-091-725-19
Sequence 19, Application US/09091725
Patent No. 6329141
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Improved methods for transforming Phaffia
TITLE OF INVENTION: and recombinant DNA for use therein
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 2000 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: United States of America
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,725
FILING DATE: 23-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95203620.0
FILING DATE: 22-DEC-1995
APPLICATION NUMBER: EP 96200943.7
FILING DATE: 11-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: E. Victor Donahue
REGISTRATION NUMBER: 35,492
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-091-725-19

Query Match 3.5%; Score 8; DB 3; Length 673;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ILGLGL 19
DB 17 ILGLGL 24

Search completed: October 27, 2004, 07:40:35
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 27, 2004, 07:22:43 : Search time 38 Seconds
(without alignments)
582.365 Million cell updates/sec

Title: US-09-787-677A-3

Perfect score: 230
Sequence: 1 MASLGLVGYILGLGLG.....PGQPKVKSSENSYLTGVY 230

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: PIR 79: *
2: p1r1: *
3: p1r2: *
4: p1r3: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	3.9	123	2	C87698 conserved hypotet
2	8	3.5	29	2	AS3145 high conductance c
3	8	3.5	120	2	S21667 Ig kappa chain V r
4	8	3.5	120	2	S21666 Ig kappa chain V r
5	8	3.5	204	2	T45270 superoxide dismuta
6	8	3.5	215	2	AD0056 probable phosphogl
7	8	3.5	296	2	A70427 conserved hypotet
8	8	3.5	300	2	T32665 hypotetrical prote
9	8	3.5	323	2	B83215 conserved hypotet
10	8	3.5	341	2	I57997 hypotetrical calci
11	8	3.5	362	2	AG1962 hypotetrical prote
12	8	3.5	404	1	G70151 pheromone shutoff
13	8	3.5	556	2	S02154 NMDH2 dehydrogenas
14	8	3.5	609	2	I38586 calcium-activated
15	8	3.5	959	2	T25704 hypotetrical prote
16	8	3.5	1113	2	S62904 calcium-regulated
17	8	3.5	1184	2	I49017 calcium-activated
18	8	3.5	1196	2	A48206 calcium-activated
19	8	3.0	57	2	E35057 MHC class II histo
20	7	3.0	57	2	D35057 MHC class II histo
21	7	3.0	66	2	AH0823 conserved hypotet
22	7	3.0	66	2	F91052 hypotetrical prote
23	7	3.0	66	2	A84408 hypotetrical prote
24	7	3.0	66	2	B85897 hypotetrical prote
25	7	3.0	66	2	C65029 hypotetrical 7.7 k
26	7	3.0	68	2	S8739 protein YOLO77w-a
27	7	3.0	82	2	I37070 gene MHC DQ-beta 1
28	7	3.0	90	2	G42518 structural protein
29	7	3.0	90	2	F36849 A14L protein - var

30	7	3.0	90	2	T28556 hypotetrical prote
31	7	3.0	90	2	D72165 A15L protein - var
32	7	3.0	92	2	S37531 Ig kappa chain V r
33	7	3.0	94	2	A83523 hypotetrical prote
34	7	3.0	95	2	B81337 probable membrane
35	7	3.0	97	2	T34765 small hydrophobic
36	7	3.0	102	1	NRPLTB ribonuclease T1 (E
37	7	3.0	109	1	KVRB37 Ig kappa chain V r
38	7	3.0	111	1	KVM869 Ig kappa chain V r
39	7	3.0	113	2	S30520 Ig kappa chain V r
40	7	3.0	128	2	H72500 hypotetrical prote
41	7	3.0	132	2	S46373 Ig kappa chain V-J
42	7	3.0	160	1	S16918 plactocquinol-plast
43	7	3.0	177	2	G75285 hypotetrical prote
44	7	3.0	184	2	H84780 probable AP2 domai
45	7	3.0	184	2	A37041 homeotic protein A

ALIGNMENTS

RESULT 1
C87698 conserved hypotetrical protein CC3621 [imported] - Caulobacter crescentus
C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C/Accession: C87698
R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.I.
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gattm, M.L.; Hart, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of Caulobacter crescentus.
A/Reference number: A87249; PMID:21173698; PMID:11259647
A/Accession: C87698
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-123 <STO>
A/Cross-references: UNIPROT:Q9A2B4; GB:AE005673; NID:G13425371; PIDN:AAK25583.1; GSPDB:GT
C/Genetics:
A/Gene: CC3621

Query Match 3.9%; Score 9; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 VFPIIGGL 131
Db 27 VFPIIGGL 35

RESULT 2
A53145 high conductance calcium-activated potassium channel, maxi-K channel - bovine (fragment)
C/Species: Bos primigenius taurus (cattle)
C/Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A53145
R/Klaus, H.G.; Garcia-Calvo, M.; Kaczorowski, G.J.; Garcia, M.L.
J. Biol. Chem. 269, 3921-3924, 1994
A/Title: Subunit composition of the high conductance calcium-activated potassium channel
A/Reference number: A53145; PMID:9410798; PMID:7508434
A/Accession: A53145
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-29 <KNA>
A/Cross-references: UNIPROT:Q9TS86
A/Note: sequence extracted from NCBI backbone (NCBI:144545)
C/Superfamily: fruit fly calcium-activated potassium channel slo

Query Match 3.5%; Score 8; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 123 VFPIIGGL 130

Db 9 VFPIGLGL 16

RESULT 3

S21667
Ig kappa chain V region (23) - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C/Accession: S21667
R/Roeschenthaler, F.; Schaeble, K.F.; Thiebe, R.; Zachau, H.G.
Biol. Chem. Hoppe-Seyler 373, 177-186, 1992
A/Title: Of orphans and UHOs. Delimitation of the germline repertoire of human immunoglobulin
A/Reference number: S21666; MUID:92281681; PMID:1596359
A/Accession: S21667
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-120 <ROE>
A/Cross-references: EMBL:X64641
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/41-115/Domain: immunoglobulin homology <IMM>

Query Match 3.5%; Score 8; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 LGHLGLG 20
Db 10 LGHLGLG 17

RESULT 4

S21666
Ig kappa chain V region (22) - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C/Accession: S21666
R/Roeschenthaler, F.; Schaeble, K.F.; Thiebe, R.; Zachau, H.G.
Biol. Chem. Hoppe-Seyler 373, 177-186, 1992
A/Title: Of orphans and UHOs. Delimitation of the germline repertoire of human immunoglobulin
A/Reference number: S21666; MUID:92281681; PMID:1596359
A/Accession: S21666
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-120 <ROE>
A/Cross-references: EMBL:X64640; NID:9432649; PIDN:CAA45914.1; PID:G1335149
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/41-115/Domain: immunoglobulin homology <IMM>

Query Match 3.5%; Score 8; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 LGHLGLG 20
Db 10 LGHLGLG 17

RESULT 5

T45270
superoxide dismutase (EC 1.15.1.1) (Mn) [similarity] - Thermus aquaticus
N/Alternate names: manganese superoxide dismutase
C/Species: Thermus aquaticus
C/Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
C/Accession: T45270
R/Motoshima, H.; Minagawa, E.; Tsukaaki, F.; Kamilogawa, S.
J. Ferment. Bioeng. 86, 21-27, 1998
A/Title: Cloning and nucleotide sequencing of genes encoding Mn-superoxide dismutase and
A/Reference number: Z22952
A/Accession: T45270
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
A/Residues: 1-204 <MOT>
A/Cross-references: UNIPROT:P53653; EMBL:D84646; PIDN:BAA12703.1
A/Experimental source: strain YT-1
C/Superfamily: superoxide dismutase (Mn)
C/Keywords: manganese; metalloprotein; oxidoreductase
F/29,84,167,171/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 3.5%; Score 8; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 LPADIQAA 80
Db 66 LPADIQAA 73

RESULT 6

AD0056
probable phosphoglycerate mutase (EC 5.4.2.1) [imported] - Yersinia pestis (strain CO92)
C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 16-Aug-2004
C/Accession: AD0056
R/Parhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Terraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, T.
Nature 413, 523-527, 2001
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: AD0056
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-215 <RUR>
A/Cross-references: UNIPROT:Q82IP0; GB:AL590842; PIDN:CAC89311.1; PID:G15978547; GSPDB:GP
C/Genetics:
A/Genes: gpmB
C/Superfamily: Cofactor-dependent phosphoglycerate mutase; phosphoglycerate mutase homol
C/Keywords: Intramolecular transferase; isomerase

Query Match 3.5%; Score 8; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 STLGLGPA 75
Db 159 STLGLGPA 166

RESULT 7

A70427
conserved hypothetical protein aq_1462 - Aquifex aeolicus
C/Species: Aquifex aeolicus
C/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C/Accession: A70427
R/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
V.
Nature 392, 353-358, 1998
A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A/Reference number: A70300; MUID:98196666; PMID:9537320
A/Accession: A70427
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-296 <NOF>
A/Cross-references: UNIPROT:O67443; GB:AE000741; NID:G2983841; PIDN:AAC07409.1; PID:G298;
A/Experimental source: strain VFS
C/Genetics:
A/Genes: aq_1462
C/Superfamily: conserved hypothetical protein AF1561

Query Match 3.5%; Score 8; DB 2; Length 296;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 FILGHLG 132
 DB 84 FILGHLG 91

RESULT 8

T32665
 hypothetical protein Fl6B4.6 - *Caenorhabditis elegans*
 C/Species: *Caenorhabditis elegans*
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T32665
 R/Davidson, S.; Mohldmann, P.; Bauer, C.; O'Neal, D.
 Submitted to the EMBL Data Library, December 1997
 A/Description: The sequence of *C. elegans* cosmid Fl6B4.
 A/Reference number: Z21208
 A/Accession: T32665
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-300 <DNV>
 A/Cross-references: UNIPROT:O44628; EMBL:AF039048; PIDD:AA94237.1; GSPDB:GN00023; CESP:
 A/Experimental source: strain Bristol N2; clone Fl6B4
 C/Genetics:
 A/Gen: CESP:Fl6B4.6
 A/Map position: 5
 A/Intons: 49/1; 128/2; 186/3; 241/3

Query Match 3.5%; Score 8; DB 2; Length 300;
 Best Local Similarity 100.0%; Pred. No. 8.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 VTSSA1SS 92
 DB 178 VTSSA1SS 185

RESULT 9
 B83215
 conserved hypothetical protein PA3445 [imported] - *Pseudomonas aeruginosa* (strain PA01)
 C/Species: *Pseudomonas aeruginosa*
 C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C/Accession: B83215
 R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mitsuuchi, S.D.; Warren, P.; Hickey, M.J.; Br
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 .; Lox, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A/Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
 A/Reference number: A82950; MUID:20437337; PMID:10984043
 A/Accession: B83215
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-323 <STO>
 A/Cross-references: UNIPROT:Q8HYG1; GB:AE004765; GB:AE004091; NID:G9949580; PIDD:AA00683
 A/Experimental source: strain PA01
 C/Genetics:

Query Match 3.5%; Score 8; DB 2; Length 323;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 LGLLPADI 77
 DB 258 LGLLPADI 265

RESULT 10
 I57937
 hypothetical calcium-binding protein - mouse
 C/Species: *Mus sp. (mouse)*
 C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 19-May-2000
 C/Accession: I57937
 R/Miyamoto, H.; Matsushiro, A.; Nozaki, M.
 Mol. Reprod. Dev. 34, 1-7, 1993

A/Title: Molecular cloning of a novel mRNA sequence expressed in cleavage stage mouse emt
 A/Reference number: I57937; MUID:93119656; PMID:8418809
 A/Accession: I57937
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-341 <RES>
 A/Cross-references: GB:851858; NID:G262933; PIDD:AA24801.1; PID:G262934
 C/Superfamily: Saccharomycetes hypothetical protein YK189w
 C/Keywords: calcium binding

Query Match 3.5%; Score 8; DB 2; Length 341;
 Best Local Similarity 100.0%; Pred. No. 9.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GLGTLVA 24
 DB 78 GLGTLVA 85

RESULT 11
 AG1962
 hypothetical protein alr1250 [imported] - *Nostoc sp.* (strain PCC 7120)

C/Species: *Nostoc sp.* PCC 7120
 A/Note: *Nostoc sp.* strain PCC 7120 is a synonym of *Anabaena sp.* strain PCC 7120
 C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C/Accession: AG1962
 R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi,
 Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001

A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anat*
 A/Reference number: AB1807; MUID:21595285; PMID:11759840
 A/Accession: AG1962
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-362 <KUR>
 A/Cross-references: UNIPROT:Q8YX33; GB:BA000019; PIDD:BA873207.1; PID:G17130597; GSPDB:G
 A/Experimental source: strain PCC 7120
 C/Genetics:
 A/Gen: alr1250
 C/Superfamily: hypothetical protein s111166

Query Match 3.5%; Score 8; DB 2; Length 362;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GLGTLVA 24
 DB 319 GLGTLVA 326

RESULT 12
 G70151
 pheromone shutdown protein (trab) homolog - Lyme disease spirochete
 C/Species: *Borrelia burgdorferi* (Lyme disease spirochete)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C/Accession: G70151
 R/Trasler, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,
 son, D.; Peterson, J.; Keriavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
 Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
 Nature 390, 580-586, 1997

A/Authors: Smith, H.O.; Venter, J.C.
 A/Title: Genomic sequence of a Lyme disease spirochete, *Borrelia burgdorferi*.
 A/Reference number: A70100; MUID:98065943; PMID:9403685
 A/Accession: G70151
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-404 <LRS>
 A/Cross-references: UNIPROT:O51377; GB:AE001146; GB:AE000783; NID:G2688312; PIDD:AA06678;
 A/Experimental source: strain B31
 C/Superfamily: pheromone shutdown protein

Query Match 3.5%; Score 8; DB 1; Length 404;
 Best Local Similarity 100.0%; Pred. No. 11;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 168 ISSLSFSL 175
 |||||
 DB 158 ISSLSFSL 165

RESULT 13

S02154
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Podospora anserina mitochondrion
 N:Alternate names: NADH-ubiquinone oxidoreductase chain 2
 C:Species: mitochondrion Podospora anserina
 C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
 C:Accession: S02154
 R: Cummings, D.J.; Domenico, J.M.
 J. Mol. Biol. 204, 815-839, 1988
 A:Title: Sequence analysis of mitochondrial DNA from Podospora anserina. Pervasiveness
 A:Reference number: S02153; WUID:89125610; PMID:2975708
 A:Accession: S02154
 A:Molecule type: DNA
 A:Residues: 1-556 <CDM>
 A:Cross-references: UNIPROT:P15578; EMBL:X14485; NID:G13296; PIDN:CAA32646.1; PID:G13297
 C:Genetics:
 A:Gene: ND2
 A:Genome: mitochondrion
 A:Genetic code: SGC3
 C:Superfamily: NADH dehydrogenase (ubiquinone) chain 2
 C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match

3.5%; Score 8; DB 2; Length 556;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 ISSLSFSLI 176
 |||||
 DB 310 ISSLSFSLI 317

RESULT 14

I38596
 calcium-activated potassium channel - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
 C:Accession: I38596
 R: Pallanck, L.; Ganetzky, B.
 Hum. Mol. Genet. 3, 1239-1243, 1994
 A:Title: Cloning and characterization of human and mouse homologs of the Drosophila calc
 A:Reference number: I38415; WUID:95078823; PMID:7967297
 A:Accession: I38596
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-609 <RES>
 A:Cross-references: UNIPROT:Q12791; EMBL:U09384; NID:9487798; PIDN:AAA50216.1; PID:94935
 C:Superfamily: fruit fly calcium-activated potassium channel s10

Query Match

3.5%; Score 8; DB 2; Length 609;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 VFFILGSL 130
 |||||
 DB 305 VFFILGSL 312

RESULT 15

T25704
 hypothetical protein F18F11.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T25704
 R: Du, Z.; Maggi, L.
 submitted to the EMBL Data Library, February 1997
 A:Description: The sequence of C. elegans cosmid F18F11.

A:Reference number: Z20072

A:Accession: T25704

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-959 <DUZ>

A:Cross-references: UNIPROT:P91263; EMBL:U88176; PIDN:AAA42287.1; GSPDB:GN00022; CESP:FL

A:Experimental source: strain Bristol N2; clone F18F11

C:Genetics:

A:Gene: CESP:F18F11.4

A:Map position: 4

A:introns: 16/3; 75/3; 104/1; 188/3; 297/3; 361/1; 400/2; 435/3; 454/1; 540/2; 607/2; 688

Query Match

3.5%; Score 8; DB 2; Length 959;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 AVAGGVFF 125
 |||||
 DB 334 AVAGGVFF 341

Search completed: October 27, 2004, 07:36:28
 Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 27, 2004, 07:22:58 ; Search time 194 Seconds
(without alignments)
682.145 Million cell updates/sec

Title: US-09-787-677A-3
Perfect score: 230
Sequence: 1 MASIGQLVGYILGLGLG.....PGQPKVSEFNSYLTGYV 230

Scoring table: OLIGO
Gapop 60.0 , Gapept 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	230	100.0	230	1 CLD2_HUMAN	P57739 homo sapien
2	230	100.0	230	2 BAC11575	Bac11575 homo sapi
3	230	100.0	230	2 AAH71747	Aah71747 homo sapi
4	59	25.7	230	2 Q765P1	Q765P1 bos taurus
5	59	25.7	230	2 BAD01111	Bad01111 bos tauru
6	58	25.2	230	1 CLD2_MOUSE	Q95K86 canis famli
7	58	25.2	230	1 CLD2_MOUSE	Q95K86 canis famli
8	58	25.2	230	2 BAB23725	Bab23725 mus muscu
9	9	3.9	123	2 Q9A2E4	Q9A2E4 cauliobacter
10	9	3.9	297	2 Q7NDS4	Q7NDS4 gloeobacter
11	9	3.9	307	2 Q9FKR4	Q9FKR4 arabidopsis
12	9	3.9	346	2 Q9NMY4	Q9NMY4 homo sapien
13	9	3.9	359	2 Q98189	Q98189 acrocephalu
14	9	3.9	359	2 Q98192	Q98192 acrocephalu
15	9	3.9	359	2 Q98193	Q98193 acrocephalu
16	9	3.9	360	2 Q98187	Q98187 acrocephalu
17	9	3.9	360	2 Q98188	Q98188 acrocephalu
18	9	3.9	360	2 Q98191	Q98191 acrocephalu
19	9	3.9	681	2 Q95RM4	Q95RM4 drosophila
20	9	3.9	930	2 Q74906	Q74906 geobacter
21	9	3.9	930	2 AAR36058	Aar36058 geobacter
22	9	3.9	1406	2 Q9U110	Q9U110 drosophila
23	9	3.9	1406	2 Q9V4D4	Q9V4D4 drosophila
24	9	3.9	1406	2 Q9XZU7	Q9XZU7 drosophila
25	8	3.5	48	2 Q9T886	Q9T886 bos taurus
26	8	3.5	100	2 Q8K116	Q8K116 pseudomonas
27	8	3.5	127	2 Q84N17	Q84N17 oryza sativ
28	8	3.5	140	2 Q9KMR1	Q9KMR1 pseudomonas
29	8	3.5	140	2 Q9KMR7	Q9KMR7 pseudomonas
30	8	3.5	140	2 Q9KHS0	Q9KHS0 pseudomonas
31	8	3.5	152	1 EXBB_PASHA	P72202 pasteurella

32	8	3.5	203	1 SODM_THEAQ	P53653 thermus aqu
33	8	3.5	205	2 Q83C97	Q83C97 coxiella bu
34	8	3.5	215	1 Q8Z1P0	Q8Z1P0 yersinia pe
35	8	3.5	233	1 AMP_ONYPE	Q7mit6 onion yello
36	8	3.5	233	2 Q9A1R8	Q9A1R8 aster yello
37	8	3.5	246	2 Q44630	Q44630 caenorhabdi
38	8	3.5	282	2 Q89RN4	Q89rn4 bradyrhizob
39	8	3.5	288	2 Q72WQ8	Q72wq8 desulfocivib
40	8	3.5	288	2 AAS94419	Aas94419 desulfovi
41	8	3.5	292	2 Q7QW15	Q7qm15 anopheles g
42	8	3.5	296	2 Q67443	Q67443 aquifex aco
43	8	3.5	296	2 Q73DC8	Q73dc8 bacillus ce
44	8	3.5	296	2 AAS39717	Aas39717 bacillus
45	8	3.5	311	2 Q88TD9	Q88td9 lactobacilli

ALIGNMENTS

RESULT 1
CLD2_HUMAN STANDARD; PRT; 230 AA.
ID P57739;
AC P57739;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Claudin-2 (UNQ705/PRO1356) (SP82).
GN Name=CLDN2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epithelium;
RA Reinacker H.-C., Sakaguchi T., Golden H.M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
RA Yu J., Han L.H.;
RT "Novel human cDNA clones with function of inhibiting cancer cell
growth."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Baton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heidens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Lao D., Mark M., Robble E., Sanchez C., Schenfeld J.,
RA Seshgiri S., Simons L., Singh V., Smith V., Stinson J., Vagstad A.,
RA Vandlen R., Watanabe C., Wileand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood M.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
RN [4]
RP SEQUENCE FROM N.A.
RA Heath P.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon, and Kidney;
RX MEDLINE=22368257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedín T.B., Toehlyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzinski M.I., Skalek U., Smalins D.E.,
 RA Schmechel A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Component of tight junction (TJ) strands.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the claudin family.
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 CC -----
 DR EMBL: AF250558; AAF98151.1; -
 DR EMBL: AF177340; AAG17984.1; -
 DR EMBL: AJ358474; AAO88838.1; -
 DR EMBL: AL158821; CAD23055.1; -
 DR EMBL: BC015252; AAH15252.1; -
 DR EMBL: BC014424; AAH14424.1; -
 DR Genew: HGNC:2041; CLDN2.
 DR InterPro: IPR006187; Claudin.
 DR InterPro: IPR005411; Claudin.
 DR InterPro: IPR006188; Claudin reg.
 DR InterPro: IPR004031; PMP22 Claudin.
 DR Pfam: PF00822; PMP22 Claudin; 1.
 DR PRINTS: PRO1077; CLAUDIN.
 DR PRINTS: PRO1589; CLAUDIN2.
 DR PROSITE: PS01346; CLAUDIN; 1.
 DR Tight Junction; Transmembrane.
 FT TRANSMEM 8 28 Potential.
 FT TRANSMEM 82 102 Potential.
 FT TRANSMEM 117 137 Potential.
 FT TRANSMEM 163 183 Potential.
 FT SEQUENCE 230 AA; 24548 MW; 52CA642DA62B70D CRC64;
 SQ
 Query Match 100.0%; Score 230; DB 1; Length 230;
 Best Local Similarity 100.0%; Pred. No. 6e-215;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MASLGQLVGYIIGLIGLIGLVAMLLPSWKTSYVGASIVTVAVGFSKGLMMECATHTSG 60
 DB 1 MASLGQLVGYIIGLIGLIGLVAMLLPSWKTSYVGASIVTVAVGFSKGLMMECATHTSG 60
 QY ITCCDIYSTLLGIPADIOAQAAMVNTSSAISLACIISVVGRCVTCQESRAKDRVAVA 120
 DB ITCCDIYSTLLGIPADIOAQAAMVNTSSAISLACIISVVGRCVTCQESRAKDRVAVA 120
 QY 61 ITCCDIYSTLLGIPADIOAQAAMVNTSSAISLACIISVVGRCVTCQESRAKDRVAVA 120
 DB 61 ITCCDIYSTLLGIPADIOAQAAMVNTSSAISLACIISVVGRCVTCQESRAKDRVAVA 120
 QY 121 GGVPFLLGLGIFPAMNLHGILRDFSPPLVDSKMFEGEALYGLIISLPSLIAGII 180
 DB 121 GGVPFLLGLGIFPAMNLHGILRDFSPPLVDSKMFEGEALYGLIISLPSLIAGII 180
 QY 121 GGVPFLLGLGIFPAMNLHGILRDFSPPLVDSKMFEGEALYGLIISLPSLIAGII 180
 DB 121 GGVPFLLGLGIFPAMNLHGILRDFSPPLVDSKMFEGEALYGLIISLPSLIAGII 180
 QY 181 LCFSCSSQNRNSNYDAYOAOPLATRSSPPGQPPKVKSEFNYSILGTGY 230
 DB 181 LCFSCSSQNRNSNYDAYOAOPLATRSSPPGQPPKVKSEFNYSILGTGY 230
 DB 181 LCFSCSSQNRNSNYDAYOAOPLATRSSPPGQPPKVKSEFNYSILGTGY 230

ID BAC11575 PRELIMINARY; PRT; 230 AA.
 AC BAC11575;
 DT 02-MAR-2004 (T-EMBLrel. 27, Created)
 DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
 DE CDNA PSEC0059 f18, clone NT2RP2000601, highly similar to Mus musculus
 DE claudin-2 mRNA.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
 RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
 RA Nagahara K., Sugano S., Isogai T.;
 RT "HRI human cDNA sequencing project.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK075371; BAC11575.1; -
 SQ SEQUENCE 230 AA; 24548 MW; 52CA642DA62B70D CRC64;
 Query Match 100.0%; Score 230; DB 2; Length 230;
 Best Local Similarity 100.0%; Pred. No. 6e-215;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MASLGQLVGYIIGLIGLIGLVAMLLPSWKTSYVGASIVTVAVGFSKGLMMECATHTSG 60
 DB 1 MASLGQLVGYIIGLIGLIGLVAMLLPSWKTSYVGASIVTVAVGFSKGLMMECATHTSG 60
 QY 61 ITCCDIYSTLLGIPADIOAQAAMVNTSSAISLACIISVVGRCVTCQESRAKDRVAVA 120
 DB 61 ITCCDIYSTLLGIPADIOAQAAMVNTSSAISLACIISVVGRCVTCQESRAKDRVAVA 120
 QY 61 ITCCDIYSTLLGIPADIOAQAAMVNTSSAISLACIISVVGRCVTCQESRAKDRVAVA 120
 DB 61 ITCCDIYSTLLGIPADIOAQAAMVNTSSAISLACIISVVGRCVTCQESRAKDRVAVA 120
 QY 121 GGVPFLLGLGIFPAMNLHGILRDFSPPLVDSKMFEGEALYGLIISLPSLIAGII 180
 DB 121 GGVPFLLGLGIFPAMNLHGILRDFSPPLVDSKMFEGEALYGLIISLPSLIAGII 180
 QY 121 GGVPFLLGLGIFPAMNLHGILRDFSPPLVDSKMFEGEALYGLIISLPSLIAGII 180
 DB 121 GGVPFLLGLGIFPAMNLHGILRDFSPPLVDSKMFEGEALYGLIISLPSLIAGII 180
 QY 181 LCFSCSSQNRNSNYDAYOAOPLATRSSPPGQPPKVKSEFNYSILGTGY 230
 DB 181 LCFSCSSQNRNSNYDAYOAOPLATRSSPPGQPPKVKSEFNYSILGTGY 230
 DB 181 LCFSCSSQNRNSNYDAYOAOPLATRSSPPGQPPKVKSEFNYSILGTGY 230

RESULT 3
 ID AAH71747 PRELIMINARY; PRT; 230 AA.
 AC AAH71747;
 DT 01-JUN-2004 (T-EMBLrel. 27, Created)
 DT 01-JUN-2004 (T-EMBLrel. 27, Last sequence update)
 DT 01-JUN-2004 (T-EMBLrel. 27, Last annotation update)
 DE CDN2 protein.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Skin and meninges pool - skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedín T.B., Toehlyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.

RC TISSUE=skin and meninges pool- skin;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC071747; AAH71747.1; -
 SQ SEQUENCE 230 AA; 24534 MW; 52CA642D4A62B70D CRC64;

Query Match 100.0%; Score 230; DB 2; Length 230;
 Best Local Similarity 100.0%; Pred. No. 66-215;

Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYILGLGLTLVAMLLPSWKTSSVYGASIVTAVGFSKGLMECATHTSG 60
 DB 1 MASLGQLVGYILGLGLTLVAMLLPSWKTSSVYGASIVTAVGFSKGLMECATHTSG 60
 QY 61 ITQCDIYSTLLGPADIOAAQAMWVTSSAISLACIIIVGKCTVFCQESRAKDRYAVA 120
 DB 61 ITQCDIYSTLLGPADIOAAQAMWVTSSAISLACIIIVGKCTVFCQESRAKDRYAVA 120
 QY 121 GGVPFLIGLGRIPVAMNHLGRDPSPLVPDSMKFEIGALYIGIISLPSLIAGI 180
 DB 121 GGVPFLIGLGRIPVAMNHLGRDPSPLVPDSMKFEIGALYIGIISLPSLIAGI 180
 QY 181 LCFSSCSQRNSRYDAYQAQPLATRSSPPRQGPVKYSEFNSYSLTGYV 230
 DB 181 LCFSSCSQRNSRYDAYQAQPLATRSSPPRQGPVKYSEFNSYSLTGYV 230

RESULT 4

Q76SP1 PRELIMINARY; PRT; 230 AA.

AC 076SP1
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Claudin 2.
 GN Name=CLDN2;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Ohta H., Takiguchi M., Inaba M.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB115779; BAD01111.1; -
 DR InterPro: IPR006187; Claudin.
 DR InterPro: IPR005411; Claudin2.
 DR InterPro: IPR006188; Claudin_reg.
 DR Pfam: PF00822; PMP22_Claudin.
 DR PRINTS: PRO1077; CLAUDIN.
 DR PRINTS: PRO1589; CLAUDIN2.
 DR PROSITE: PS01346; CLAUDIN.
 KW Transmembrane.
 SQ SEQUENCE 230 AA; 24533 MW; ED241778B0E541CA CRC64;

Query Match 25.7%; Score 59; DB 2; Length 230;
 Best Local Similarity 100.0%; Pred. No. 1.2e-48;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GGVPFLIGLGRIPVAMNHLGRDPSPLVPDSMKFEIGALYIGIISLPSLIAGI 179
 DB 121 GGVPFLIGLGRIPVAMNHLGRDPSPLVPDSMKFEIGALYIGIISLPSLIAGI 179

RESULT 5

QY BAD01111 PRELIMINARY; PRT; 230 AA.

AC BAD01111
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Claudin 2.
 GN CLDN2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Ohta H., Takiguchi M., Inaba M.;
 RL "Localization of claudin proteins in bovine kidneys.";
 DR EMBL: AB115779; BAD01111.1; -
 SQ SEQUENCE 230 AA; 24533 MW; ED241778B0E541CA CRC64;

Query Match 25.7%; Score 59; DB 2; Length 230;
 Best Local Similarity 100.0%; Pred. No. 1.2e-48;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GGVPFLIGLGRIPVAMNHLGRDPSPLVPDSMKFEIGALYIGIISLPSLIAGI 179
 DB 121 GGVPFLIGLGRIPVAMNHLGRDPSPLVPDSMKFEIGALYIGIISLPSLIAGI 179

RESULT 6
 CLDN2_CANFA STANDARD; PRT; 230 AA.
 AC 095KM6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Claudin-2.
 GN Name=CLDN2;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=21206012; PubMed=11309408;
 RA Furuse M., Furuse K., Sasaki H., Tsukita S.;
 RT "Conversion of zonulae occludentes from tight to leaky strand type by
 RT introducing claudin-2 into Madin-Darby canine kidney I cells.";
 RL J. Cell Biol. 153:263-272(2001).
 CC -1- FUNCTION: Component of tight junction (TJ) strands.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the claudin family.
 CC -----
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 CC -----
 CC EMBL: AF358907; AAK51433.1; -
 DR InterPro: IPR006187; Claudin.
 DR InterPro: IPR005411; Claudin2.
 DR InterPro: IPR006188; Claudin_reg.
 DR InterPro: IPR004031; PMP22_Claudin.
 DR Pfam: PF00822; PMP22_Claudin.
 DR

DR PRINTS; PRO1077; CLAUDIN.
 DR PRINTS; PRO1589; CLAUDIN2.
 DR PROSITE; PS01346; CLAUDIN.1.
 KW Tight junction; Transmembrane.
 FT TRANSMEM 8 28 Potential.
 FT TRANSMEM 82 102 Potential.
 FT TRANSMEM 117 137 Potential.
 FT TRANSMEM 163 183 Potential.
 SQ SEQUENCE 230 AA; 24502 MW; 91B7LCIE5CDC4BB9 CRC64;

Query Match 25.2%; Score 58; DB 1; Length 230;
 Best Local Similarity 100.0%; Pred. No. 1.1e-47;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 SIYTAAGFSKGLMECATHTSTGTCDDIYSTLLGLPADIOAQAQMMVTSSAISLACI 96
 DB 39 SIYTAAGFSKGLMECATHTSTGTCDDIYSTLLGLPADIOAQAQMMVTSSAISLACI 96

RESULT 7
 CLD2_MOUSE STANDARD; PRT; 230 AA.
 AC 088552;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Claudin-2.
 GN Name=Cldn2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98311639; PubMed=9647647;
 RA Furness M., Fujita K., Hiltag T., Fujimoto K., Tsukita S.;
 RT "Claudin-1 and -2: novel integral membrane proteins localizing at
 tight junctions with no sequence similarity to occludin.";
 RL J. Cell Biol. 141:1539-1550(1998).
 CC -1- FUNCTION: Component of tight junction (TJ) strands.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the claudin family.
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 CC -----
 CC EMBL; AF072128; AAC27079.1; -
 CC MGD; MG11276110; Cldn2.
 DR InterPro; IPR006187; Claudin.
 DR InterPro; IPR005411; Claudin2.
 DR InterPro; IPR006188; Claudin.reg.
 DR InterPro; IPR004031; PMP22 Claudin.
 DR Pfam; PF00822; PMP22 Claudin; 1.
 DR PRINTS; PRO1077; CLAUDIN.
 DR PRINTS; PRO1589; CLAUDIN2.
 DR PROSITE; PS01346; CLAUDIN.1.
 KW Tight junction; Transmembrane.
 FT TRANSMEM 8 28 Potential.
 FT TRANSMEM 82 102 Potential.
 FT TRANSMEM 117 137 Potential.
 FT TRANSMEM 163 183 Potential.
 SQ SEQUENCE 230 AA; 24483 MW; 38A7C074A1E0D5D2 CRC64;

Query Match 25.2%; Score 58; DB 1; Length 230;
 Best Local Similarity 100.0%; Pred. No. 1.1e-47;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 TSSYVAGSIYTAAGFSKGLMECATHTSTGTCDDIYSTLLGLPADIOAQAQMMVTSSA 89

DB 32 TSSYVAGSIYTAAGFSKGLMECATHTSTGTCDDIYSTLLGLPADIOAQAQMMVTSSA 89

RESULT 8
 BAB3725 PRELIMINARY; PRT; 230 AA.
 ID BAB3725;
 AC BAB3725;
 DT 14-APR-2004 (TrEMBLrel. 27, Created)
 DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Adult male liver cDNA, RIKEN full-length enriched library,
 DE clone:1300013G06 product:claudin 2, full insert sequence.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium,
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=2049374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama Y., Nishi K., Katsunai T., Taahiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Hatada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Washigaki K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Bono H.,
 RA Arawaka T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Nunazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito K., Sakai C., Sakai K.,

RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK004990; BAB3725.1; -
 SQ SEQUENCE 230 AA; 24483 MW; 38A7C074A1E0D5D2 CRC64;

Query Match 25.2%; Score 58; DB 2; Length 230;
 Best Local Similarity 100.0%; Pred. No. 1.1e-47; Indels 0; Gaps 0;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 TSSYVGSIVTAVGFSKGLMMECATHTSTGTCTDIYSTLLGLPADIQAAQAMVVTSSA 89
 DB 32 TSSYVGSIVTAVGFSKGLMMECATHTSTGTCTDIYSTLLGLPADIQAAQAMVVTSSA 89

RESULT 9
 Q9A2E4 PRELIMINARY; PRT; 123 AA.
 AC O9A2E4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein CC3621.
 GN OrderedLocNames=CC3621;
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
 OC Caulobacteraceae; Caulobacter.
 NCBI TaxID=155892;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19089 / CB15;
 RX MEDLINE=21173688; PubMed=11259647; DOI=10.1073/pnas.061029298;
 RA Nieman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwin M.L., Haft D.H.,
 RA Kolony J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
 RA Berry K.J., Uettermann T.R., Tran K., Wolf A.M., Vamathevan J.J.,
 RA Brumley M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
 RA Fraser C.M.;
 RT "Complete genome sequence of Caulobacter crescentus.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 DR EMBL: AEO06020; AAK25583.1; -
 DR PIR: C87698; C87698.
 DR TIGR: CC3621; -
 DR GO: GO:0016020; C:membrane; IEA.
 DR InterPro: IPR003425; Unk_YGGR.
 DR Pfam: PF02325; YGGR; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 123 AA; 13427 MW; 15F76F23C280DAC2 CRC64;

Query Match 3.9%; Score 9; DB 2; Length 123;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 VFFILGGL 131
 DB 27 VFFILGGL 35

RESULT 10
 Q7NDS4 PRELIMINARY; PRT; 297 AA.
 AC Q7NDS4;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE G1r4158 protein.
 GN OrderedLocNames=G1r4158;
 OS Gloeobacter violaceus.
 OC Bacteria; Cyanobacteria; Chroococcales; Gloeobacter.

OX NCBI TaxID=33072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC 7421;
 RX MEDLINE=22977040; PubMed=14621292;
 RA Nakamura Y., Kaneko T., Sato S., Muro M., Miyashita H., Tsuchiya T.,
 RA Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
 RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a
 cyanobacterium that lacks thylakoids.";
 RL DNA Res. 10:137-145 (2003).
 DR EMBL: AP006582; BAC92099.1; -
 DR InterPro: IPR001279; Blactamase-like.
 DR Pfam: PF00753; Lactamase_B; 1.
 KW Complete proteome.
 SQ SEQUENCE 297 AA; 33846 MW; 720044C2AD2AB4B CRC64;

Query Match 3.9%; Score 9; DB 2; Length 297;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 PADIOAQA 82
 DB 76 PADIOAQA 84

RESULT 11
 Q9FKF4 PRELIMINARY; PRT; 307 AA.
 AC Q9FKF4;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1139
 GN (Hypothetical protein At5g61670) (AT5g61670/k1139_190).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI TaxID=3702;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98403884; PubMed=9734815;
 RA Kocani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
 RT Sequence features of the regions of 1,367,185 bp covered by 19
 RT physically assigned pi and TAC clones.";
 RL DNA Res. 5:203-216(1998).
 [2]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
 RA Gerninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
 RA Seki M., Shim P., Southwick A., Shinzaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22088475; PubMed=12093376;
 RA Haas B.J., Volfovsky N., Town C.D., Trukhan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 RT annotation.";
 RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
 [4]
 RP SEQUENCE FROM N.A.
 RP Brover V., Trukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,
 RA Bower L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
 RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 RA Tang C., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
 RA Dang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bower L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
 RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Bower L., Carninci P.,
 RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,
 RA Heuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,
 RA Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
 RA Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP EMBL: AB012339; BAB09011.1; -
 DR EMBL: AY065401; AAL38842.1; -
 DR EMBL: AY084568; AAM61134.1; -
 DR EMBL: AY094431; AAM19804.1; -
 DR EMBL: AY117226; AAM51301.1; -
 DR EMBL: AY149953; AAN3107.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 307 AA; 33789 MW; CB0C5C0C7CD80BA CRC64;
 QY Query Match 3.9%; Score 9; DB 2; Length 307;
 Db Best Local Similarity 100.0%; Pred. No. 6.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 173 FSLIAGIIL 181
 Db 152 FSLIAGIIL 160
 RESULT 12
 ID O9NMW4 PRELIMINARY; PRT; 346 AA.
 AC O9NMW4;
 DT 01-OCT-2000 (TEMBLrel. 15, Created)
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
 DT 01-OCT-2004 (TEMBLrel. 28, Last annotation update)
 DE Hypothetical protein FLJ20534 (Hypothetical protein
 DE DKF25664H1372).
 GN Name=FLJ20534; Synonyms=DKF2564H1372;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Matsumoto K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
 RA Suzuki Y., Ohtsuka M., Nishii T., Shibahara T., Tanaka T.,
 RA Nakamura Y., Ieigai T., Sugano S.,
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Maruska K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gilwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywicki M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maier M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Blum H., Baerzachs S., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK000541; BAA91241.1; -
 DR EMBL: BC010367; AAL10367.1; -
 DR EMBL: AL136673; CAB66608.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 346 AA; 39408 MW; 6089F075C8B50B CRC64;
 QY Query Match 3.9%; Score 9; DB 2; Length 346;
 Db Best Local Similarity 100.0%; Pred. No. 7.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ASLGLQLVG 10
 Db 74 ASLGLQLVG 82
 RESULT 13
 ID O98189 PRELIMINARY; PRT; 359 AA.
 AC O98189;
 DT 01-MAY-1999 (TEMBLrel. 10, Created)
 DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
 DE MHC class I antigen.
 OS Acropetalus arundinaceus (great reed warbler).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Passeriformes; Sylvidae; Acropetalus.
 OX NCBI_TaxID=39621;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=99115500; PubMed=9914330;
 RA Westerdahl H., Witzell H., von Schantz T.,
 RT "Polymorphism and transcription of Mhc class I genes in a passerine
 bird, the great reed warbler.";
 RL Immunogenetics 49:158-170 (1999).
 DR EMBL: AJ005505; CAA06562.1; -
 DR HSP: O9HC68; 1A6Z.
 DR GO: GO:0016020; C-membrane; IEA.
 DR GO: GO:0006955; P-immune response; IEA.
 DR InterPro: IPR007110; Ig-like.

